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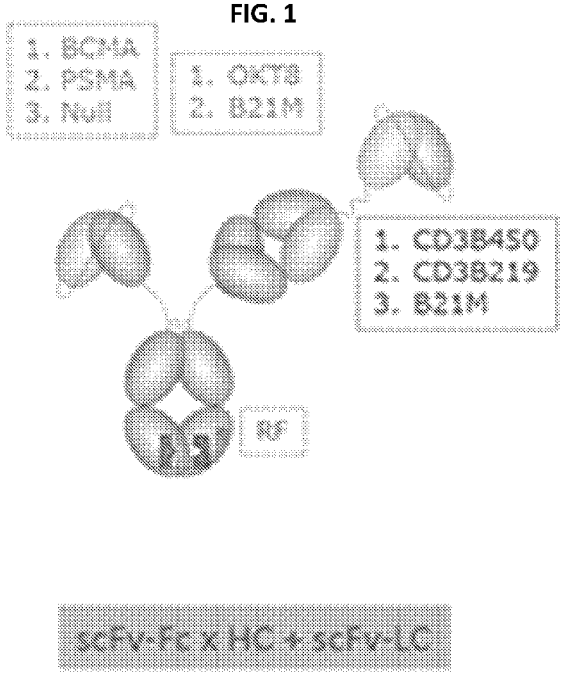
FIG. 1



(57) Abstract: An isolated molecule, comprising: a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds a T cell receptor (TCR) complex. In another aspect, the disclosure provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CDS, the second antigen binding domain specifically binds a TCR complex, and the third antigen binding domain binds a third antigen.

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MATERIALS AND METHODS FOR IN VIVO BIOLOGICAL TARGETING

CROSS -REFERENCE TO RELATED APPLICATIONS

[0001] This application claims benefit of priority of U.S. Serial No. 62/949,486 filed on December 18, 2019, U.S. Serial No. 62/949,492 filed on December 18, 2019, U.S. Serial No. 62/949,499 filed on December 18, 2019, U.S. Serial No. 62/949,502 filed on December 18, 2019, U.S. Serial No. 62/949,507 filed on December 18, 2019, U.S. Serial No. 62/949,513 filed on December 18, 2019, U.S. Serial No. 62/949,519 filed on December 18, 2019, U.S. Serial No. 62/949,526 filed on December 18, 2019, and U.S. Serial No. 63/091,100 filed on October 13, 2020, the contents of each of which is incorporated herein by reference in its entirety.

SEQUENCE LISTING

[0002] This application incorporates by reference a Sequence Listing submitted with this application as a text format, entitled "14620-329-228_SL.txt," created on December 14, 2020 and having a size of 1,037,532 bytes.

TECHNICAL FIELD

[0003] Provided herein are molecules comprising multiple binding domains, compositions comprising same, and methods for uses thereof, *e.g.*, for treating a disease or disorder such as cancer.

BACKGROUND

[0004] T cell redirection has become an alternative to cancer therapies with the approval of BENLYSTA® (blinatumomab). T cell redirection utilizing CD3 binding domains however poses challenges as the approach results in unselective recruitment of pan-T cells, including exhausted T cells, helper and regulatory cells such as $CD4^+$, Th1, Th2, Th9, Th17, Th22, Tfh, Tregs, Tr1 and non-CTL $CD8^+$ cells, *i.e.*, cells that are incapable of mediating tumor cell lysis. Only fraction of the cells recruited by engaging CD3 are cytotoxic T lymphocytes (CTLs). Further, even low doses of T cell redirection molecules based on CD3 may result in cytokine release syndrome. Therefore, there is a need to develop additional strategies to redirect subsets of T cells to enhance selectivity and safety profile of T cell redirecting molecules for improved treatment of cancers and other diseases in which depletion or partial depletion of cells contributing to disease pathogenesis is beneficial.

SUMMARY

[0005] In one aspect, the disclosure provides an isolated molecule, comprising: a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds a T cell receptor (TCR) complex.

[0006] In another aspect, the disclosure provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex, and the third antigen binding domain binds a third antigen.

[0007] In another aspect, the disclosure provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex, and the third antigen binding domain binds an antigen expressed by an undesired cell.

[0008] In some embodiments, the molecule further comprises a third antigen binding domain that specifically binds an third antigen. In some embodiments, the third antigen comprises an antigen expressed by undesired cells.

[0009] In some embodiments, the isolated molecule activates or recruits CD8+ CTLs upon co-engagement of the TCR complex and CD8. In some embodiments, the isolated molecule is unable to activate or recruit CD8+ CTLs in the absence of co-engagement of the TCR complex and CD8. In some embodiments, the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds the TCR complex with affinities that result in activation or recruitment of CD8+ CTLs only upon co-engagement of the TCR complex and CD8.

[0010] In some embodiments, the first antigen binding domain, the second antigen binding domain or the third antigen binding domain comprises a scFv, a Fab, a Fab', a F(ab')2, a Fd, a Fv, a domain antibody (dAb), a VHH, a heavy chain variable domain (VH), a light chain variable domain (VL), a non-antibody scaffold, or fragments thereof. In some embodiments, the first antigen binding domain comprises the Fab. In some embodiments, the second antigen

binding domain comprises the scFv. In some embodiments, the third antigen binding domain comprises the scFv.

[0011] In some embodiments, the first antigen binding domain comprising the Fab, the second antigen binding domain comprising the scFv or the third antigen binding domain comprising the scFv is conjugated to the Fc or the fragment of the Fc, to the VH that is capable of specifically biding CD8, to the CL domain or to the CH3 domain via a linker. In some embodiments, the linker comprises a polypeptide of SEQ ID NOs: 2183-2290. In some embodiments, the fragment of the Fc comprises a CH2 domain and a CH3 domain. In some embodiments, the CH3 domain comprises one or more substitutions when compared to a wild-type CH3 domain. In some embodiments, the one or more substitutions comprise T350V, L351Y, F405A,Y407V, T366Y, T366W, F405W, T394W, T394S, Y407T, Y407A, T366S/L368A/Y407V, L351Y/F405A/Y407V, T366I/K392M/T394W, F405A/Y407V, T366L/K392M/T394W, L351Y/Y407A, T366A/K409F, L351Y/Y407A, T366V/K409F, T366A/K409F, T350V/L351Y/F405A/Y407V or T350V/T366L/K392L/T394W, wherein residue numbering is according to the EU index.

[0012] In yet another aspect, the disclosure also provides an isolated molecule, comprising: a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a second antigen binding domain comprising a scFv that specifically binds a TCR complex, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain; the second polypeptide comprises, from N- to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc.

[0013] In yet another aspect, the disclosure also provides an isolated molecule, comprising: a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain; the second polypeptide comprises, from N- to C-terminus, a VL that is capable of specifically binding CD8, a CL domain and a second antigen binding domain comprising a scFv that specifically binds a TCR complex; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a

scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc.

[0014] In yet another aspect, the disclosure also provides an isolated molecule, comprising: a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a VH that is capable of specifically CD8, a CH1 domain, a hinge, a CH2 domain, a CH3 domain and a second antigen binding domain comprising a scFv that specifically binds a TCR complex; the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc.

[0015] In some embodiments, the first polypeptide comprises a CH3 domain comprising one or more substitutions when compared to a wild-type CH3 domain which promote heterodimerization of the first polypeptide with the third polypeptide; the third polypeptide comprises a CH3 domain comprising one or more substitutions when compared to the wild-type CH3 domain which promote heterodimerization of the third polypeptide with the first polypeptide; or the first polypeptide comprises the CH3 domain comprising one or more substitutions when compared to the wild-type CH3 which promote heterodimerization of the first polypeptide with the third polypeptide and the third polypeptide comprises the CH3 domain comprising one or more substitutions when compared to the wild-type CH3 which promote heterodimerization of the third polypeptide with the first polypeptide.

[0016] In some embodiments, the one or more substitutions comprise T350V, L351Y, F405A,Y407V, T366Y, T366W, F405W, T394W, T394S, Y407T, Y407A, T366S/L368A/Y407V, L351Y/F405A/Y407V, T366I/K392M/T394W, F405A/Y407V, T366L/K392M/T394W, L351Y/Y407A, T366A/K409F, L351Y/Y407A, T366V/K409F, T366A/K409F, T350V/L351Y/F405A/Y407V or T350V/T366L/K392L/T394W, wherein residue numbering is according to the EU index.

[0017] In some embodiments, the Fc, the CH2 domain or the CH3 domain is an IgG1, IgG2, IgG3 or IgG4 isotype. In some embodiments, the second antigen binding domain specifically binds CD3, TCRα chain, TCRβ chain, TCRγ chain or TCRδ chain, or any combination thereof. In some embodiments, the TCRβ chain comprises TCRVB17. In some embodiments, CD3

comprises CD3ε, CD3γ, CD3δ or CD3ζ. In some embodiments, the second antigen binding domain that specifically binds CD3 comprises a heavy chain complementarity determining region 1 (HCDR1_ of SEQ ID NO: 2291, a HCDR2 of SEQ ID NO: 2292, a HCDR3 of SEQ ID NO: 2293, a LCDR1 of SEQ ID NO: 2294, a LCDR2 of SEQ ID NO: 2295 and a LCDR3 of SEQ ID NO: 2296. In some embodiments, the second antigen binding domain that specifically binds CD3 comprises the VH of SEQ ID NO: 2297 and the VL of SEQ ID NO: 2298. In some embodiments, the first antigen binding domain comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312. In some embodiments, the first antigen binding domain comprises the VH of SEQ ID NO: 2313 and the VL of SEQ ID NO: 2314.

[0018] In some embodiments, the undesired cell is a pathogenic cell. In some embodiments, the undesired cell is a cancer cell, an infected cell, a virus infected cell, a bacterial infected cell, an immune cell, an inflamed cell, a damaged cells, a foreign cell, an apoptotic cell, a dysplastic cell, an immunogenic cell, a metaplastic cell or a mutant cell, or any combination thereof. In some embodiments, the isolated molecule is an antibody or a non-antibody molecule. In some embodiments, the antibody comprises a first half molecule and a second half molecule, wherein the first half molecule comprises the first antigen binding domain and the second antigen binding domain and the second half molecule comprises the third antigen binding domain.

[0019] In some embodiments, the antigen expressed by the undesired cell comprises mesothelin, alpha-fetoprotein (ALP), BAGE, BCR-ABL, beta-catenin, beta-HCG, BrE3-antigen, BCA225, BCMA, BTAA, CA125, CA195, CA242, CA-50, CAM43, CAMEL, CAP-l, carbonic anhydrase IX, CA19-9, CA72-4, CAM 17.1, CASP-8, CCCL19, CCCL21, CD1, CD la, CD2, CD4, CD5, CD11A, CD14, CD15, CD16, CD18, CD19, CD20, CD21, CD22, CD23, CD25, CD29, CD30, CD32b, CD33, CD37, CD38, CD40, CD40L, CD44, CD45, CD46, CD47, CD52, CD54, CD55, CD59, CD64, CD66a-e, CD67, CD68, CD70, CD70L, CD74, CD79a, CD79b, CD80, CD83, CD95, CD123, CD126, CD132, CD133, CD138, CD147, CD154, CDC27, CDK4, CDK4m, CDKN2A, CO-029, CTLA4, CXCR4, CXCR7, CXCL12, HIF-la, colon- specific antigen-p (CSAp), CEACAM5) CEACAM6, c-Met, DAM, E2A-PRL, EGFR, EGFRvIII, EGP-l , EGP-2, ELF2-M, Ep-CAM, FGF, FGF-5, Flt-l, Flt- 3, folate receptor, G250 antigen, Ga733VEpCAM, GAGE, gplOO, GRO-b, H4-RET, HLA-DR, HM1.24, human

chorionic gonadotropin (HCG) HER2, HER3, HMGB-l, HIF-l, HSP70-2M, HST-2, HTgp-l75, la, IGF-1R, IFN-g, IFN-a, IFN-b, IFN- l, IL-4R, IL-6R, IL-13R, IL-15R, IL-17R, IL-18R, IL-2, IL-6, IL-8, IL-12, IL-15, IL-17, IL-18, IL-23, IL-25, insulin-like growth factor- 1 (IGF-l), KC4-antigen, KLK2, KSA, KS-l-antigen, KS1-4, LAGE-la, Le-Y, LDR/FUT, M344, MA-50, macrophage migration inhibitory factor (MIF), MAGE, MAGE-l, MAGE-3, MAGE-4, MAGE-5, MAGE-6, MART-l, MART-2, TRAG-3, MCP-l, MIP-1A, MIP-1B, MIF, MG7-Ag, MOV18, MUC1, MUC2, MUC3, MUC4, MUC5ac, MUC13, MUC16, MUM- 1/2, MUM-3, MYL-RAR, NB/70K, Nm23Hl, NuMA, NCA66, NCA95, NCA90, NY-ESO-l, pl5, pl6, pl85erbB2, pl80erbB3, PAM4 antigen, pancreatic cancer mucin, PD-l, PD-L1, PD-L2, PI5, placental growth factor, p53, PLAGL2, Pmell7 prostatic acid phosphatase, PSA, PRAME, PSMA, P1GF, ILGF, ILGF-1R, IL-6, IL-25, RCAS1, RS5, RAGE, RANTES, Ras, T101, SAGE, S100, SLAMF7, survivin, survivin-2B, SDDCAG16, TA-90\Mac2 binding protein, TAAL6, TAC, TAG-72, TLP, tenascin, TMEFF2, TRAIL receptors, TRP-l, TRP-2, TSP-180, VEGFR, ED-B fibronectin, WT-l, l7-lA-antigen, C3, C3a, C3b, C5a, C5, bcl-2, K-ras, tumor neoantigen, a viral antigen associated with cancer, FcγRIIB, IL-12β2R, CD28, CD56, CD11c, CD66b, CD41, CD61, CD62, CD235a, CD146, CD326, or CD203c.

[0020] In yet another aspect, provided herein is a kit, comprising the isolated molecule provided herein. In some embodiments, the kit further comprises means for diluting or administering the isolated molecule provided herein. In yet another aspect, provided herein is a pharmaceutical composition, comprising the isolated molecule provided herein and a pharmaceutically acceptable excipient.

[0021] In yet another aspect, the disclosure provides a method of selectively activating or recruiting CD8+ CTLs towards an undesired cell, comprising: contacting a population of lymphocytes with an isolated molecule comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[0022] In yet another aspect, the disclosure also provides a method of selectively activating or recruiting $CD8^+$ CTLs towards an undesired cell, comprising: contacting a population of lymphocytes with an isolated molecule comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a second antigen binding domain comprising a scFv that specifically binds a TCR complex, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain; the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[0023] In yet another aspect, the disclosure also provides a method of selectively activating or recruiting $CD8^+$ CTLs towards an undesired cell, comprising: contacting a population of lymphocytes with an isolated molecule comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain; the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8, a CL domain and a second antigen binding domain comprising a scFv that specifically binds a TCR complex; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[0024] In yet another aspect, the disclosure also provides a method of selectively activating or recruiting $CD8^+$ CTLs towards an undesired cell, comprising: contacting a population of lymphocytes with an isolated molecule comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a VH that is capable of specifically CD8, a CH1 domain, a hinge, a CH2 domain, a CH3 domain and a

second antigen binding domain comprising a scFv that specifically binds a TCR complex; the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[0025] In yet another aspect, the disclosure also provides a method of selectively activating or recruiting $CD8^+$ CTLs towards an undesired cell in a subject, comprising: administering to the subject an isolated molecule comprising a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[0026] In yet another aspect, the disclosure provides a method of providing an improved T cell redirection therapy for a subject in need thereof, comprising: administering to the subject an isolated molecule comprising a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[0027] In yet another aspect, the disclosure also provides a method of providing an improved T cell redirection therapy to a subject in need thereof, comprising: administering to the subject an isolated molecule comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a second antigen binding domain comprising a scFv that specifically binds a TCR complex, a VH that is capable

of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain; the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[0028] In yet another aspect, the disclosure also provides a method of providing an improved T cell redirection therapy to a subject in need thereof, comprising: administering to the subject an isolated molecule comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain; the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8, a CL domain and a second antigen binding domain comprising a scFv that specifically binds a TCR complex; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[0029] In yet another aspect, the disclosure also provides a method of providing an improved T cell redirection therapy to a subject in need thereof, comprising: administering to the subject an isolated molecule comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a VH that is capable of specifically CD8, a CH1 domain, a hinge, a CH2 domain, a CH3 domain and a second antigen binding domain comprising a scFv that specifically binds a TCR complex; the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc, wherein the isolated molecule selectively

activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[0030] In yet another aspect, the disclosure provides a method of targeting $CD8^+$ CTLs to an undesired cell in a subject, comprising administering to the subject an isolated molecule comprising a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex and the third antigen binding domain specifically binds an antigen expressed by the undesired cell, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[0031] In yet another aspect, the disclosure also provides a method of targeting $CD8^+$ CTLs to an undesired cell in a subject, comprising administering to the subject an isolated molecule comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a second antigen binding domain comprising a scFv that specifically binds a TCR complex, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain; the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by the undesired cell and a Fc or a fragment of the Fc, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[0032] In yet another aspect, the disclosure also provides a method of targeting $CD8^+$ CTLs to an undesired cell in a subject, comprising administering to the subject an isolated molecule comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain; the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8, a CL domain and a second antigen binding domain comprising a scFv that specifically binds a TCR

complex; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by the undesired cell and a Fc or a fragment of the Fc, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8

[0033] In yet another aspect, the disclosure also provides a method of targeting $CD8^+$ CTLs to an undesired cell in a subject, comprising administering to the subject an isolated molecule comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a VH that is capable of specifically CD8, a CH1 domain, a hinge, a CH2 domain, a CH3 domain and a second antigen binding domain comprising a scFv that specifically binds a TCR complex; the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by the undesired cell and a Fc or a fragment of the Fc, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[0034] In yet another aspect, the disclosure provides a method of treating a cancer in a subject, comprising: administering to the subject an isolated molecule comprising a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[0035] In yet another aspect, the disclosure also provides a method of treating a cancer in a subject, comprising administering to the subject an isolated molecule comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a second antigen binding domain comprising a scFv that specifically binds a TCR complex, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain; the second polypeptide comprises, from N-

to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[0036] In yet another aspect, the disclosure also provides a method of treating a cancer in a subject, comprising administering to the subject an isolated molecule comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain; the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8, a CL domain and a second antigen binding domain comprising a scFv that specifically binds a TCR complex; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[0037] In yet another aspect, the disclosure also provides a method of treating a cancer in a subject, comprising administering to the subject an isolated molecule comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a VH that is capable of specifically CD8, a CH1 domain, a hinge, a CH2 domain, a CH3 domain and a second antigen binding domain comprising a scFv that specifically binds a TCR complex; the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[0038] In yet another aspect, the disclosure provides a method of enhancing a $CD8^+$ CTL response against an undesired cell in a subject, comprising: administering to the subject an isolated molecule comprising a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[0039] In yet another aspect, the disclosure also provides a method of enhancing a $CD8^+$ CTL response against an undesired cell in a subject, comprising administering to the subject an isolated molecule comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a second antigen binding domain comprising a scFv that specifically binds a TCR complex, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain; the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[0040] In yet another aspect, the disclosure also provides a method of enhancing a $CD8^+$ CTL response against an undesired cell in a subject, comprising administering to the subject an isolated molecule comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain; the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8, a CL domain and a second antigen binding domain comprising a scFv that specifically binds a TCR complex; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed

by an undesired cell and a Fc or a fragment of the Fc, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[0041] In yet another aspect, the disclosure also provides a method of enhancing a $CD8^+$ CTL response against an undesired cell in a subject, comprising administering to the subject an isolated molecule comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a VH that is capable of specifically CD8, a CH1 domain, a hinge, a CH2 domain, a CH3 domain and a second antigen binding domain comprising a scFv that specifically binds a TCR complex; the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[0042] In some embodiments, the subject has a cancer, an infection, or an immune-mediated disease. In some embodiments, the cancer is a hematological malignancy or a solid tumor. In some embodiments, the hematological malignancy comprises acute lymphoblastic leukemia, acute myeloid leukemia, anaplastic large-cell lymphoma, Burkitt's lymphoma, chronic lymphocytic leukemia, chronic myeloid leukemia, diffuse large B-cell lymphoma, dendritic cell neoplasm, follicular lymphoma, hairy cell leukemia, Hodgkin's lymphoma, leukemia, B cell leukemia, T cell leukemia, light chain amyloidosis, lymphoma, B cell lymphoma, NK cell lymphoma, T cell lymphoma, mantle-cell lymphoma, marginal zone B-cell lymphoma, monoclonal gammopathy of undetermined significance, mucosa-associated lymphatic tissue lymphoma, multiple myeloma, myelodysplastic syndrome, non-Hodgkin's lymphoma, plasma cell leukemia, precursor B-cell lymphoblastic leukemia, smoldering multiple myeloma, Waldenstrom's macroglobulinemia, B cell malignancy, T cell malignancy, NK cell malignancy, or any combination thereof.

[0043] In some embodiments, the solid tumor comprises adenocarcinoma, anal cancer, basal cell carcinoma, biliary tract cancer, bladder cancer, bone cancer, breast cancer, cancer

associated with infection, cancer of the adrenal gland, cancer of the endocrine system, cancer of the head or neck, cancer of the parathyroid gland, cancer of the penis, cancer of the thyroid gland, cancer of the urethra, cervical cancer, carcinoma of the breast, carcinoma of the fallopian tubes, carcinoma of the liver, carcinoma of the lung, carcinoma of the prostate, carcinoma of the renal pelvis, carcinoma of the vagina, carcinoma of the vulva, choriocarcinoma, clear cell carcinoma, colon cancer, colon carcinoma, colorectal cancer, connective tissue cancer, cutaneous or intraocular malignant melanoma, environmentally induced cancer, gastric cancer, gastrointestinal cancer, glioma, glioblastoma, endometrial cancer, epithelial cancer, esophageal cancer, eye cancer, larynx cancer, liver cancer, hepatocellular carcinoma, hormone refractory prostate adenocarcinoma, Kaposi's sarcoma, kidney cancer, lung cancer gastro-esophageal cancer, melanoma, mesothelioma, Merkel cell cancer, neuroblastoma, non-small cell lung cancer (NSCLC), osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, rectal cancer, renal cell carcinoma, retinoblastoma rhabdomyosarcoma, squamous cell cancer, soft tissue sarcoma, solid tumors of childhood, spinal axis tumor, stomach cancer, testicular cancer, thyroid cancer, uterine cancer, urothelial carcinoma or sarcomas, or any combination thereof.

[0044] In some embodiments, the infection comprises infection with adenovirus, arboviral encephalitis virus, coronavirus, coxsackie virus, cytomegalovirus (CMV), dengue virus, echovirus, Epstein Barr virus, flaviviruses, human immunodeficiency virus (HIV), hepatitis A virus, hepatitis B virus, hepatitis C virus, herpes virus, HTLV virus, influenza virus, JC virus, measles virus, molluscum virus, mumps virus, papillomavirus, parvovirus, poliovirus, rabies virus, respiratory syncytial virus, rhinovirus, rotavirus, rubella virus or vaccinia virus, bacteria, virus, fungi, protozoa, parasite or prion, or any combination thereof.

[0045] In some embodiments, the immune-mediated disease comprises systemic lupus erythematosus (SLE), ankylosing spondylitis, Chagas disease, chronic obstructive pulmonary disease, Crohn's Disease, dermatomyositis, diabetes mellitus type 1, endometriosis, Goodpasture's syndrome, Graves' disease, Guillain-Barre syndrome (GBS), Hashimoto's disease, hidradenitis suppurativa, Kawasaki disease, IgA nephropathy, idiopathic thrombocytopenic purpura, interstitial cystitis, mixed connective tissue disease, morphea, multiple sclerosis, myasthenia gravis, narcolepsy, neuromyotonia, pemphigus vulgaris, pernicious anaemia, psoriasis, psoriatic arthritis, polymyositis, primary biliary cirrhosis, relapsing polychondritis, rheumatoid arthritis (RA), sarcoidosis, schizophrenia, scleroderma,

Sjogren's syndrome, temporal arteritis, ulcerative colitis, vasculitis, vitiligo, Wegener's granulomatosis, IgG4-related disease, anti-synthetase syndrome, and autoimmunity associated with immunodeficiency including chronic variable immunodeficiency, Wiskott-Aldrich syndrome, Good syndrome, IgA deficiency, Hyper IgM syndrome, complement disorders, seropositive RA, SLE, postmyocardial infarction syndrome, subacute bacterial endocarditis, anti-glomerular basement membrane nephritis, autoimmune hepatitis, primary biliary cirrhosis, alopecia areata, bullous pemphigoid, cicatricial pemphigoid, dermatitis herpetiformis, gestational pemphigoid, pemphigus vulgaris, systemic scleroderma, Addison's disease, autoimmune polyendocrine syndrome type 2, autoimmune pancreatitis, diabetes mellitus type 1, autoimmune thyroiditis, Graves' disease, Sjogren's syndrome, celiac disease, antiphospholipid syndrome, autoimmune thrombocytopenic purpura, cold agglutinin disease, pernicious anemia, thrombocytopenia, adult onset Still's disease, CREST syndrome, drug-induced lupus, enthesitis-related arthritis, juvenile arthritis, mixed connective tissue disease, palindromic rheumatism, Parry Romberg syndrome, rheumatic fever, undifferentiated connective tissue disease, dermatomysitis, myasthenia gravis, neuromyotonia, paraneoplastic cerebellar degeneration, polymyositis, Bickerstaff's encephalitis, chronic inflammatory demyelinating polyneuropathy, Guillain-Barre syndrome, Hashimoto's encephalopathy, Lambert-Eaton myasthenic syndrome, multiple sclerosis, progressive inflammatory neuropathy, Stiff person syndrome, autoimmune uveitis, neuromyelitis optica, symphathetic ophthalmia, Meniere's disease, anti-neutrophil cytoplasmic antibody-associated vasculitis, Churg-Strauss syndrome, Henoch-Schonlein purpura, microscopic polyangiitis, urticarial vasculitis, and vasculitis. Examples of autoantibody-associated autoimmune conditions include gastritis and POEMS syndrome. Examples of autoantibody-associated (non-autoimmune) diseases include agammaglobulinemia, amyotrophic lateral sclerosis, Castleman's disease, cutaneous leukocytoclastic angiitis, eczema, eosinophilic gastroenteritis, erythroblastosis fetalis, fibrodysplasia ossificans progressive, hypogammaglobulinemia, idiopathic pulmonary fibrosis, IgA nephropathy, Majeed syndrome, narcolepsy, Rasmussen's encephalitis, spondyloarthropathy or Sweet's syndrome, or any combination thereof.

[0046] In yet another aspect, the disclosure provides a system comprising a means for selective activation or recruitment of $CD8^+$ CTLs.

[0047] In yet another aspect, the disclosure also provides a composition comprising an antibody comprising a first antigen binding domain and a second antigen binding domain, and means for selective activation or recruitment of $CD8^+$ CTLs.

[0048] In yet another aspect, the disclosure also provides a composition for enhancing an immune response against an antigen expressed by an undesired cell, comprising means for selective activation or recruitment of $CD8^+$ CTLs.

[0049] In yet another aspect, the disclosure also provides a composition for treating a cancer in subject, comprising means for selective activation or recruitment of $CD8^+$ CTLs.

[0050] In yet another aspect, the disclosure also provides a system comprising a means for providing an improved T cell redirecting therapeutic treatment to a subject.

[0051] In yet another aspect, the disclosure also provides a T cell redirecting therapeutic comprising a means for improving safety of the T cell redirecting therapeutic.

[0052] In yet another aspect, the disclosure also provides a process for generating an improved T cell redirecting therapeutic, comprising: a step for performing a function of designing the T cell redirecting therapeutic comprising the means of the disclosure; and a step for performing a function of producing the T cell redirecting therapeutic comprising the means of the disclosure.

[0053] In yet another aspect, the disclosure provides a method of isolating, separating, purifying, sorting, selecting or capturing a CD8+ CTL comprising: providing a sample comprising the CD8+ CTL; contacting the sample with an isolated molecule comprising a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds a TCR complex; and isolating, separating, purifying, sorting, selecting or capturing the $CD8^+$ CTL bound to the isolated molecule.

[0054] In yet another aspect, the disclosure also provides a method of isolating, separating, purifying, sorting, selecting or capturing a CD8+ CTL, comprising contacting the $CD8^+$ CTL with an isolated molecule comprising a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds a TCR complex; and isolating, separating, purifying, sorting, selecting or capturing the CD8+ CTL based on binding of the CD8+ CTL to the isolated molecule.

BRIEF DESCRIPTION OF THE DRAWINGS

[0055] **FIG. 1** shows the design of the Protein Format 1. In the Protein Format 1, the tumor associated antigen (TAA) binding arm was incorporated as a scFv coupled to a Fc (HC1_scFv), the CD8 binding arm was incorporated as a HC/LC chain (HC2 N-term and LC2 2nd N-term), and the CD3 binding arm was incorporated as a scFv attached to the N-terminus of the CD8 binding HC (LC2 1st N-term).

[0056] **FIG. 2** shows the design of the Protein Format 2. In the Protein Format 2, the TAA binding arm was incorporated as a scFv coupled to the Fc (HC1_scFv), the CD8 binding arm was incorporated as a HC/LC chain (HC2 N-term and LC2 1st N-term), and the CD3 binding arm was incorporated as a scFv attached to the C-terminus of the CD8 binding LC (LC2 C-term).

[0057] **FIG. 3** shows the design of the Protein Format 3. In the Protein Format 3, the TAA binding arm was incorporated as a scFv coupled to the Fc (HC1_scFv), the CD8 binding arm was incorporated as a HC/LC chain (HC2 N-term and LC1 1st N-term), and the CD3 binding arm was incorporated as a scFv attached to the C-terminus of the CD8 binding HC (HC2 C-term).

[0058] **FIG. 4A-4B** show low affinity CD3 multispecifics paired with CD8 binders show selective binding to CD8 T cells. **FIG. 4A** shows that the trispecific binds to and specifically recruits CD8 T cells. **FIG. 4B** shows that Pan T cells were isolated from the PBMCs of healthy volunteers and stained with the test multispecifics at room temperature for 30min followed by detection using an anti-human IgG antibody and staining with anti-human CD3, CD4 and CD8 antibodies. % binding was determined using the secondary antibody-stained samples as negative controls.

[0059] **FIG. 5A** shows in the top panel cytotoxicity assay on C4-2B (target) and PBMCs (effector) at 3 different E:T ratios incubated for 72h in the presence of CD8xCD3xPSMA trispecific Ab (black circle), CD8xPSMA bispecific Ab (black square) and CD3xPSMA bispecific Ab (grey triangle). EC50 values listed in the table are for the CD8xCD3xPSMA trispecific Ab (CD8B573.001). The low panel in **FIG. 5A** shows cytotoxicity assay on C4-2B (target) and PBMCs (effector) with E:T ratio of 3:1 and incubated for 72h (left) and 48h (right) in the presence of indicated Ab. Table list EC50 values for CD3xCD8xPSMA (low affinity

CD3), CD3xPSMA (CD8B52, CD3B376) [medium affinity CD3], CD3xPSMA (CD3B220, HA) [high affinity CD3].

[0060] **FIG. 5B** shows the IncuCyte cytotoxicity assay on target cell line C4-2B and PBMCs (2 donors: 19054280 and 19053791) in the presence of indicated Ab ranging from 0 (NBS) to 60 nM.

[0061] **FIG. 6** shows low affinity CD3 multispecifics paired with CD8 binders show potent cytotoxicity against target cell lines in a CD8 T cell dependent manner. PBMCs of healthy volunteers were either depleted of CD8 T cells or used as such. CD8 depleted and non depleted PBMCs were cocultured with C4-2B target cells as a 1:1 effector to target ratio (CD3 to target cells) for 72hrs in the presence of the test multispecifics. Cytotoxicity was monitored using the Incucyte automated live cell analysis system and EC50 values were calculated after normalizing to no multispecific containing wells.

[0062] **FIG. 7** shows low affinity CD3 multispecifics paired with CD8 binders specifically and potently activate only CD8 T cells. PBMCs were cocultured with C4-2B target cells as a 1:1 effector to target ratio (CD3 to target cells) for the indicated time points in the presence of the test multispecifics. At each time point, cells were harvested and CD3, CD4 and CD8 T cells were analyzed for the presence of the indicated activation and exhaustion markers.

[0063] **FIG. 8** shows low affinity CD3 multispecifics paired with CD8 binders show reduced anti-inflammatory cytokine release. PBMCs were cocultured with C4-2B target cells as a 1:1 effector to target ratio (CD3 to target cells) for the indicated time points in the presence of the test multispecifics. At each time point, supernatants were harvested and analyzed for the indicated cytokines using a multiplex Luminex analysis system.

DETAILED DESCRIPTION

[0064] The disclosed methods may be understood more readily by reference to the following detailed description taken in connection with the accompanying Figures, which form a part of this disclosure. It is to be understood that the disclosed methods are not limited to the specific methods described and/or shown herein, and that the terminology used herein is for the purpose of describing particular embodiments by way of example only and is not intended to be limiting of the claimed compositions or methods.

[0065] All patents, published patent applications and publications cited herein are incorporated by reference as if set forth fully herein.

[0066] When a list is presented, unless stated otherwise, it is to be understood that each individual element of that list, and every combination of that list, is a separate embodiment. For example, a list of embodiments presented as "**A, B, or C**" is to be interpreted as including the embodiments, "A," "B," "C," "A or B," "A or C," "B or C," or "A, B, or C."

[0067] As used in this specification and the appended claims, the singular forms "**a**," "**an**," and "**the**" include plural referents unless the content clearly dictates otherwise. Thus, for example, reference to "a cell" includes a combination of two or more cells, and the like.

[0068] The transitional terms "**comprising**," "**consisting essentially of**," and "**consisting of**" are intended to connote their generally accepted meaning, that is, (i) "comprising," which is synonymous with "including," "containing," or "characterized by," is inclusive or open-ended and does not exclude additional, unrecited elements or method steps; (ii) "consisting of" excludes any element, step, or ingredient not specified in the claim; and (iii) "consisting essentially of" limits the scope of a claim to the specified materials or steps "and those that do not materially affect the basic and novel characteristic(s)" of the claimed invention. Embodiments described in terms of the phrase "comprising" (or its equivalents) also provide as embodiments those independently described in terms of "consisting of" and "consisting essentially of."

[0069] "**About**" means within an acceptable error range for the particular value as determined by one of ordinary skill in the art, which will depend in part on how the value is measured or determined, *i.e.*, the limitations of the measurement system. Unless explicitly stated otherwise within the Examples or elsewhere in the Specification in the context of a particular assay, result or embodiment, "about" means within one standard deviation per the practice in the art, or a range of up to 5%, whichever is larger.

[0070] "**Activate**" or "**activation**" or "**activated**" refers to induction of a change in the biologic state of a cell resulting in expression of activation markers, cytokine production, proliferation or mediating cytotoxicity of target cells. Cells may be activated by primary stimulatory signals. Co-stimulatory signals may amplify the magnitude of the primary signals and suppress cell death following initial stimulation resulting in a more durable activation state and thus a higher cytotoxic capacity. An exemplary activated cell is an activated $CD8^+$ CTL that expresses CD25 and/or produces cytokines such as IFNγ.

[0071] "**Affinity**" or "**binding affinity**" or "**binds with affinity**" refers to the strength of the sum total of noncovalent interactions between a single binding site of a molecule (such as molecules and multispecific antibodies described herein) and its binding partner (*i.e.*., an antigen). Unless indicated otherwise, "affinity" refers to intrinsic binding affinity which reflects a 1:1 interaction between members of a binding pair. The affinity can generally be represented by the dissociation constant (K_D). Affinity can be measured by known methods, such as using biolayer interferometry (BLI) or surface plasmon resonance (SPR) assays by Octet®, using, for example, an Octet®Red96 system, or by Biacore®, using, for example, a Biacore®TM-2000 or a Biacore®TM-3000. An "on-rate" or "rate of association" or "association rate" or "kon" and an "of-rate" or "rate of dissociation" or "dissociation rate" or "koff" may also be determined with the same methods. "High affinity" within the context of this disclosure refers to molecules which demonstrate stronger binding to an antigen (*e.g.*, lower K_D). "Low affinity" within the context of this disclosure refers to molecules which demonstrate weaker binding to an antigen (*e.g.*, higher K_D).

[0072] "**Non-antibody scaffold**" refers to a single chain protein framework that contains a structured core associated with variable domains of high conformational tolerance. The variable domains tolerate variation to be introduced without compromising scaffold integrity, and hence the variable domains can be engineered and selected for binding to a specific antigen.

[0073] "**Antigen**" refers to any molecule (*e.g.*, protein, peptide, polysaccharide, glycoprotein, glycolipid, nucleic acid, portions thereof, or combinations thereof) that is capable of mediating an immune response either alone or in complex in MHC. Exemplary immune responses include antibody production and activation of immune cells, such as T cells, B cells or NK cells. Antigens may be expressed by genes, synthetized, or purified from biological samples such as a tissue sample, a tumor sample, a cell or a fluid with other biological components, organisms, subunits of proteins/antigens, killed or inactivated whole cells or lysates.

[0074] "**Antigen binding domain**" or "**antigen binding fragment**" or "**domain that binds an antigen**" refers to a portion of a molecule that specifically binds an antigen. Antigen binding domain may include portions of an immunoglobulin that bind an antigen, such as a VH, a VL, the VH and the VL, Fab, Fab', $F(ab')_2$, Fd and Fv fragments, domain antibodies (dAb) consisting of one VH or one VL, shark variable IgNAR domains, camelized VH domains,

VHH, minimal recognition units consisting of the amino acid residues that mimic the CDRs of an antibody, such as FR3-CDR3-FR4 portions, the HCDR1, the HCDR2 and/or the HCDR3 and the LCDR1, the LCDR2 and/or the LCDR3 and non-antibody scaffolds that bind an antigen.

[0075] "**Antibodies**" is meant in a broad sense and includes immunoglobulin molecules including monoclonal antibodies including murine, human, humanized and chimeric monoclonal antibodies, antigen binding domains, multispecific antibodies, such as bispecific, trispecific, tetraspecific, dimeric, trimeric, tetrameric or multimeric antibodies, single chain antibodies, domain antibodies and any other modified configuration of the immunoglobulin molecule that comprises an antigen binding site of the required specificity. "Full length antibodies" are comprised of two heavy chains (HC) and two light chains (LC) inter-connected by disulfide bonds as well as multimers thereof (*e.g.*, IgM). Each heavy chain is comprised of a heavy chain variable region (VH) and a heavy chain constant region (comprised of domains CH1, hinge, CH2 and CH3). Each light chain is comprised of a light chain variable region (VL) and a light chain constant region (CL). The VH and the VL regions may be further subdivided into regions of hypervariability, termed complementarity determining regions (CDR), interspersed with framework regions (FR). Each VH and VL is composed of three CDRs and four FR segments, arranged from amino-to-carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3 and FR4. Immunoglobulins may be assigned to five major classes, IgA, IgD, IgE, IgG and IgM, depending on the heavy chain constant domain amino acid sequence. IgA and IgG are further sub-classified as the isotypes IgA1, IgA2, IgG1, IgG2, IgG3 and IgG4. Antibody light chains of any vertebrate species may be assigned to one of two clearly distinct types, namely kappa (κ) and lambda (λ), based on the amino acid sequences of their constant domains.

[0076] "**Bispecific**" refers to a molecule that specifically binds two distinct antigens or two distinct epitopes within the same antigen. The bispecific molecule may have cross-reactivity to other related antigens, for example to the same antigen from other species (homologs), such as human or monkey, for example *Macaca cynomolgus* (cynomolgus, cyno) or *Pan troglodytes*, or may bind an epitope that is shared between two or more distinct antigens.

[0077] "**Cancer**" refers to a broad group of various diseases characterized by the uncontrolled growth of abnormal cells in the body. Unregulated cell division and growth results in the formation of malignant tumors that invade neighboring tissues and may also metastasize

to distant parts of the body through the lymphatic system or bloodstream. A "cancer" or "cancer tissue" can include a tumor.

[0078] "**Cancer cell**" or "**tumor cell**" refers to a cancerous, pre-cancerous or transformed cell, either *in vivo*, *ex vivo*, or in tissue culture, that has spontaneous or induced phenotypic changes. Cancer cells may exhibit characteristics such as morphological changes, immortalization, aberrant growth, foci formation, proliferation, malignancy, modulation of tumor specific marker levels or invasiveness.

[0079] "**CH2 domain**" or "**CH2 region**" refers to the CH2 region of an immunoglobulin. The CH2 region of a human IgG1 antibody corresponds to amino acid residues 231-340 (EU numbering) of IgG1 constant domain. The amino acid sequence of a wild-type IGG1 CH2 domain is shown in SEQ ID NO: 2318.

[0080] SEQ ID NO: 2318 (IgG1 CH2)
APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA

[0081] "**CH3 domain**" or "**CH3 region**" refers to the CH3 region of an immunoglobulin. The CH3 region of human IgG1 antibody corresponds to amino acid residues 341-446 (EU numbering) of IgG1 constant domain. The amino acid sequence of a wild-type IgG1 CH3 domain is shown in SEQ ID NO: 2319.

[0082] SEQ ID NO: 2319
GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

[0083] "**CD3ε**" refers to CD3ε from any species, such as from primate or rodent, such as human, monkey, rat or mouse. Human CD3ε comprises the amino acid sequence of SEQ ID NO: 2180.

[0084] SEQ ID NO: 2180 (CD3ε)
DGNEEMGGITQTPYKVSISGTTVILTCPQYPGSEILWQHNDKNIGGDEDDKNIGSDEDH
LSLKEFSELEQSGYYVCYPRGSKPEDANFYLYLRARVCENCMEMDVMSVATIVIVDICI
TGGLLLLVYYWSKNRKAKAKPVTRGAGAGGRQRGQNKERPPPVPNPDYEPIRKGQRD
LYSGLNQRRI

[0085] "**CD8**" refers to CD8 from any species, such as from primate or rodent, such as human, monkey, rat or mouse. Human CD8 is a homodimer of alpha chains (CD8α) or a heterodimer of CD8α (SEQ ID NO: 2181) and CD8β (SEQ ID NO: 2182) chains.

[0086] SEQ ID NO: 2181 (CD8α chain)

SQFRVSPLDRTWNLGETVELKCQVLLSNPTSGCSWLFQPRGAAASPTFLLYLSQNKPKA AEGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPAKPTTT PAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSL VITLYCNHRNRRRVCKCPRPVVKSGDKPSLSARYV

[0087] SEQ ID NO: 2182 (CD8β chain)

LQQTPAYIKVQTNKMVMLSCEAKISLSNMRIYWLRQRQAPSSDSHHEFLALWDSAKGT IHGEEVEQEKIAVFRDASRFILNLTSVKPEDSGIYFCMIVGSPELTFGKGTQLSVVDFLPT TAQPTKKSTLKKRVCRLPRPETQKGPLCSPITLGLLVAGVLVLLVSLGVAIHLCCRRRR ARLRFMKQFYK

[0088] "**Complementarity determining regions**" (CDR) are regions of an antibody that bind an antigen. There are three CDRs in the VH (HCDR1, HCDR2, HCDR3) and three CDRs in the VL (LCDR1, LCDR2, LCDR3). CDRs may be defined using various delineations such as Kabat (Wu et al. (1970) J Exp Med 132: 211-50; Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md., 1991; Kabat *et al., J. Biol. Chem.* 252:6609-6616 (1977); Kabat, *Adv. Prot. Chem.* 32:1-75 (1978)), Chothia (Chothia et al. (1987) J Mol Biol 196: 901-17), IMGT (Lefranc et al. (2003) Dev Comp Immunol 27: 55-77). Both terminologies are well recognized in the art. CDR region sequences have also been defined by AbM, AbM (Martin and Thornton J Bmol Biol 263: 800-15, 1996), Contact and IMGT. The correspondence between the various delineations and variable region numbering is described (see *e.g.,* Lefranc et al. (2003) Dev Comp Immunol 27: 55-77; Honegger and Pluckthun, J Mol Biol (2001) 309:657-70; International ImMunoGeneTics (IMGT) database; Web resources, http://www_imgt_org). Available programs such as abYsis by UCL Business PLC may be used to delineate CDRs. The term "CDR", "HCDR1", "HCDR2", "HCDR3", "LCDR1", "LCDR2" and "LCDR3" as used herein includes CDRs defined by any of the methods described supra, Kabat, Chothia, IMGT, AbM or Contact, unless otherwise explicitly stated in the specification.

[0089] The light chain variable region CDR1 domain is interchangeably referred to herein as LCDR1 or VL CDR1. The light chain variable region CDR2 domain is interchangeably referred to herein as LCDR2 or VL CDR2. The light chain variable region CDR3 domain is interchangeably referred to herein as LCDR3 or VL CDR3. The heavy chain variable region CDR1 domain is interchangeably referred to herein as HCDR1 or VH CDR1. The heavy chain variable region CDR2 domain is interchangeably referred to herein as HCDR2 or VH CDR2. The heavy chain variable region CDR1 domain is interchangeably referred to herein as HCDR3 or VH CDR3.

[0090] Exemplary CDR region sequences are illustrated herein, for example, in the tables provided in the Examples below. The positions of CDRs within a canonical antibody variable region have been determined by comparison of numerous structures (Al-Lazikani *et al., J. Mol. Biol.* 273:927-948 (1997); *Morea et al., Methods* 20:267-279 (2000)). Because the number of residues within a hypervariable region varies in different antibodies, additional residues relative to the canonical positions are conventionally numbered with a, b, c and so forth next to the residue number in the canonical variable region numbering scheme (Al-Lazikani *et al., supra* (1997)). Such nomenclature is similarly well known to those skilled in the art.

[0091] The term "hypervariable region", such as a VH or VL, when used herein refers to the regions of an antibody variable region that are hypervariable in sequence and/or form structurally defined loops. Generally, antibodies comprise six hypervariable regions; three in the VH (HCDR1, HCDR2, HCDR3), and three in the VL (LCDR1, LCDR2, LCDR3). A number of hypervariable region delineations are in use and are encompassed herein. The "Kabat" CDRs are based on sequence variability and are the most commonly used (see, *e.g.,* Kabat *et al.*, Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD. (1991)). "Chothia" refers instead to the location of the structural loops (see, *e.g.,* Chothia and Lesk, *J. Mol. Biol.* 196:901-917 (1987)). The end of the Chothia CDR-HCDR1 loop when numbered using the Kabat numbering convention varies between H32 and H34 depending on the length of the loop (this is because the Kabat numbering scheme places the insertions at H35A and H35B; if neither 35A nor 35B is present, the loop ends at 32; if only 35A is present, the loop ends at 33; if both 35A and 35B are present, the loop ends at 34). The "AbM" hypervariable regions represent a compromise between the Kabat CDRs and Chothia structural loops, and are used by Oxford Molecular's AbM antibody

modeling software (see, *e.g.*, Martin, in Antibody Engineering, Vol. 2, Chapter 3, Springer Verlag). "Contact" hypervariable regions are based on an analysis of the available complex crystal structures.

[0092] Recently, a universal numbering system has been developed and widely adopted, ImMunoGeneTics (IMGT) Information System® (Lafranc *et al.*, *Dev. Comp. Immunol.* 27(1):55-77 (2003)). IMGT is an integrated information system specializing in immunoglobulins (IG), T cell receptors (TR) and major histocompatibility complex (MHC) of human and other vertebrates. Herein, the CDRs are referred to in terms of both the amino acid sequence and the location within the light or heavy chain. As the "location" of the CDRs within the structure of the immunoglobulin variable domain is conserved between species and present in structures called loops, by using numbering systems that align variable domain sequences according to structural features, CDR and framework residues and are readily identified. This information can be used in grafting and replacement of CDR residues from immunoglobulins of one species into an acceptor framework from, typically, a human antibody. An additional numbering system (AHon) has been developed by Honegger and Plückthun, *J. Mol. Biol.* 309: 657-670 (2001). Correspondence between the numbering system, including, for example, the Kabat numbering and the IMGT unique numbering system, is well known to one skilled in the art (see, *e.g.*, Kabat, *supra*; Chothia and Lesk, *supra*; Martin, *supra*; Lefranc *et al.*, *supra*). An Exemplary system, shown herein, combines Kabat and Chothia.

	Exemplary	**IMGT**	**Kabat**	**AbM**	**Chothia**	**Contact**
V_H CDR1	26-35	27-38	31-35	26-35	26-32	30-35
V_H CDR2	50-65	56-65	50-65	50-58	53-55	47-58
V_H CDR3	95-102	105-117	95-102	95-102	96-101	93-101
V_L CDR1	24-34	27-38	24-34	24-34	26-32	30-36
V_L CDR2	50-56	56-65	50-56	50-56	50-52	46-55
V_L CDR3	89-97	105-117	89-97	89-97	91-96	89-96

[0093] Hypervariable regions may comprise "extended hypervariable regions" as follows: 24-36 or 24-34 (LCDR1), 46-56 or 50-56 (LCDR2) and 89-97 or 89-96 (LCDR3) in the VL and 26-35 or 26-35A (HCDR1), 50-65 or 49-65 (HCDR2) and 93-102, 94-102, or 95-102 (HCDR3)

in the VH. CDR sequences, reflecting each of the above numbering schemes, are provided herein, including in the tables provided in the Examples below.

[0094] "**Reduce**" or "**reduced**" refers to a decrease in a measured response mediated by a test molecule in any system *in vitro* or *in vivo* when compared to a control. Measured response may be an Fc-mediated effector function such as ADCC, CDC and/or ADCP, cellular proliferation or activation, or cell killing. "Reduced" may be a reduction of about 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100% or more, or a statistically significant reduction when compared to a control. Suitable controls depend on the assay or response and are known.

[0095] "**Enhance**" or "**enhanced**" refers to an increase in a measured response mediated by a test molecule in any system *in vitro* or *in vivo* when compared to a control. Measured response may be an Fc-mediated effector function such as ADCC, CDC and/or ADCP, cellular proliferation or activation, or cell killing. "Enhanced" may be an increase of about 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100% or more, or a statistically significant increase when compared to a control. Suitable controls depend on the assay or response and are known.

[0096] "**Domain antibody**" or "**dAb**" refers to an antibody fragment composed of a VH domain.

[0097] "**Fab**" or "**Fab fragment**" refers to an antibody fragment composed of VH, CH1, VL and CL domains.

[0098] "**F(ab')$_2$**" or "**F(ab')$_2$ fragment**" refers to an antibody fragment containing two Fab fragments connected by a disulfide bridge in the hinge region.

[0099] "**Fc**" or "**Fc region**" or "**Fc domain**" refers to an antibody region comprising at least a portion of a hinge region, a CH2 domain and a CH3 domain. The Fc may be generated by digestion of an antibody with papain, or pepsin where the Fc is the fragment obtained thereby, which includes one or both CH2-CH3 domains of and a portion of the hinge region.

[00100] "**Fd**" or "**Fd fragment**" refers to an antibody fragment composed of VH and CH1 domains.

[00101] "**Fv**" or "**Fv fragment**" refers to an antibody fragment composed of the VH and the VL domains from a single arm of the antibody.

[00102] "**Full length antibody**" is comprised of two heavy chains (HC) and two light chains (LC) inter-connected by disulfide bonds as well as multimers thereof (*e.g.,* IgM). Each heavy chain is comprised of a VH and a heavy chain constant domain, the heavy chain constant

domain comprised of subdomains CH1, hinge, CH2 and CH3. Each light chain is comprised of a VL and a light chain constant domain (CL). The VH and the VL may be further subdivided into regions of hypervariability, termed complementarity determining regions (CDR), interspersed with framework regions (FR). Each VH and VL is composed of three CDRs and four FR segments, arranged from amino-to-carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3 and FR4.

[00103] "**Half molecule**", in the context of an antibody that comprises two heavy chains of fragments thereof (such as two Fc regions), refers to one heavy chain or a fragment thereof and any additional polypeptides that associate with the one heavy chain or fragment thereof or are conjugated to the one heavy chain or fragment thereof. An exemplary half molecule is a molecule comprising a scFv conjugated to Fc. Another exemplary half molecule is a molecule comprising a HC conjugated to scFv.

[00104] "**Human antibody**" refers to an antibody that is optimized to have minimal immune response when administered to a human subject. Variable regions of human antibody are derived from human immunoglobulin sequences. If human antibody contains a constant region or a portion of the constant region, the constant region is also derived from human immunoglobulin sequences. Human antibody comprises heavy and light chain variable regions that are "derived from" sequences of human origin if the variable regions of the human antibody are obtained from a system that uses human germline immunoglobulin or rearranged immunoglobulin genes. Such exemplary systems are human immunoglobulin gene libraries displayed on phage, and transgenic non-human animals such as mice, rats or chicken carrying human immunoglobulin loci. "Human antibody" typically contains amino acid differences when compared to the immunoglobulins expressed in humans due to differences between the systems used to obtain the human antibody and human immunoglobulin loci, introduction of somatic mutations or intentional introduction of substitutions into the frameworks or CDRs, or both. Typically, "human antibody" is at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical in amino acid sequence to an amino acid sequence encoded by human germline immunoglobulin or rearranged immunoglobulin genes. In some instances, "human antibody" may contain consensus framework sequences derived from human framework sequence analyses, for example as described in Knappik et al., (2000) J Mol Biol 296:57-86, or a synthetic HCDR3

incorporated into human immunoglobulin gene libraries displayed on phage, for example as described in Shi et al., (2010) J Mol Biol 397:385-96, and in Int. Patent Publ. No. WO2009/085462. Antibodies in which at least one CDR is derived from a non-human species are not included in the definition of "human antibody".

[00105] "**Humanized antibody**" refers to an antibody in which at least one CDR is derived from non-human species and at least one framework is derived from human immunoglobulin sequences. Humanized antibody may include substitutions in the frameworks so that the frameworks may not be exact copies of expressed human immunoglobulin or human immunoglobulin germline gene sequences.

[00106] The terms **"identical"** or percent **"identity,"** in the context of two or more nucleic acids or polypeptide sequences (*e.g.*, CD8 antibody and polynucleotides that encode them), refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same, when compared and aligned for maximum correspondence, as measured using one of the following sequence comparison algorithms or by visual inspection.

[00107] For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are input into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters.

[00108] Optimal alignment of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith & Waterman, Adv. Appl. Math. 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, J. Mol. Biol. 48:443 (1970), by the search for similarity method of Pearson & Lipman, Proc. Nat'l. Acad. Sci. USA 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by visual inspection (see generally, Current Protocols in Molecular Biology, F.M. Ausubel *et al.*, eds., Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc., (1995 Supplement) (Ausubel)).

[00109] Examples of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.* (1990) J. Mol. Biol. 215: 403-410 and Altschul *et al.* (1997) Nucleic Acids Res. 25: 3389-3402, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased.

[00110] Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a word length (W) of 11, an expectation (E) of 10, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a word length (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, Proc. Natl. Acad. Sci. USA 89:10915 (1989)).

[00111] In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, *e.g.*, Karlin & Altschul, Proc. Nat'l. Acad. Sci. USA 90:5873-5787 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference

nucleic acid is less than about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001.

[00112] A further indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the polypeptide encoded by the second nucleic acid, as described below. Thus, a polypeptide is typically substantially identical to a second polypeptide, for example, where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules hybridize to each other under stringent conditions.

[00113] "**Isolated**" refers to a homogenous population of molecules (such as synthetic polynucleotides or polypeptides) which have been substantially separated and/or purified away from other components of the system the molecules are produced in, such as a recombinant cell, as well as a protein that has been subjected to at least one purification or isolation step. "Isolated" refers to a molecule that is substantially free of other cellular material and/or chemicals and encompasses molecules that are isolated to a higher purity, such as to 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% purity.

[00114] "**Monoclonal antibody**" refers to an antibody obtained from a substantially homogenous population of antibody molecules, *i.e.*, the individual antibodies comprising the population are identical except for possible well-known alterations such as removal of C-terminal lysine from the antibody heavy chain or post-translational modifications such as amino acid isomerization or deamidation, methionine oxidation or asparagine or glutamine deamidation. Monoclonal antibodies typically bind one antigenic epitope. A bispecific monoclonal antibody binds two distinct antigenic epitopes. Monoclonal antibodies may have heterogeneous glycosylation within the antibody population. Monoclonal antibody may be monospecific or multispecific such as bispecific, trispecific, monovalent, bivalent, trivalent or multivalent.

[00115] "**Multispecific**" refers to a molecule that specifically binds two or more distinct antigens or two or more distinct epitopes within the same antigen. Multispecific molecule may have cross-reactivity to other related antigens, for example to the same antigen from other species (homologs), such as human or monkey, for example *Macaca fascicularis* (cynomolgus,

cyno) or *Pan troglodytes*, or may bind an epitope that is shared between two or more distinct antigens.

[00116] "**Molecule**" refers to a protein that may be monomeric, multimeric, homodimeric or heterodimeric protein. Multimeric protein may be composed of two or more identical or distinct subunits. Trimeric protein is composed of three subunits which may be identical or distinct, or alternatively, two subunits may be identical and the third subunit distinct.

[00117] "**Pharmaceutical composition**" refers to a composition that results from combining an active ingredient and one or more pharmaceutically acceptable carriers.

[00118] "**Pharmaceutically acceptable carrier**" or "excipient" refers to an ingredient in a pharmaceutical composition, other than the active ingredient, which is nontoxic to a subject. Exemplary pharmaceutically acceptable carriers are a buffer, stabilizer or preservative.

[00119] "**Prevent,**" "**preventing,**" or "**prophylaxis**" of a disease or disorder means preventing that a disorder occurs in a subject.

[00120] "**Protein**" or "**polypeptide**" are used interchangeably herein are refers to a molecule that comprises one or more polypeptides each comprised of at least two amino acid residues linked by a peptide bond. Protein may be a monomer, or may be protein complex of two or more subunits, the subunits being identical or distinct. Small polypeptides of less than 50 amino acids may be referred to as "peptides". Protein may be a heterologous fusion protein, a glycoprotein, or a protein modified by post-translational modifications such as phosphorylation, acetylation, myristoylation, palmitoylation, glycosylation, oxidation, formylation, amidation, citrullination, polyglutamylation, ADP-ribosylation, pegylation or biotinylation. Protein may be recombinantly expressed.

[00121] "**Recombinant**" refers to polynucleotides, polypeptides, vectors, viruses and other macromolecules that are prepared, expressed, created or isolated by recombinant means.

[00122] "**Sample**" refers to a collection of similar fluids, cells, or tissues isolated from a subject, as well as fluids, cells, or tissues present within a subject. Exemplary samples are biological fluids such as blood, serum and serosal fluids, plasma, lymph, urine, saliva, cystic fluid, tear drops, feces, sputum, mucosal secretions of the secretory tissues and organs, vaginal secretions, ascites fluids such as those associated with non-solid tumors, fluids of the pleural, pericardial, peritoneal, abdominal and other body cavities, fluids collected by bronchial lavage, liquid solutions contacted with a subject or biological source, for example, cell and organ

culture medium including cell or organ conditioned medium, lavage fluids and the like, tissue biopsies, fine needle aspirations or surgically resected tumor tissue.

[00123] "**Single chain Fv**" or "**scFv**" refers to a fusion protein comprising a VH and a VL, which are optionally linked via a polypeptide linker. scFv may have the VL and VH variable regions in either order, *e.g.*, with respect to the N- terminal and C-terminal ends of the polypeptide, the scFv may comprise VL-linker-VH or may comprise VH-linker-VL. scFv may comprise one or more disulfide bonds to stabilize the scFv.

[00124] "**Specifically binds,**" "**specific binding,**" "**specifically binding**" or "**binds**" refer to a molecule comprising an antigen binding domain that binds the antigen with greater affinity than other antigens. Typically, the molecule binds the antigen with a dissociation constant (K_D) of about $1x10^{-7}$ M or less, for example about $5x10^{-8}$ M or less, about $1x10^{-8}$ M or less, about $1x10^{-9}$ M or less, about $1x10^{-10}$ M or less, about $1x10^{-11}$ M or less, or about $1x10^{-12}$ M or less, typically with the K_D that is at least one hundred fold less than its K_D for binding to a non-specific antigen (*e.g.*, BSA, casein).

[00125] "**Subject**" includes any human or nonhuman animal. "Nonhuman animal" includes all vertebrates, *e.g.,* mammals and non-mammals, such as nonhuman primates, sheep, dogs, cats, horses, cows, chickens, amphibians, reptiles, etc. The terms "subject" and "patient" can be used interchangeably herein.

[00126] "**T cell receptor complex**" (TCR complex) refers to a known TCR complex comprising of a TCRα and TCRβ chains, CD3ε, CD3γ, CD3δ and CD3ζ molecules. In some instances, TCRα and TCRβ chains are replaced by TCRγ and TCRδ chains. The amino acid sequences of the various proteins forming the TCR complex are well-known.

[00127] "**Therapeutically effective amount**" or "**effective amount**" used interchangeably herein, refers to an amount effective, at dosages and for periods of time necessary, to achieve a desired therapeutic result. A therapeutically effective amount may vary according to factors such as the disease state, age, sex, and weight of the individual, and the ability of a therapeutic or a combination of therapeutics to elicit a desired response in the individual. Example indicators of an effective therapeutic or combination of therapeutics that include, for example, improved wellbeing of the patient, reduction of a tumor burden, arrested or slowed growth of a tumor, and/or absence of metastasis of cancer cells to other locations in the body.

[00128] "**Treat,**" "**treating**" or "**treatment**" of a disease or disorder such as cancer refers to accomplishing one or more of the following: reducing the severity and/or duration of the disorder, inhibiting worsening of symptoms characteristic of the disorder being treated, limiting or preventing recurrence of the disorder in subjects that have previously had the disorder, or limiting or preventing recurrence of symptoms in subjects that were previously symptomatic for the disorder.

[00129] "**Trispecific"** refers to a molecule that specifically binds three distinct antigens or three distinct epitopes within the same antigen. Trispecific molecule may have cross-reactivity to other related antigens, for example to the same antigen from other species (homologs), such as human or monkey, for example *Macaca cynomolgus* (cynomolgus, cyno) or *Pan troglodytes*, or may bind an epitope that is shared between two or more distinct antigens.

[00130] "**Unable to activate**" in the context of $CD8^+$ CTL activation refers to a molecule that exhibits no measurable activation of $CD8^+$ CTLs in a system, such as in an *in vitro* assay. $CD8^+$ CTL activation may be measured using known methods, such as assessing increased CD25 expression or by production IFNγ by the $CD8^+$ CTL.

[00131] "**Undesired cell**" refers to a cell that is desired or intended to be removed from a system, such as an *in vitro* system an *ex vivo* system, a tissue, blood, sample, or from a subject.

[00132] "**Expressed by an undesired cell**" refers to a measurable intracellular or surface expression of an antigen by the undesired cell.

[00133] "**VHH**" refers to a single chain antigen binding domain derived from camelid antibodies which are devoid of light chains.

[00134] "**BCMA**" refers to **B cell maturation antigen** (TNFRSF17, CD269), a transmembrane protein belonging to the tumor necrosis family receptor (TNFR) superfamily that is primarily expressed on terminally differentiated B cells. BCMA expression is restricted to the B cell lineage and mainly present on plasma cells and plasmablasts and to some extent on memory B cells, but virtually absent on peripheral and naive B cells. BCMA is also expressed on multiple myeloma (MM) cells, on leukemia cells and lymphoma cells. The amino acid sequence of human BCMA is shown in SEQ ID NO: 2320. The extracellular domain spans residues 1-54, the transmembrane domain spans residues 55-77 and the cytoplasmic domain spans residues 78-184 of SEQ ID NO: 2320.

[00135] SEQ ID NO: 2320 (BCMA)

MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWT
CLGLSLIISLAVFVLMFLLRKINSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGL
EYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEK
SISAR

[00136] "**PSMA**" refers to Prostate Specific Membrane Antigen. The amino acid sequence of the human PSMA is shown in SEQ ID NO: 2321. The extracellular domain spans residues 44 - 750, the transmembrane domain spans residues 20 - 43 and the cytoplasmic domain spans residues 1 - 19 of SEQ ID NO: 2321.

[00137] SEQ ID NO: 2321 (PSMA)

MWNLLHETDSAVATARRPRWLCAGALVLAGGFFLLGFLFGWFIKSSNEATNITPKHN
MKAFLDELKAENIKKFLYNFTQIPHLAGTEQNFQLAKQIQSQWKEFGLDSVELAHYDV
LLSYPNKTHPNYISIINEDGNEIFNTSLFEPPPPGYENVSDIVPPFSAFSPQGMPEGDLVYV
NYARTEDFFKLERDMKINCSGKIVIARYGKVFRGNKVKNAQLAGAKGVILYSDPADYF
APGVKSYPDGWNLPGGGVQRGNILNLNGAGDPLTPGYPANEYAYRRGIAEAVGLPSIP
VHPIGYYDAQKLLEKMGGSAPPDSSWRGSLKVPYNVGPGFTGNFSTQKVKMHIHSTNE
VTRIYNVIGTLRGAVEPDRYVILGGHRDSWVFGGIDPQSGAAVVHEIVRSFGTLKKEG
WRPRRTILFASWDAEEFGLLGSTEWAEENSRLLQERGVAYINADSSIEGNYTLRVDCTP
LMYSLVHNLTKELKSPDEGFEGKSLYESWTKKSPSPEFSGMPRISKLGSGNDFEVFFQR
LGIASGRARYTKNWETNKFSGYPLYHSVYETYELVEKFYDPMFKYHLTVAQVRGGMV
FELANSIVLPFDCRDYAVVLRKYADKIYSISMKHPQEMKTYSVSFDSLFSAVKNFTEIAS
KFSERLQDFDKSNPIVLRMMNDQLMFLERAFIDPLGLPDRPFYRHVIYAPSSHNKYAGE
SFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAAETLSEVA

[00138] The numbering of amino acid residues in the antibody constant region throughout the specification is according to the EU index as described in Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD. (1991), unless otherwise explicitly stated. Various antibody numbering schemes are available at ImMunoGeneTics (IMGT) website via IMGT scientific charts.

[00139] Mutations in the Ig constant regions are referred to as follows: L351Y_F405A_Y407V refers to L351Y, F405A and Y407V mutations in an immunoglobulin chain. L351Y_F405A_Y407V/T394W refers to L351Y, F405A and Y407V mutations in a first

immunoglobulin chain and T394W mutation in the second immunoglobulin chain in a heterodimeric molecule comprising both the first and the second immunoglobulin chains.

[00140] Compositions of matter

[00141] The disclosure provides molecules having improved characteristics and functionality. The molecules of the disclosure selectively activate or recruit $CD8^+$ CTLs without activating or recruiting non-CTL CD8 expressing cells. Without wishing to be bound by any particular theory, it is expected that the molecules of the disclosure provide a benefit in terms of therapeutic treatment when compared to other T cell redirecting molecules, mediating more efficient killing or undesired cells and exhibiting reduced side effect profile, particularly cytokine release syndrome observed with CD3 binding T cell redirecting molecules. The molecules of the disclosure may be utilized broadly to deplete or partially deplete any undesired cell, such as cancer cell, a virus infected cell, an immune cell, an inflamed cell, a damaged cell, a dysplastic cell, an immunogenic cell, a metaplastic cell or a mutant cell, or any combination thereof. The molecules of the disclosure therefore have utility across a spectrum of disease indications including cancer, infectious disease and immune-mediated diseases. The molecules of the disclosure have been designed in a manner that co-engagement of CD8 and CD3 is needed for activation and/or recruitment of the $CD8^+$ CTLs. The molecules of the disclosure may be used to treat any mammalian or non-mammalian subject. The molecules of the disclosure may also be used to isolate, separate, purify, sort, select or capture $CD8^+$ CTLs.

[00142] The disclosure provides an isolated molecule, comprising: a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds a TCR complex.

[00143] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex, and the third antigen binding domain specifically binds a third antigen.

[00144] In some embodiments, the third antigen comprises an antigen expressed by an undesired cell.

[00145] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first

antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell.

[00146] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8.

[00147] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[00148] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds the TCR with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of the TCR complex and CD8.

[00149] In some embodiments, the isolated molecule is an isolated antibody.

[00150] In some embodiments, the isolated molecule is based on one or more non-antibody scaffolds.

[00151] The disclosure also provides an isolated multispecific antibody, comprising: a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds a TCR complex.

[00152] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex, and the third antigen binding domain specifically binds a third antigen.

[00153] In some embodiments, the third antigen comprises an antigen expressed by an undesired cell.

[00154] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell.

[00155] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8.

[00156] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and wherein the isolated multispecific antibody is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[00157] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds the TCR complex with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of the TCR complex and CD8.

[00158] The affinities (*e.g.,* binding affinities) with which the isolated molecules or isolated multispecific antibodies of the disclosure bind to the various antigens are expressed as dissociation constants (K_D).

[00159] In some embodiments, the first antigen binding domain specifically binds CD8 with the K_D of about $0.1x10^{-9}$ M or higher, such as about $0.2x10^{-9}$ M or higher, about $0.3x10^{-9}$ M or higher, about $0.4x10^{-9}$ M or higher, about $0.5x10^{-9}$ M or higher, about $0.6x10^{-9}$ M or higher, about $0.7x10^{-9}$ M or higher, about $0.8x10^{-9}$ M or higher, about $0.9x10^{-9}$ M or higher, $1x10^{-9}$ M or higher, about $2x10^{-9}$ M or higher, about $3x10^{-9}$ M or higher, about $4x10^{-9}$ M or higher, about $5x10^{-9}$ M or higher, about $6x10^{-9}$ M or higher, about $7x10^{-9}$ M or higher, about $8x10^{-9}$ M or higher, about $9x10^{-9}$ M or higher, about $10x10^{-9}$ M or higher, about $15x10^{-9}$ M or higher, about $20x10^{-9}$ M or higher, about $25x10^{-9}$ M or higher, about $30x10^{-9}$ M or higher, about $35x10^{-9}$ M or higher, about $40x10^{-9}$ M or higher, about $45x10^{-9}$ M or higher, $50x10^{-9}$ M or higher, about $55x10^{-9}$ M or higher, about $60x10^{-9}$ M or higher, about $65x10^{-9}$ M or higher, about $70x10^{-9}$ M or higher, about $75x10^{-9}$ M or higher, about $80x10^{-9}$ M or higher, about $85x10^{-9}$ M or higher, about $90x10^{-9}$ M or higher, about $95x10^{-9}$ M or higher, about $100x10^{-9}$ M or higher, about $110x10^{-9}$ M or higher, about $120x10^{-9}$ M or higher, about $130x10^{-9}$ M or higher, about $140x10^{-9}$ M or higher, about $150x10^{-9}$ M or higher, about $160x10^{-9}$ M or higher, about $170x10^{-9}$ M or higher, about $180x10^{-9}$ M or higher, about $190x10^{-9}$ M or higher, about $200x10^{-9}$ M or higher, about $210x10^{-9}$ M or higher, about $220x10^{-9}$ M or higher, about $230x10^{-9}$ M or higher, about $240x10^{-9}$ M or higher, about $250x10^{-9}$ M or higher, about $260x10^{-9}$ M or higher, about $270x10^{-9}$ M or higher, about $280x10^{-9}$ M or higher, about $290x10^{-9}$ M or higher, about $300x10^{-9}$ M or higher, about $310x10^{-9}$ M or higher, about $320x10^{-9}$ M or higher, about $330x10^{-9}$ M or higher, about $340x10^{-9}$

M or higher, about $350x10^{-9}$ M or higher, about $360x10^{-9}$ M or higher, about $370x10^{-9}$ M or higher, about $380x10^{-9}$ M or higher, about $390x10^{-9}$ M or higher, about $400x10^{-9}$ M or higher, about $410x10^{-9}$ M or higher, about $420x10^{-9}$ M or higher, about $430x10^{-9}$ M or higher, about $440x10^{-9}$ M or higher, about $450x10^{-9}$ M or higher, about $460x10^{-9}$ M or higher, about $470x10^{-9}$ M or higher, about $480x10^{-9}$ M or higher, about $490x10^{-9}$ M or higher, about $400x10^{-9}$ M or higher, about $510x10^{-9}$ M or higher, about $520x10^{-9}$ M or higher, about $530x10^{-9}$ M or higher, about $540x10^{-9}$ M or higher, about $550x10^{-9}$ M or higher, about $560x10^{-9}$ M or higher, about $570x10^{-9}$ M or higher, about $580x10^{-9}$ M or higher, about $590x10^{-9}$ M or higher, about $600x10^{-9}$ M or higher, about $610x10^{-9}$ M or higher, about $620x10^{-9}$ M or higher, about $630x10^{-9}$ M or higher, about $640x10^{-9}$ M or higher, about $650x10^{-9}$ M or higher, about $660x10^{-9}$ M or higher, about $670x10^{-9}$ M or higher, about $680x10^{-9}$ M or higher, about $690x10^{-9}$ M or higher, about $700x10^{-9}$ M or higher, about $710x10^{-9}$ M or higher, about $720x10^{-9}$ M or higher, about $730x10^{-9}$ M or higher, about $740x10^{-9}$ M or higher, about $750x10^{-9}$ M or higher, about $760x10^{-9}$ M or higher, about $770x10^{-9}$ M or higher, about $780x10^{-9}$ M or higher, about $790x10^{-9}$ M or higher, about $800x10^{-9}$ M or higher, about $810x10^{-9}$ M or higher, about $820x10^{-9}$ M or higher, about $830x10^{-9}$ M or higher, about $840x10^{-9}$ M or higher, about $850x10^{-9}$ M or higher, about $860x10^{-9}$ M or higher, about $870x10^{-9}$ M or higher, about $880x10^{-9}$ M or higher, about $890x10^{-9}$ M or higher, about $900x10^{-9}$ M or higher, about $910x10^{-9}$ M or higher, about $920x10^{-9}$ M or higher, about $930x10^{-9}$ M or higher, about $940x10^{-9}$ M or higher, about $950x10^{-9}$ M or higher, about $960x10^{-9}$ M or higher, about $970x10^{-9}$ M or higher, about $980x10^{-9}$ M or higher, about $990x10^{-9}$ M or higher or about $1,000x10^{-9}$ M or higher.

[00160] In some embodiments, the first antigen binding domain specifically binds CD8 with the K_D of from about $0.1x10^{-9}$ M to about $1,000x10^{-9}$ M. In some embodiments, the first antigen binding domain specifically binds CD8 with the K_D of from about $0.5x10^{-9}$ M to about $700x10^{-9}$ M. In some embodiments, the first antigen binding domain specifically binds CD8 with the K_D of from about $0.5x10^{-9}$ M to about $500x10^{-9}$ M. In some embodiments, the first antigen binding domain specifically binds CD8 with the K_D of from about $0.5x10^{-9}$ M to about $400x10^{-9}$ M. In some embodiments, the first antigen binding domain specifically binds CD8 with the K_D of from about $1x10^{-9}$ M to about $400x10^{-9}$ M. In some embodiments, the first antigen binding domain specifically binds CD8 with the K_D of from about $0.5x10^{-9}$ M to about $300x10^{-9}$ M. In

some embodiments, the first antigen binding domain specifically binds CD8 with the K_D of from about $1x10^{-9}$ M to about $300x10^{-9}$ M.

[00161] In some embodiments, the first antigen binding domain specifically binds CD8 with the K_D of about $0.1x10^{-9}$ M, such as about $0.2x10^{-9}$ M, about $0.3x10^{-9}$ M, about $0.4x10^{-9}$ M, about $0.5x10^{-9}$ M, about $0.6x10^{-9}$ M, about $0.7x10^{-9}$ M, about $0.8x10^{-9}$ M, about $0.9x10^{-9}$ M, about $50x10^{-9}$ M, about $55x10^{-9}$ M, about $60x10^{-9}$ M, about $65x10^{-9}$ M, about $70x10^{-9}$ M, about $75x10^{-9}$ M, about $80x10^{-9}$ M, about $85x10^{-9}$ M, about $90x10^{-9}$ M, about $95x10^{-9}$ M, about $100x10^{-9}$ M, about $110x10^{-9}$ M, about $120x10^{-9}$ M, about $130x10^{-9}$ M, about $140x10^{-9}$ M, about $150x10^{-9}$ M, about $160x10^{-9}$ M, about $170x10^{-9}$ M, about $180x10^{-9}$ M, about $190x10^{-9}$ M, about $200x10^{-9}$ M, about $210x10^{-9}$ M, about $220x10^{-9}$ M, about $230x10^{-9}$ M, about $240x10^{-9}$ M, about $250x10^{-9}$ M, about $260x10^{-9}$ M, about $270x10^{-9}$ M, about $280x10^{-9}$ M, about $290x10^{-9}$ M, about $300x10^{-9}$ M, about $310x10^{-9}$ M, about $320x10^{-9}$ M, about $330x10^{-9}$ M, about $340x10^{-9}$ M, about $350x10^{-9}$ M, about $360x10^{-9}$ M, about $370x10^{-9}$ M, about $380x10^{-9}$ M, about $390x10^{-9}$ M, about $400x10^{-9}$ M, about $410x10^{-9}$ M, about $420x10^{-9}$ M, about $430x10^{-9}$ M, about $440x10^{-9}$ M, about $450x10^{-9}$ M, about $460x10^{-9}$ M, about $470x10^{-9}$ M, about $480x10^{-9}$ M, about $490x10^{-9}$ M, about $400x10^{-9}$ M, about $510x10^{-9}$ M, about $520x10^{-9}$ M, about $530x10^{-9}$ M, about $540x10^{-9}$ M, about $550x10^{-9}$ M, about $560x10^{-9}$ M, about $570x10^{-9}$ M, about $580x10^{-9}$ M, about $590x10^{-9}$ M, about $600x10^{-9}$ M, about $610x10^{-9}$ M, about $620x10^{-9}$ M, about $630x10^{-9}$ M, about $640x10^{-9}$ M, about $650x10^{-9}$ M, about $660x10^{-9}$ M, about $670x10^{-9}$ M, about $680x10^{-9}$ M, about $690x10^{-9}$ M, about $700x10^{-9}$ M, about $710x10^{-9}$ M, about $720x10^{-9}$ M, about $730x10^{-9}$ M, about $740x10^{-9}$ M, about $750x10^{-9}$ M, about $760x10^{-9}$ M, about $770x10^{-9}$ M, about $780x10^{-9}$ M, about $790x10^{-9}$ M, about $800x10^{-9}$ M, about $810x10^{-9}$ M, about $820x10^{-9}$ M, about $830x10^{-9}$ M, about $840x10^{-9}$ M, about $850x10^{-9}$ M, about $860x10^{-9}$ M, about $870x10^{-9}$ M, about $880x10^{-9}$ M, about $890x10^{-9}$ M, about $900x10^{-9}$ M, about $910x10^{-9}$ M, about $920x10^{-9}$ M, about $930x10^{-9}$ M, about $940x10^{-9}$ M, about $950x10^{-9}$ M, about $960x10^{-9}$ M, about $970x10^{-9}$ M, about $980x10^{-9}$ M, about $990x10^{-9}$M, or about $1,000x10^{-9}$ M.

[00162] In some embodiments, the second antigen binding domain specifically binds the TCR complex with the K_D of about $10x10^{-9}$ M or higher, such as about $20x10^{-9}$ M or higher, about $30x10^{-9}$ M or higher, about $40x10^{-9}$ M or higher, about $50x10^{-9}$ M or higher, such as about $55x10^{-9}$ M or higher, about $60x10^{-9}$ M or higher, about $65x10^{-9}$ M or higher, about $70x10^{-9}$ M or higher, about $75x10^{-9}$ M or higher, about $80x10^{-9}$ M or higher, about $85x10^{-9}$ M or higher, about

$90x10^{-9}$ M or higher, about $95x10^{-9}$ M or higher, about $100x10^{-9}$ M or higher, about $110x10^{-9}$ M or higher, about $120x10^{-9}$ M or higher, about $130x10^{-9}$ M or higher, about $140x10^{-9}$ M or higher, about $150x10^{-9}$ M or higher, about $160x10^{-9}$ M or higher, about $170x10^{-9}$ M or higher, about $180x10^{-9}$ M or higher, about $190x10^{-9}$ M or higher, about $200x10^{-9}$ M or higher, about $210x10^{-9}$ M or higher, about $220x10^{-9}$ M or higher, about $230x10^{-9}$ M or higher, about $240x10^{-9}$ M or higher, about $250x10^{-9}$ M or higher, about $260x10^{-9}$ M or higher, about $270x10^{-9}$ M or higher, about $280x10^{-9}$ M or higher, about $290x10^{-9}$ M or higher, about $300x10^{-9}$ M or higher, about $310x10^{-9}$ M or higher, about $320x10^{-9}$ M or higher, about $330x10^{-9}$ M or higher, about $340x10^{-9}$ M or higher, about $350x10^{-9}$ M or higher, about $360x10^{-9}$ M or higher, about $370x10^{-9}$ M or higher, about $380x10^{-9}$ M or higher, about $390x10^{-9}$ M or higher, about $400x10^{-9}$ M or higher, about $410x10^{-9}$ M or higher, about $420x10^{-9}$ M or higher, about $430x10^{-9}$ M or higher, about $440x10^{-9}$ M or higher, about $450x10^{-9}$ M or higher, about $460x10^{-9}$ M or higher, about $470x10^{-9}$ M or higher, about $480x10^{-9}$ M or higher, about $490x10^{-9}$ M or higher, about $400x10^{-9}$ M or higher, about $510x10^{-9}$ M or higher, about $520x10^{-9}$ M or higher, about $530x10^{-9}$ M or higher, about $540x10^{-9}$ M or higher, about $550x10^{-9}$ M or higher, about $560x10^{-9}$ M or higher, about $570x10^{-9}$ M or higher, about $580x10^{-9}$ M or higher, about $590x10^{-9}$ M or higher, about $600x10^{-9}$ M or higher, about $610x10^{-9}$ M or higher, about $620x10^{-9}$ M or higher, about $630x10^{-9}$ M or higher, about $640x10^{-9}$ M or higher, about $650x10^{-9}$ M or higher, about $660x10^{-9}$ M or higher, about $670x10^{-9}$ M or higher, about $680x10^{-9}$ M or higher, about $690x10^{-9}$ M or higher, about $700x10^{-9}$ M or higher, about $710x10^{-9}$ M or higher, about $720x10^{-9}$ M or higher, about $730x10^{-9}$ M or higher, about $740x10^{-9}$ M or higher, about $750x10^{-9}$ M or higher, about $760x10^{-9}$ M or higher, about $770x10^{-9}$ M or higher, about $780x10^{-9}$ M or higher, about $790x10^{-9}$ M or higher, about $800x10^{-9}$ M or higher, about $810x10^{-9}$ M or higher, about $820x10^{-9}$ M or higher, about $830x10^{-9}$ M or higher, about $840x10^{-9}$ M or higher, about $850x10^{-9}$ M or higher, about $860x10^{-9}$ M or higher, about $870x10^{-9}$ M or higher, about $880x10^{-9}$ M or higher, about $890x10^{-9}$ M or higher, about $900x10^{-9}$ M or higher, about $910x10^{-9}$ M or higher, about $920x10^{-9}$ M or higher, about $930x10^{-9}$ M or higher, about $940x10^{-9}$ M or higher, about $950x10^{-9}$ M or higher, about $960x10^{-9}$ M or higher, about $970x10^{-9}$ M or higher, about $980x10^{-9}$ M or higher, about $990x10^{-9}$ M or higher or about $1{,}000x10^{-9}$ M or higher.

[00163] In some embodiments, the second antigen binding domain specifically binds the TCR complex with the K_D of from about $50x10^{-9}$ M to about $1{,}000x10^{-9}$ M. In some embodiments, the

second antigen binding domain specifically binds the TCR complex with the K_D of from about $50x10^{-9}$ M to about $700x10^{-9}$ M. In some embodiments, the second antigen binding domain specifically binds the TCR complex with the K_D of from about $50x10^{-9}$ M to about $500x10^{-9}$ M. In some embodiments, the second antigen binding domain specifically binds the TCR complex with the K_D of from about $50x10^{-9}$ M to about $400x10^{-9}$ M. In some embodiments, the second antigen binding domain specifically binds the TCR complex with the K_D of from about $100x10^{-9}$ M to about $400x10^{-9}$ M. In some embodiments, the second antigen binding domain specifically binds the TCR complex with the K_D of from about $50x10^{-9}$ M to about $300x10^{-9}$ M. In some embodiments, the second antigen binding domain specifically binds the TCR complex with the K_D of from about $100x10^{-9}$ M to about $300x10^{-9}$ M.

[00164] In some embodiments, the second antigen binding domain specifically binds the TCR complex with the K_D of about $50x10^{-9}$ M, about $55x10^{-9}$ M, about $60x10^{-9}$ M, about $65x10^{-9}$ M, about $70x10^{-9}$ M, about $75x10^{-9}$ M, about $80x10^{-9}$ M, about $85x10^{-9}$ M, about $90x10^{-9}$ M, about $95x10^{-9}$ M, about $100x10^{-9}$ M, about $110x10^{-9}$ M, about $120x10^{-9}$ M, about $130x10^{-9}$ M, about $140x10^{-9}$ M, about $150x10^{-9}$ M, about $160x10^{-9}$ M, about $170x10^{-9}$ M, about $180x10^{-9}$ M, about $190x10^{-9}$ M, about $200x10^{-9}$ M, about $210x10^{-9}$ M, about $220x10^{-9}$ M, about $230x10^{-9}$ M, about $240x10^{-9}$ M, about $250x10^{-9}$ M, about $260x10^{-9}$ M, about $270x10^{-9}$ M, about $280x10^{-9}$ M, about $290x10^{-9}$ M, about $300x10^{-9}$ M, about $310x10^{-9}$ M, about $320x10^{-9}$ M, about $330x10^{-9}$ M, about $340x10^{-9}$ M, about $350x10^{-9}$ M, about $360x10^{-9}$ M, about $370x10^{-9}$ M, about $380x10^{-9}$ M, about $390x10^{-9}$ M, about $400x10^{-9}$ M, about $410x10^{-9}$ M, about $420x10^{-9}$ M, about $430x10^{-9}$ M, about $440x10^{-9}$ M, about $450x10^{-9}$ M, about $460x10^{-9}$ M, about $470x10^{-9}$ M, about $480x10^{-9}$ M, about $490x10^{-9}$ M, about $400x10^{-9}$ M, about $510x10^{-9}$ M, about $520x10^{-9}$ M, about $530x10^{-9}$ M, about $540x10^{-9}$ M, about $550x10^{-9}$ M, about $560x10^{-9}$ M, about $570x10^{-9}$ M, about $580x10^{-9}$ M, about $590x10^{-9}$ M, about $600x10^{-9}$ M, about $610x10^{-9}$ M, about $620x10^{-9}$ M, about $630x10^{-9}$ M, about $640x10^{-9}$ M, about $650x10^{-9}$ M, about $660x10^{-9}$ M, about $670x10^{-9}$ M, about $680x10^{-9}$ M, about $690x10^{-9}$ M, about $700x10^{-9}$ M, about $710x10^{-9}$ M, about $720x10^{-9}$ M, about $730x10^{-9}$ M, about $740x10^{-9}$ M, about $750x10^{-9}$ M, about $760x10^{-9}$ M, about $770x10^{-9}$ M, about $780x10^{-9}$ M, about $790x10^{-9}$ M, about $800x10^{-9}$ M, about $810x10^{-9}$ M, about $820x10^{-9}$ M, about $830x10^{-9}$ M, about $840x10^{-9}$ M, about $850x10^{-9}$ M, about $860x10^{-9}$ M, about $870x10^{-9}$ M, about $880x10^{-9}$ M, about $890x10^{-9}$ M, about $900x10^{-9}$ M, about $910x10^{-9}$ M, about $920x10^{-9}$ M, about $930x10^{-9}$ M, about

940x10^{-9} M, about 950x10^{-9} M, about 960x10^{-9} M, about 970x10^{-9} M, about 980x10^{-9} M, about 990x10^{-9} M, or about 1,000x10^{-9} M.

[00165] In some embodiments, the third antigen binding domain specifically binds the antigen expressed by the undesired cell with the K_D of about 5x10^{-8} M or less, such as about 1x10^{-8} M or less, about 5x10^{-9} M or less, about 1x10^{-9} M or less, about 5x10^{-10} M or less, about 1x10^{-10} M or less, about 5x10^{-11} M or less, about 1x10^{-11} M or less, about 5x10^{-12} M or less, about 1x10^{-12} M or less, about 5x10^{-13} M or less, about 1x10^{-13} M or less, about 5x10^{-14} M or less, about 1x10^{-14} M or less, about 5x10^{-15} M or less or about 1x10^{-15}M or less.

[00166] In some embodiments, the third antigen binding domain specifically binds the antigen expressed by the undesired cell with the K_D of from about 5x10^{-8} M to about 1x10^{-15} M. In some embodiments, the third antigen binding domain specifically binds the antigen expressed by the undesired cell with the K_D of from about 1x10^{-9} M to about 1x10^{-15} M. In some embodiments, the third antigen binding domain specifically binds the antigen expressed by the undesired cell with the K_D of from about 5x10^{-10} M to about 1x10^{-15} M. In some embodiments, the third antigen binding domain specifically binds the antigen expressed by the undesired cell with the K_D of from about 1x10^{-10} M to about 1x10^{-15} M. In some embodiments, the third antigen binding domain specifically binds the antigen expressed by the undesired cell with the K_D of from about 5x10^{-11} M to about 1x10^{-15} M. In some embodiments, the third antigen binding domain specifically binds the antigen expressed by the undesired cell with the K_D of from about 1x10^{-11} M to about 1x10^{-15} M.

[00167] In some embodiments, the third antigen binding domain specifically binds the antigen expressed by the undesired cell with the K_D of about 5x10^{-8} M, such as about 1x10^{-8} M, about 5x10^{-9} M, about 1x10^{-9} M, about 5x10^{-10} M, about 1x10^{-10} M, about 5x10^{-11} M, about 1x10^{-11} M, about 5x10^{-12} M, about 1x10^{-12} M, about 5x10^{-13} M, about 1x10^{-13} M, about 5x10^{-14} M, about 1x10^{-14} M, about 5x10^{-15} M, or about 1x10^{-15} M.

[00168] In some embodiments, the first antigen binding domain specifically binds CD8 with the K_D of from about 0.1x10^{-9} M to about 1,000x10^{-9} M and the second antigen binding domain specifically binds the TCR complex with the K_D of from about 50x10^{-9} M to about 1,000x10^{-9} M. In some embodiments, the first antigen binding domain specifically binds CD8 with the K_D of from about 0.5x10^{-9} M to about 500x10^{-9} M and the second antigen binding domain specifically binds the TCR complex with the K_D of from about 50x10^{-9} M to about 500x10^{-9} M.

In some embodiments, the first antigen binding domain specifically binds CD8 with the K_D of from about $1x10^{-9}$ M to about $500x10^{-9}$ M and the second antigen binding domain specifically binds the TCR complex with the K_D of from about $100x10^{-9}$ M to about $500x10^{-9}$ M.

[00169] In some embodiments, the first antigen binding domain specifically binds CD8 with the K_D about $0.5x10^{-9}$ M or higher and the second antigen binding domain specifically binds the TCR complex with the K_D of about $50x10^{-9}$ M or higher. In some embodiments, the first antigen binding domain specifically binds CD8 with the K_D about $1x10^{-9}$ M or higher and the second antigen binding domain specifically binds the TCR complex with the K_D of about $100x10^{-9}$ M or higher.

[00170] In some embodiments, the first antigen binding domain specifically binds CD8 with the K_D of from about $0.1x10^{-9}$ M to about $1,000x10^{-9}$ M, the second antigen binding domain specifically binds the TCR complex with the K_D of from about $50x10^{-9}$ M to about $1,000x10^{-9}$ M, and the third antigen binding domain specifically binds the antigen expressed by the undesired cell with the K_D of from about $5x10^{-8}$ M to about $1x10^{-15}$ M. In some embodiments, the first antigen binding domain specifically binds CD8 with the K_D of from about $0.5x10^{-9}$ M to about $500x10^{-9}$ M, the second antigen binding domain specifically binds the TCR complex with the K_D of from about $50x10^{-9}$ M to about $500x10^{-9}$ M, and the third antigen binding domain specifically binds the antigen expressed by the undesired cell with the K_D of from about $1x10^{-9}$ M to about $1x10^{-15}$ M. In some embodiments, the first antigen binding domain specifically binds CD8 with the K_D of from about $1x10^{-9}$ M to about $500x10^{-9}$ M, the second antigen binding domain specifically binds the TCR complex with the K_D of from about $100x10^{-9}$ M to about $500x10^{-9}$ M, and the third antigen binding domain specifically binds the antigen expressed by the undesired cell with the K_D of from about $1x10^{-10}$ M to about $1x10^{-15}$ M.

[00171] In some embodiments, the first antigen binding domain specifically binds CD8 with the K_D about $0.5x10^{-9}$ M or higher, the second antigen binding domain specifically binds the TCR complex with the K_D of about $50x10^{-9}$ M or higher, and the third antigen binding domain specifically binds the antigen expressed by the undesired cell with the K_D of about $1x10^{-8}$ M or less. In some embodiments, the first antigen binding domain specifically binds CD8 with the K_D about $1x10^{-9}$ M or higher, the second antigen binding domain specifically binds the TCR complex with the K_D of about $100x10^{-9}$ M or higher, and the third antigen binding domain

specifically binds the antigen expressed by the undesired cell with the K_D of about $1x10^{-9}$ M or less.

[00172] In some embodiments, the first antigen binding domain comprises a scFv, a Fab, a Fab', a $F(ab')_2$, a Fd, a Fv, a domain antibody (dAb), a VHH domain, a VH, a VL, a non-antibody scaffold, or fragments thereof. In some embodiments, the second antigen binding domain comprises a scFv, a Fab, a Fab', a $F(ab')_2$, a Fd, a Fv, a dAb, a VHH domain, a VH, a VL, a non-antibody scaffold, or fragments thereof. In some embodiments, the third antigen binding domain comprises a scFv, a Fab, a Fab', a $F(ab')_2$, a Fd, a Fv, a dAb, a VHH domain, a VH, a VL, a non-antibody scaffold, or fragments thereof.

[00173] In some embodiments, the first antigen binding domain comprises a scFv. In some embodiments, the first antigen binding domain comprises a Fab. In some embodiments, the first antigen binding domain comprises a Fab'. In some embodiments, the first antigen binding domain comprises a $F(ab')_2$. In some embodiments, the first antigen binding domain comprises a Fd. In some embodiments, the first antigen binding domain comprises a Fv. In some embodiments, the first antigen binding domain comprises a dAb. In some embodiments, the first antigen binding domain comprises a VHH. In some embodiments, the first antigen binding domain comprises a VH. In some embodiments, the first antigen binding domain comprises a VL. In some embodiments, the first antigen binding domain comprises a non-antibody scaffold. In some embodiments, the second antigen binding domain comprises a scFv. In some embodiments, the second antigen binding domain comprises a Fab. In some embodiments, the second antigen binding domain comprises a Fab'. In some embodiments, the second antigen binding domain comprises a $F(ab')_2$. In some embodiments, the second antigen binding domain comprises a Fd. In some embodiments, the second antigen binding domain comprises a Fv. In some embodiments, the second antigen binding domain comprises a dAb. In some embodiments, the second antigen binding domain comprises a VHH. In some embodiments, the second antigen binding domain comprises a VH. In some embodiments, the second antigen binding domain comprises a VL. In some embodiments, the second antigen binding domain comprises a non-antibody scaffold. In some embodiments, the third antigen binding domain comprises a scFv. In some embodiments, the third antigen binding domain comprises a Fab. In some embodiments, the third antigen binding domain comprises a Fab'. In some embodiments, the third antigen binding domain comprises a $F(ab')_2$. In some embodiments, the

third antigen binding domain comprises a Fd. In some embodiments, the third antigen binding domain comprises a Fv. In some embodiments, the third antigen binding domain comprises a dAb. In some embodiments, the third antigen binding domain comprises a VHH. In some embodiments, the third antigen binding domain comprises a VH. In some embodiments, the third antigen binding domain comprises a VL. In some embodiments, the third antigen binding domain comprises a non-antibody scaffold. In some embodiments, the first antigen binding domain comprises a scFv, the second antigen binding domain comprises a scFv and the third antigen binding domain comprises a Fab.

[00174] The disclosure also provides an isolated molecule, comprising: a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a second antigen binding domain comprising a scFv that specifically binds a TCR complex, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain; the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc.

[00175] The disclosure also provides an isolated molecule, comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain; the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8, a CL domain and a second antigen binding domain comprising a scFv that specifically binds a TCR complex; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc.

[00176] The disclosure also provides an isolated molecule, comprising: a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a VH that is capable of specifically CD8, a CH1 domain, a hinge, a CH2 domain, a CH3 domain and a second antigen binding domain comprising a scFv that specifically binds a TCR complex; the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and the third polypeptide comprises, from N- to C-

terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc.

[00177] "**Capable of specifically binding**" in the context of CD8 refers to VH and VL which specifically bind CD8 when they associate to form an antigen binding domain. The VH that is capable of specifically binding CD8 may specifically bind CD8 in the absence of the VL in instances when most paratope residues reside in the VH.

[00178] In some embodiments, first antigen binding domain comprising the Fab, the second antigen binding domain comprising the scFv or the third antigen binding domain comprising the scFv is conjugated to the Fc or the fragment of the Fc, to the VH that is capable of specifically biding CD8, to the CL domain or to the CH3 domain via a linker.

[00179] In some embodiments, the linker comprises a polypeptide having an amino acid sequence of any one of SEQ ID NOs: 2183-2290.

[00180] In some embodiments, the fragment of the Fc comprises a CH2 domain and a CH3 domain.

[00181] In some embodiments, the CH3 domain comprises one or more substitutions when compared to a wild-type CH3 domain. An exemplary wild-type CH3 domain is an IgG1 CH3 domain having the amino acid sequence of SEQ ID NO: 2319.

[00182] In some embodiments, the one or more substitutions comprise T350V, L351Y, F405A,Y407V, T366Y, T366W, F405W, T394W, T394S, Y407T, Y407A, T366S/L368A/Y407V, L351Y/F405A/Y407V, T366I/K392M/T394W, F405A/Y407V, T366L/K392M/T394W, L351Y/Y407A, T366A/K409F, L351Y/Y407A, T366V/K409F, T366A/K409F, T350V/L351Y/F405A/Y407V or T350V/T366L/K392L/T394W, wherein residue numbering is according to the EU index.

[00183] In some embodiments, the Fc, the CH2 domain or the CH3 domain is an IgG1 isotype. In some embodiments, the Fc, the CH2 domain or the CH3 domain is an IgG2 isotype. In some embodiments, the Fc, the CH2 domain or the CH3 domain is an IgG3 isotype. In some embodiments, the Fc, the CH2 domain or the CH3 domain is an IgG4 isotype.

[00184] In some embodiments, the second antigen binding domain specifically binds CD3, TCRα chain, TCRβ chain, TCRγ chain or TCRδ chain, or any combination thereof. In some embodiments, the second antigen binding domain specifically binds CD3. In some embodiments, the second antigen binding domain specifically binds CD3ε. In some

embodiments, the second antigen binding domain specifically binds TCRα chain. In some embodiments, the second antigen binding domain specifically binds TCRβ chain. In some embodiments, the second antigen binding domain specifically binds TCRγ chain. In some embodiments, the second antigen binding domain specifically binds TCRδ chain.

[00185] In some embodiments, the TCRβ chain comprises TCRVB17.

[00186] In some embodiments, CD3 comprises CD3ε, CD3γ, CD3δ or CD3ζ. In some embodiments, CD3 comprises CD3ε. In some embodiments, CD3 comprises CD3γ. In some embodiments, CD3 comprises CD3δ. In some embodiments, CD3 comprises CD3ζ.

[00187] In some embodiments, the TCR complex and the CD8 are from a mammal. In some embodiments, the TCR complex and the CD8 are from a rodent. In some embodiments, the TCR complex and the CD8 are from a human. In some embodiments, the TCR complex and the CD8 are from a monkey. In some embodiments, the TCR complex and the CD8 are from a dog. In some embodiments, the TCR complex and the CD8 are from a rat. In some embodiments, the TCR complex and the CD8 are from a mouse.

[00188] In some embodiments, the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312.

[00189] In some embodiments, the first antigen binding domain that specifically binds CD8 comprises the VH of SEQ ID NO: 2313 and the VL of SEQ ID NO: 2314.

[00190] In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:31; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:32. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:65; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an

amino acid sequence of SEQ ID NO:66. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:99; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:100. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:133; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:134. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:167; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:168. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:201; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:202. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:235; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:236. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH

CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:269; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:270. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:303; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:304. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:337; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:338. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:371; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:372. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:405; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:406. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:439; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL

CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:440. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:473; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:474. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:507; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:508. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:541; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:542. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:575; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:576. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:609; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:610. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an

amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:643; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:644. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:677; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:678. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:711; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:712. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:745; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:746. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:779; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:780. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:813; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL

CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:814. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:847; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:848. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:881; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:882. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:915; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:916. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:949; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:950. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:983; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:984. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH

CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1017; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1018. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1051; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1052. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1085; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1086. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1119; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1120. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1153; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1154. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1187; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having

an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1188. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1221; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1222. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1255; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1256. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1289; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1290. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1323; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1324. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1357; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1358. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH

comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1391; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1392. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1425; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1426. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1459; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1460. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1493; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1494. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1527; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1528. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1561; and (ii) a VL comprising a VL CDR1, a

VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1562. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1595; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1596. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1629; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1630. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1663; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1664. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1697; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1698. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1731; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1732. In some embodiments, the first antigen binding domain that specifically

binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1765; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1766. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1799; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1800. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1833; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1834. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1867; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1868. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1901; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1902. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1935; and (ii) a VL

comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1936. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1969; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1970. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:2003; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:2004. In another aspect, provided herein is an antibody that binds CD8. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:2037; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:2038. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:2071; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:2072. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:2105; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL

having an amino acid sequence of SEQ ID NO:2106. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:2139; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:2140. In some embodiments, the first antigen binding domain that specifically binds CD8 comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:2173; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:2174.

[00191] In some embodiments, the VH CDR1, VH CDR2, VH CDR3, VL CDR1, VL CDR2, and VL CDR3 amino acid sequences of the first antigen binding domain that specifically binds CD8 are according to the Kabat numbering system. In some embodiments, the VH CDR1, VH CDR2, VH CDR3, VL CDR1, VL CDR2, and VL CDR3 amino acid sequences of the first antigen binding domain that specifically binds CD8 are according to the Chothia numbering system. In some embodiments, the VH CDR1, VH CDR2, VH CDR3, VL CDR1, VL CDR2, and VL CDR3 amino acid sequences of the first antigen binding domain that specifically binds CD8 are according to the AbM numbering system. In some embodiments, the VH CDR1, VH CDR2, VH CDR3, VL CDR1, VL CDR2, and VL CDR3 amino acid sequences of the first antigen binding domain that specifically binds CD8 are according to the Contact numbering system. In some embodiments, the VH CDR1, VH CDR2, VH CDR3, VL CDR1, VL CDR2, and VL CDR3 amino acid sequences of the first antigen binding domain that specifically binds CD8 are according to the IMGT numbering system.

[00192] In some embodiments, the first antigen binding domain that specifically binds CD8 binds a CD8 antigen. In some embodiments, the first antigen binding domain that specifically binds CD8 binds a CD8 epitope. In some embodiments, the VH CDR1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 and VL CDR3 form a binding site for an antigen of the CD8. In some embodiments, the VH CDR1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 and VL CDR3

form a binding site for an epitope of the CD8. In some embodiments, the CD8 is present on the surface of a T cell.

[00193] In some embodiments, the first antigen binding domain that specifically binds CD8 binds to CD8α. In some embodiments, the first antigen binding domain that specifically binds CD8 binds a CD8α antigen. In some embodiments, the first antigen binding domain that specifically binds CD8 binds a CD8α epitope. In some embodiments, the VH CDR1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 and VL CDR3 form a binding site for an antigen of the CD8α. In some embodiments, the VH CDR1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 and VL CDR3 form a binding site for an epitope of the CD8α. In some embodiments, the CD8α is present on the surface of a T cell.

[00194] In some embodiments, the first antigen binding domain that specifically binds CD8 binds to CD8β. In some embodiments, the first antigen binding domain that specifically binds CD8 binds a CD8β antigen. In some embodiments, the first antigen binding domain that specifically binds CD8 binds a CD8β epitope. In some embodiments, the VH CDR1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 and VL CDR3 form a binding site for an antigen of the CD8β. In some embodiments, the VH CDR1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 and VL CDR3 form a binding site for an epitope of the CD8β. In some embodiments, the CD8β is present on the surface of a T cell.

[00195] In some embodiments, the first antigen binding domain that specifically binds CD8 binds at the interface of CD8α and CD8β. In some embodiments, the first antigen binding domain that specifically binds CD8 binds an antigen at the interface of CD8α and CD8β. In some embodiments, the first antigen binding domain that specifically binds CD8 binds an epitope at the interface of CD8α and CD8β. In some embodiments, the VH CDR1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 and VL CDR3 form a binding site for an antigen at the interface of CD8α and CD8β. In some embodiments, the VH CDR1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 and VL CDR3 form a binding site for an epitope at the interface of CD8α and CD8β. In some embodiments, the interface of CD8α and CD8β is present on the surface of a T cell.

[00196] In some embodiments, the VH CDR1, VH CDR2, VH CDR3, VL CDR1, VL CDR2, and VL CDR3 sequences are according to the Kabat numbering system. In some embodiments, the VH CDR1, VH CDR2, VH CDR3, VL CDR1, VL CDR2, and VL CDR3 sequences are

according to the Chothia numbering system. In some embodiments, the VH CDR1, VH CDR2, VH CDR3, VL CDR1, VL CDR2, and VL CDR3 sequences are according to the Exemplary numbering system. In some embodiments, the VH CDR1, VH CDR2, VH CDR3, VL CDR1, VL CDR2, and VL CDR3 sequences are according to the Contact numbering system. In some embodiments, the VH CDR1, VH CDR2, VH CDR3, VL CDR1, VL CDR2, and VL CDR3 sequences are according to the IMGT numbering system. In some embodiments, the VH CDR1, VH CDR2, VH CDR3, VL CDR1, VL CDR2, and VL CDR3 sequences are according to the AbM numbering system. Exemplary sets of 6 CDRs (VH CDR1-3 and VL CDR1-3) of certain antibody embodiments are provided herein. Other sets of CDRs are contemplated and within the scope of the antibody embodiments provided herein.

[00197] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1, 2, and 3, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:4, 5, and 6, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:7, 8, and 9, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:10, 11, and 12, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:13, 14, and 15, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:16, 17, and 18, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:19, 20, and 21, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:22, 23, and 24, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:25, 26, and 27, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:28, 29, and 30, respectively. In one embodiment, the first antigen binding domain that specifically

binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:31; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:32. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence of SEQ ID NO:31. In one aspect, provided herein is an antibody that binds CD8, comprising a VL having an amino acid sequence of SEQ ID NO:32. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence of SEQ ID NO:31, and a VL having an amino acid sequence of SEQ ID NO:32. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence of SEQ ID NO:33. In one aspect, provided herein is an antibody that binds CD8, comprising a light chain having an amino acid sequence of SEQ ID NO:34. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence of SEQ ID NO:33, and a light chain having an amino acid sequence of SEQ ID NO:34. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:31. In one aspect, provided herein is an antibody that binds CD8, comprising a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:32. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:31, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:32. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:33. In one aspect, provided herein is an antibody that binds CD8, comprising a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:34. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:33, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:34.

[00198] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:35, 36, and 37, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:38, 39, and 40, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:41, 42, and 43, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:44, 45, and 46, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:47, 48, and 49, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:50, 51, and 52, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:53, 54, and 55, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:56, 57, and 58, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:59, 60, and 61, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:62, 63, and 64, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:65; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:66. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence of SEQ ID NO:65. In one aspect, provided herein is an antibody that binds CD8, comprising a VL having an amino acid sequence of SEQ ID NO:66. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence of SEQ ID NO:65, and a VL having an amino acid sequence of SEQ ID NO:66. In one aspect, provided herein is

an antibody that binds CD8, comprising a heavy chain having an amino acid sequence of SEQ ID NO:67. In one aspect, provided herein is an antibody that binds CD8, comprising a light chain having an amino acid sequence of SEQ ID NO:68. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence of SEQ ID NO:67, and a light chain having an amino acid sequence of SEQ ID NO:68. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:65. In one aspect, provided herein is an antibody that binds CD8, comprising a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:66. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:65, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:66. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:67. In one aspect, provided herein is an antibody that binds CD8, comprising a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:68. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:67, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:68.

[00199] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:69, 70, and 71, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:72, 73, and 74, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:75, 76, and 77, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:78, 79, and 80, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:81, 82, and 83, respectively, and (ii) a VL comprising a

VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:84, 85, and 86, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:87, 88, and 89, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:90, 91, and 92, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:93, 94, and 95, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:96, 97, and 98, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:99; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:100. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence of SEQ ID NO:99. In one aspect, provided herein is an antibody that binds CD8, comprising a VL having an amino acid sequence of SEQ ID NO:100. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence of SEQ ID NO:99, and a VL having an amino acid sequence of SEQ ID NO:100. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence of SEQ ID NO:101. In one aspect, provided herein is an antibody that binds CD8, comprising a light chain having an amino acid sequence of SEQ ID NO:102. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence of SEQ ID NO:101, and a light chain having an amino acid sequence of SEQ ID NO:102. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:99. In one aspect, provided herein is an antibody that binds CD8, comprising a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:100. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:99, and a VL having an

amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:100. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:101. In one aspect, provided herein is an antibody that binds CD8, comprising a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:102. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:101, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:102.

[00200] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:103, 104, and 105, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:106, 107, and 108, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:109, 110, and 111, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:112, 113, and 114, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:115, 116, and 117, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:118, 119, and 120, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:121, 122, and 123, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:124, 125, and 126, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:127, 128, and 129, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:130, 131, and 132, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a

VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:133; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:134. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence of SEQ ID NO:133. In one aspect, provided herein is an antibody that binds CD8, comprising a VL having an amino acid sequence of SEQ ID NO:134. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence of SEQ ID NO:133, and a VL having an amino acid sequence of SEQ ID NO:134. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence of SEQ ID NO:135. In one aspect, provided herein is an antibody that binds CD8, comprising a light chain having an amino acid sequence of SEQ ID NO:136. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence of SEQ ID NO:135, and a light chain having an amino acid sequence of SEQ ID NO:136. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:133. In one aspect, provided herein is an antibody that binds CD8, comprising a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:134. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:133, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:134. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:135. In one aspect, provided herein is an antibody that binds CD8, comprising a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:136. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:135, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:136.

[00201] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:137, 138, and 139, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:140, 141, and 142, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:143, 144, and 145, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:146, 147, and 148, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:149, 150, and 151, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:152, 153, and 154, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:155, 156, and 157, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:158, 159, and 160, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:161, 162, and 163, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:164, 165, and 166, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:167; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:168. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence of SEQ ID NO:167. In one aspect, provided herein is an antibody that binds CD8, comprising a VL having an amino acid sequence of SEQ ID NO:168. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence of SEQ ID NO:167, and a VL having an amino acid

sequence of SEQ ID NO:168. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence of SEQ ID NO:169. In one aspect, provided herein is an antibody that binds CD8, comprising a light chain having an amino acid sequence of SEQ ID NO:170. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence of SEQ ID NO:169, and a light chain having an amino acid sequence of SEQ ID NO:170. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:167. In one aspect, provided herein is an antibody that binds CD8, comprising a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:168. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:167, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:168. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:169. In one aspect, provided herein is an antibody that binds CD8, comprising a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:170. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:169, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:170.

[00202] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:171, 172, and 173, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:174, 175, and 176, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:177, 178, and 179, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:180, 181, and 182, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH

CDR3 having an amino acid sequence of SEQ ID NOs:183, 184, and 185, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:186, 187, and 188, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:189, 190, and 191, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:192, 193, and 194, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:195, 196, and 197, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:198, 199, and 200, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:201; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:202. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence of SEQ ID NO:201. In one aspect, provided herein is an antibody that binds CD8, comprising a VL having an amino acid sequence of SEQ ID NO:202. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence of SEQ ID NO:201, and a VL having an amino acid sequence of SEQ ID NO:202. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence of SEQ ID NO:203. In one aspect, provided herein is an antibody that binds CD8, comprising a light chain having an amino acid sequence of SEQ ID NO:204. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence of SEQ ID NO:203, and a light chain having an amino acid sequence of SEQ ID NO:204. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:201. In one aspect, provided herein is an antibody that binds CD8, comprising a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:202. In one aspect, provided herein is an

antibody that binds CD8, comprising a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:201, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:202. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:203. In one aspect, provided herein is an antibody that binds CD8, comprising a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:204. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:203, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:204.

[00203] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:205, 206, and 207, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:208, 209, and 210, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:211, 212, and 213, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:214, 215, and 216, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:217, 218, and 219, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:220, 221, and 222, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:223, 224, and 225, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:226, 227, and 228, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:229, 230, and 231, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having

an amino acid sequence of SEQ ID NOs:232, 233, and 234, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:235; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:236. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence of SEQ ID NO:235. In one aspect, provided herein is an antibody that binds CD8, comprising a VL having an amino acid sequence of SEQ ID NO:236. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence of SEQ ID NO:235, and a VL having an amino acid sequence of SEQ ID NO:236. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence of SEQ ID NO:237. In one aspect, provided herein is an antibody that binds CD8, comprising a light chain having an amino acid sequence of SEQ ID NO:238. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence of SEQ ID NO:237, and a light chain having an amino acid sequence of SEQ ID NO:238. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:235. In one aspect, provided herein is an antibody that binds CD8, comprising a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:236. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:235, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:236. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:237. In one aspect, provided herein is an antibody that binds CD8, comprising a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:238. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of

SEQ ID NO:237, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:238.

[00204] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:239, 240, and 241, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:242, 243, and 244, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:245, 246, and 247, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:248, 249, and 250, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:251, 252, and 253, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:254, 255, and 256, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:257, 258, and 259, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:260, 261, and 262, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:263, 264, and 265, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:266, 267, and 268, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:269; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:270. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence of SEQ ID NO:269. In one aspect, provided herein is an antibody that binds CD8, comprising a VL having an amino acid sequence

of SEQ ID NO:270. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence of SEQ ID NO:269, and a VL having an amino acid sequence of SEQ ID NO:270. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence of SEQ ID NO:271. In one aspect, provided herein is an antibody that binds CD8, comprising a light chain having an amino acid sequence of SEQ ID NO:272. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence of SEQ ID NO:271, and a light chain having an amino acid sequence of SEQ ID NO:272. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:269. In one aspect, provided herein is an antibody that binds CD8, comprising a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:270. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:269, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:270. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:271. In one aspect, provided herein is an antibody that binds CD8, comprising a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:272. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:271, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:272.

[00205] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:273, 274, and 275, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:276, 277, and 278, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:279, 280, and 281, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:282,

283, and 284, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:285, 286, and 287, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:288, 289, and 290, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:291, 292, and 293, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:294, 295, and 296, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:297, 298, and 299, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:300, 301, and 302, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:303; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:304. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence of SEQ ID NO:303. In one aspect, provided herein is an antibody that binds CD8, comprising a VL having an amino acid sequence of SEQ ID NO:304. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence of SEQ ID NO:303, and a VL having an amino acid sequence of SEQ ID NO:304. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence of SEQ ID NO:305. In one aspect, provided herein is an antibody that binds CD8, comprising a light chain having an amino acid sequence of SEQ ID NO:306. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence of SEQ ID NO:305, and a light chain having an amino acid sequence of SEQ ID NO:306. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:303. In one aspect, provided herein is an

antibody that binds CD8, comprising a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:304. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:303, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:304. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:305. In one aspect, provided herein is an antibody that binds CD8, comprising a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:306. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:305, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:306.

[00206] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:307, 308, and 309, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:310, 311, and 312, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:313, 314, and 315, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:316, 317, and 318, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:319, 320, and 321, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:322, 323, and 324, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:325, 326, and 327, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:328, 329, and 330, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH

CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:331, 332, and 333, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:334, 335, and 336, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:337; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:338. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence of SEQ ID NO:337. In one aspect, provided herein is an antibody that binds CD8, comprising a VL having an amino acid sequence of SEQ ID NO:338. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence of SEQ ID NO:337, and a VL having an amino acid sequence of SEQ ID NO:338. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence of SEQ ID NO:339. In one aspect, provided herein is an antibody that binds CD8, comprising a light chain having an amino acid sequence of SEQ ID NO:340. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence of SEQ ID NO:339, and a light chain having an amino acid sequence of SEQ ID NO:340. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:337. In one aspect, provided herein is an antibody that binds CD8, comprising a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:338. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:337, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:338. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:339. In one aspect, provided herein is an antibody that binds CD8, comprising a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:340. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy

chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:339, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:340.

[00207] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:341, 342, and 343, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:344, 345, and 346, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:347, 348, and 349, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:350, 351, and 352, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:353, 354, and 355, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:356, 357, and 358, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:359, 360, and 361, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:362, 363, and 364, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:365, 366, and 367, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:368, 369, and 370, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:371; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:372. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence of SEQ ID NO:371. In one aspect,

provided herein is an antibody that binds CD8, comprising a VL having an amino acid sequence of SEQ ID NO:372. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence of SEQ ID NO:371, and a VL having an amino acid sequence of SEQ ID NO:372. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence of SEQ ID NO:373. In one aspect, provided herein is an antibody that binds CD8, comprising a light chain having an amino acid sequence of SEQ ID NO:374. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence of SEQ ID NO:373, and a light chain having an amino acid sequence of SEQ ID NO:374. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:371. In one aspect, provided herein is an antibody that binds CD8, comprising a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:372. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:371, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:372. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:373. In one aspect, provided herein is an antibody that binds CD8, comprising a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:374. In one aspect, provided herein is an antibody that binds CD8, comprising a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:373, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:374.

[00208] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:375, 376, and 377, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:378, 379, and 380, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:381, 382, and 383, respectively, and (ii) a VL comprising

a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:384, 385, and 386, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:387, 388, and 389, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:390, 391, and 392, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:393, 394, and 395, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:396, 397, and 398, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:399, 400, and 401, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:402, 403, and 404, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:405; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:406. In one aspect, provided herein is an antibody that binds CD8, comprising a VH having an amino acid sequence of SEQ ID NO:405. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:406. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:405, and a VL having an amino acid sequence of SEQ ID NO:406. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:407. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:408. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:407, and a light chain having an amino acid sequence of SEQ ID NO:408. In one

embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:405. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:406. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:405, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:406. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:407. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:408. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:407, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:408.

[00209] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:409, 410, and 411, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:412, 413, and 414, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:415, 416, and 417, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:418, 419, and 420, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:421, 422, and 423, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:424, 425, and 426, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2,

and a VH CDR3 having an amino acid sequence of SEQ ID NOs:427, 428, and 429, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:430, 431, and 432, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:433, 434, and 435, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:436, 437, and 438, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:439; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:440. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:439. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:440. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:439, and a VL having an amino acid sequence of SEQ ID NO:440. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:441. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:442. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:441, and a light chain having an amino acid sequence of SEQ ID NO:442. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:439. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:440. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:439, and a VL having an amino acid

sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:440. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:441. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:442. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:441, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:442.

[00210] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:443, 444, and 445, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:446, 447, and 448, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:449, 450, and 451, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:452, 453, and 454, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:455, 456, and 457, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:458, 459, and 460, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:461, 462, and 463, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:464, 465, and 466, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:467, 468, and 469, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:470, 471, and 472, respectively. In one embodiment,

the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:473; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:474. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:473. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:474. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:473, and a VL having an amino acid sequence of SEQ ID NO:474. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:475. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:476. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:475, and a light chain having an amino acid sequence of SEQ ID NO:476. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:473. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:474. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:473, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:474. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:475. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:476. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at

least 95% identity to an amino acid sequence of SEQ ID NO:475, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:476.

[00211] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:477, 478, and 479, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:480, 481, and 482, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:483, 484, and 485, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:486, 487, and 488, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:489, 490, and 491, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:492, 493, and 494, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:495, 496, and 497, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:498, 499, and 500, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:501, 502, and 503, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:504, 505, and 506, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:507; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:508. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID

NO:507. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:508. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:507, and a VL having an amino acid sequence of SEQ ID NO:508. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:509. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:510. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:509, and a light chain having an amino acid sequence of SEQ ID NO:510. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:507. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:508. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:507, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:508. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:509. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:510. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:509, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:510.

[00212] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:511, 512, and 513, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:514, 515, and

516, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:517, 518, and 519, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:520, 521, and 522, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:523, 524, and 525, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:526, 527, and 528, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:529, 530, and 531, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:532, 533, and 534, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:535, 536, and 537, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:538, 539, and 540, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:541; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:542. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:541. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:542. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:541, and a VL having an amino acid sequence of SEQ ID NO:542. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:543. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino

acid sequence of SEQ ID NO:544. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:543, and a light chain having an amino acid sequence of SEQ ID NO:544. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:541. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:542. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:541, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:542. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:543. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:544. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:543, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:544.

[00213] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:545, 546, and 547, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:548, 549, and 550, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:551, 552, and 553, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:554, 555, and 556, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:557, 558, and 559, respectively, and (ii)

a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:560, 561, and 562, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:563, 564, and 565, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:566, 567, and 568, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:569, 570, and 571, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:572, 573, and 574, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:575; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:576. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:575. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:576. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:575, and a VL having an amino acid sequence of SEQ ID NO:576. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:577. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:578. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:577, and a light chain having an amino acid sequence of SEQ ID NO:578. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:575. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid

sequence of SEQ ID NO:576. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:575, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:576. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:577. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:578. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:577, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:578.

[00214] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:579, 580, and 581, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:582, 583, and 584, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:585, 586, and 587, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:588, 589, and 590, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:591, 592, and 593, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:594, 595, and 596, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:597, 598, and 599, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:600, 601, and 602, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH

CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:603, 604, and 605, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:606, 607, and 608, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:609; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:610. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:609. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:610. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:609, and a VL having an amino acid sequence of SEQ ID NO:610. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:611. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:612. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:611, and a light chain having an amino acid sequence of SEQ ID NO:612. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:609. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:610. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:609, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:610. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:611. In one embodiment, the first antigen binding domain that specifically binds

CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:612. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:611, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:612.

[00215] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:613, 614, and 615, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:616, 617, and 618, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:619, 620, and 621, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:622, 523, and 624, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:625, 626, and 627, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:628, 629, and 630, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:631, 632, and 633, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:634, 635, and 636, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:637, 638, and 639, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:640, 641, and 642, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:643; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino

acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:644. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:643. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:644. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:643, and a VL having an amino acid sequence of SEQ ID NO:644. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:645. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:646. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:645, and a light chain having an amino acid sequence of SEQ ID NO:646. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:643. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:644. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:643, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:644. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:645. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:646. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:645, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:646.

[00216] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:647, 648, and 649, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:650, 651, and 652, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:653, 654, and 655, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:656, 657, and 658, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:659, 660, and 661, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:662, 663, and 664, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:665, 666, and 667, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:668, 669, and 670, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:671, 672, and 673, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:674, 675, and 676, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:677; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:678. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:677. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:678. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid

sequence of SEQ ID NO:677, and a VL having an amino acid sequence of SEQ ID NO:678. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:679. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:680. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:679, and a light chain having an amino acid sequence of SEQ ID NO:680. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:677. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:678. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:677, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:678. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:679. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:680. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:679, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:680.

[00217] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:681, 682, and 683, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:684, 685, and 686, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:687, 688, and 689, respectively, and (ii) a VL comprising

a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:690, 691, and 692, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:693, 694, and 695, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:696, 697, and 698, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:699, 700, and 701, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:702, 703, and 704, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:705, 706, and 707, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:708, 709, and 710, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:711; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:712. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:711. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:712. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:711, and a VL having an amino acid sequence of SEQ ID NO:712. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:713. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:714. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:713, and a light chain having an amino acid sequence of SEQ ID NO:714. In one

embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:711. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:712. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:711, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:712. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:713. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:714. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:713, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:714.

[00218] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:715, 716, and 717, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:718, 719, and 720, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:721, 722, and 723, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:724, 725, and 726, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:727, 728, and 729, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:730, 731, and 732, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2,

and a VH CDR3 having an amino acid sequence of SEQ ID NOs:733, 734, and 735, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:736, 737, and 738, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:739, 740, and 741, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:742, 743, and 744, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:745; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:746. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:745. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:746. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:745, and a VL having an amino acid sequence of SEQ ID NO:746. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:747. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:748. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:747, and a light chain having an amino acid sequence of SEQ ID NO:748. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:745. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:746. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:745, and a VL having an amino acid

sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:746. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:747. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:748. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:747, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:748.

[00219] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:749, 750, and 751, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:752, 753, and 754, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:755, 756, and 757, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:758, 759, and 760, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:761, 762, and 763, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:764, 765, and 766, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:767, 768, and 769, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:770, 771, and 772, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:773, 774, and 775, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:776, 777, and 778, respectively. In one embodiment,

the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:779; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:780. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:779. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:780. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:779, and a VL having an amino acid sequence of SEQ ID NO:780. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:781. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:782. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:781, and a light chain having an amino acid sequence of SEQ ID NO:782. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:779. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:780. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:779, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:780. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:781. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:782. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at

least 95% identity to an amino acid sequence of SEQ ID NO:781, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:782.

[00220] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:783, 784, and 785, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:786, 787, and 788, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:789, 790, and 791, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:792, 793, and 794, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:795, 796, and 797, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:798, 799, and 800, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:801, 802, and 803, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:804, 805, and 806, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:807, 808, and 809, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:810, 811, and 812, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:813; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:814. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID

NO:813. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:814. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:813, and a VL having an amino acid sequence of SEQ ID NO:814. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:815. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:816. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:815, and a light chain having an amino acid sequence of SEQ ID NO:816. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:813. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:814. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:813, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:814. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:815. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:816. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:815, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:816.

[00221] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:817, 818, and 819, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:820, 821, and

822, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:823, 824, and 825, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:826, 827, and 828, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:829, 830, and 831, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:832, 833, and 834, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:835, 836, and 837, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:838, 839, and 840, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:841, 842, and 843, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:844, 845, and 846, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:847; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:848. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:847. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:848. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:847, and a VL having an amino acid sequence of SEQ ID NO:848. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:849. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino

acid sequence of SEQ ID NO:850. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:849, and a light chain having an amino acid sequence of SEQ ID NO:850. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:847. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:848. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:847, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:848. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:849. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:850. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:849, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:850.

[00222] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:851, 852, and 853, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:854, 855, and 856, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:857, 858, and 859, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:860, 861, and 862, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:863, 864, and 865, respectively, and (ii)

a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:866, 867, and 868, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:869, 870, and 871, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:872, 873, and 874, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:875, 876, and 877, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:878, 879, and 880, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:881; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:882. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:881. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:882. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:881, and a VL having an amino acid sequence of SEQ ID NO:882. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:883. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:884. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:883, and a light chain having an amino acid sequence of SEQ ID NO:884. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:881. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid

sequence of SEQ ID NO:882. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:881, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:882. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:883. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:884. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:883, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:884.

[00223] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:885, 886, and 887, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:888, 889, and 890, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:891, 892, and 893, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:894, 895, and 896, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:897, 898, and 899, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:900, 901, and 902, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:903, 904, and 905, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:906, 907, and 908, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH

CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:909, 910, and 911, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:912, 913, and 914, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:915; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:916. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:915. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:916. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:915, and a VL having an amino acid sequence of SEQ ID NO:916. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:917. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:918. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:917, and a light chain having an amino acid sequence of SEQ ID NO:918. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:915. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:916. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:915, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:916. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:917. In one embodiment, the first antigen binding domain that specifically binds

CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:918. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:917, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:918.

[00224] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:919, 920, and 921, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:922, 923, and 924, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:925, 926, and 927, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:928, 929, and 930, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:931, 932, and 933, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:934, 935, and 936, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:937, 938, and 939, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:940, 941, and 942, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:943, 944, and 945, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:946, 947, and 948, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:949; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino

acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:950. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:949. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:950. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:949, and a VL having an amino acid sequence of SEQ ID NO:950. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:951. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:952. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:951, and a light chain having an amino acid sequence of SEQ ID NO:952. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:949. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:950. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:949, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:950. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:951. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:952. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:951, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:952.

[00225] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:953, 954, and 955, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:956, 957, and 958, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:959, 960, and 961, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:962, 963, and 964, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:965, 966, and 967, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:968, 969, and 970, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:971, 972, and 973, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:974, 975, and 976, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:977, 978, and 979, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:980, 981, and 982, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:983; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:984. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:983. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:984. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid

sequence of SEQ ID NO:983, and a VL having an amino acid sequence of SEQ ID NO:984. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:985. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:986. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:985, and a light chain having an amino acid sequence of SEQ ID NO:986. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:983. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:984. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:983, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:984. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:985. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:986. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:985, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:986.

[00226] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:987, 988, and 989, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:990, 991, and 992, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:993, 994, and 995, respectively, and (ii) a VL comprising

a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:996, 997, and 998, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:999, 1000, and 1001, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1002, 1003, and 1004, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1005, 1006, and 1007, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1008, 1009, and 1010, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1011, 1012, and 1013, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1014, 1015, and 1016, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1017; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1018. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1017. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:1018. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1017, and a VL having an amino acid sequence of SEQ ID NO:1018. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1019. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:1020. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1019, and a light chain having an amino acid sequence of SEQ ID

NO:1020. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1017. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1018. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1017, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1018. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1019. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1020. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1019, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1020.

[00227] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1021, 1022, and 1023, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1024, 1025, and 1026, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1027, 1028, and 1029, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1030, 1031, and 1032, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1033, 1034, and 1035, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1036, 1037, and 1038, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH

CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1039, 1040, and 1041, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1042, 1043, and 1044, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1045, 1046, and 1047, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1048, 1049, and 1050, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1051; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1052. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1051. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:1052. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1051, and a VL having an amino acid sequence of SEQ ID NO:1052. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1053. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:1054. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1053, and a light chain having an amino acid sequence of SEQ ID NO:1054. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1051. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1052. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1051, and a VL having

an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1052. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1053. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1054. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1053, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1054.

[00228] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1055, 1056, and 1057, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1058, 1059, and 1060, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1061, 1062, and 1063, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1064, 1065, and 1066, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1067, 1068, and 1069, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1070, 1071, and 1072, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1073, 1074, and 1075, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1076, 1077, and 1078, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1079, 1080, and 1081, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1082, 1083, and 1084,

respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1085; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1086. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1085. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:1086. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1085, and a VL having an amino acid sequence of SEQ ID NO:1086. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1087. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:1088. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1087, and a light chain having an amino acid sequence of SEQ ID NO:1088. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1085. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1086. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1085, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1086. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1087. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1088. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino

acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1087, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1088.

[00229] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1089, 1090, and 1091, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1092, 1093, and 1094, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1095, 1096, and 1097, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1098, 1099, and 1100, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1101, 1102, and 1103, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1104, 1105, and 1106, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1107, 1108, and 1109, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1110, 1111, and 1112, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1113, 1114, and 1115, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1116, 1117, and 1118, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1119; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1120. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino

acid sequence of SEQ ID NO:1119. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:1120. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1119, and a VL having an amino acid sequence of SEQ ID NO:1120. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1121. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:1122. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1121, and a light chain having an amino acid sequence of SEQ ID NO:1122. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1119. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1120. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1119, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1120. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1121. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1122. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1121, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1122.

[00230] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1123, 1124, and 1125, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1126,

1127, and 1128, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1129, 1130, and 1131, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1132, 1133, and 1134, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1135, 1136, and 1137, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1138, 1139, and 1140, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1141, 1142, and 1143, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1144, 1145, and 1146, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1147, 1148, and 1149, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1150, 1151, and 1152, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1153; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1154. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1153. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:1154. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1153, and a VL having an amino acid sequence of SEQ ID NO:1154. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1155. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light

chain having an amino acid sequence of SEQ ID NO:1156. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1155, and a light chain having an amino acid sequence of SEQ ID NO:1156. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1153. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1154. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1153, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1154. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1155. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1156. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1155, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1156.

[00231] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1157, 1158, and 1159, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1160, 1161, and 1162, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1163, 1164, and 1165, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1166, 1167, and 1168, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1169, 1170, and 1171,

respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1172, 1173, and 1174, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1175, 1176, and 1177, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1178, 1179, and 1180, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1181, 1182, and 1183, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1184, 1185, and 1186, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1187; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1188. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1187. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:1188. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1187, and a VL having an amino acid sequence of SEQ ID NO:1188. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1189. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:1190. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1189, and a light chain having an amino acid sequence of SEQ ID NO:1190. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1187. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95%

identity to an amino acid sequence of SEQ ID NO:1188. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1187, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1188. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1189. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1190. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1189, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1190.

[00232] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1191, 1192, and 1193, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1194, 1195, and 1196, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1197, 1198, and 1199, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1200, 1201, and 1202, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1203, 1204, and 1205, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1206, 1207, and 1208, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1209, 1210, and 1211, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1212, 1213, and 1214, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH

comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1215, 1216, and 1217, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1218, 1219, and 1220, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1221; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1222. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1221. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:1222. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1221, and a VL having an amino acid sequence of SEQ ID NO:1222. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1223. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:1224. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1223, and a light chain having an amino acid sequence of SEQ ID NO:1224. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1221. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1222. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1221, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1222. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1223. In one embodiment, the first antigen binding domain

that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1224. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1223, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1224.

[00233] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1225, 1226, and 1227, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1228, 1229, and 1230, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1231, 1232, and 1233, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1234, 1235, and 1236, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1237, 1238, and 1239, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1240, 1241, and 1242, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1243, 1244, and 1245, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1246, 1247, and 1248, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1249, 1250, and 1251, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1252, 1253, and 1254, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1255; and (ii) a VL comprising a VL CDR1, a VL CDR2,

and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1256. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1255. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:1256. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1255, and a VL having an amino acid sequence of SEQ ID NO:1256. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1257. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:1258. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1257, and a light chain having an amino acid sequence of SEQ ID NO:1258. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1255. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1256. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1255, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1256. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1257. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1258. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1257, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1258.

[00234] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1259, 1260, and 1261, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1262, 1263, and 1264, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1265, 1266, and 1267, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1268, 1269, and 1270, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1271, 1272, and 1273, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1274, 1275, and 1276, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1277, 1278, and 1279, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1280, 1281, and 1282, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1283, 1284, and 1285, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1286, 1287, and 1288, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1289; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1290. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1289. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:1290. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH

having an amino acid sequence of SEQ ID NO:1289, and a VL having an amino acid sequence of SEQ ID NO:1290. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1291. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:1292. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1291, and a light chain having an amino acid sequence of SEQ ID NO:1292. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1289. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1290. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1289, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1290. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1291. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1292. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1291, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1292.

[00235] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1293, 1294, and 1295, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1296, 1297, and 1298, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1299, 1300, and 1301, respectively, and

(ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1302, 1303, and 1304, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1305, 1306, and 1307, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1308, 1309, and 1310, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1311, 1312, and 1313, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1314, 1315, and 1316, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1317, 1318, and 1319, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1320, 1321, and 1322, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1323; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1324. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1323. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:1324. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1323, and a VL having an amino acid sequence of SEQ ID NO:1324. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1325. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:1326. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1325, and a light chain having an amino acid sequence of SEQ ID

NO:1326. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1323. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1324. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1323, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1324. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1325. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1326. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1325, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1326.

[00236] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1327, 1328, and 1329, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1330, 1331, and 1332, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1333, 1334, and 1335, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1336, 1337, and 1338, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1339, 1340, and 1341, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1342, 1343, and 1344, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH

CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1345, 1346, and 1347, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1348, 1349, and 1350, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1351, 1352, and 1353, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1354, 1355, and 1356, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1357; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1358. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1357. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:1358. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1357, and a VL having an amino acid sequence of SEQ ID NO:1358. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1359. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:1360. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1359, and a light chain having an amino acid sequence of SEQ ID NO:1360. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1357. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1358. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1357, and a VL having

an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1358. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1359. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1360. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1359, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1360.

[00237] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1361, 1362, and 1363, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1364, 1365, and 1366, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1367, 1368, and 1369, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1370, 1371, and 1372, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1373, 1374, and 1375, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1376, 1377, and 1378, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1379, 1380, and 1381, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1382, 1383, and 1384, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1385, 1386, and 1387, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1388, 1389, and 1390,

respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1391; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1392. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1391. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:1392. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1391, and a VL having an amino acid sequence of SEQ ID NO:1392. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1393. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:1394. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1393, and a light chain having an amino acid sequence of SEQ ID NO:1394. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1391. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1392. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1391, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1392. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1393. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1394. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino

acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1393, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1394.

[00238] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1395, 1396, and 1397, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1398, 1399, and 1400, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1401, 1402, and 1403, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1404, 1405, and 1406, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1407, 1408, and 1409, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1410, 1411, and 1412, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1413, 1414, and 1415, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1416, 1417, and 1418, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1419, 1420, and 1421, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1422, 1423, and 1424, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1425; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1426. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino

acid sequence of SEQ ID NO:1425. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:1426. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1425, and a VL having an amino acid sequence of SEQ ID NO:1426. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1427. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:1428. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1427, and a light chain having an amino acid sequence of SEQ ID NO:1428. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1425. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1426. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1425, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1426. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1427. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1428. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1427, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1428.

[00239] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1429, 1430, and 1431, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1432,

1433, and 1434, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1435, 1436, and 1437, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1438, 1439, and 1440, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1441, 1442, and 1443, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1444, 1445, and 1446, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1447, 1448, and 1449, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1450, 1451, and 1452, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1453, 1454, and 1455, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1456, 1457, and 1458, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1459; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1460. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1459. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:1460. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1459, and a VL having an amino acid sequence of SEQ ID NO:1460. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1461. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light

chain having an amino acid sequence of SEQ ID NO:1462. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1461, and a light chain having an amino acid sequence of SEQ ID NO:1462. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1459. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1460. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1459, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1460. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1461. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1462. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1461, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1462.

[00240] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1463, 1464, and 1465, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1466, 1467, and 1468, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1469, 1470, and 1471, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1472, 1473, and 1474, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1475, 1476, and 1477,

respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1478, 1479, and 1480, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1481, 1482, and 1483, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1484, 1485, and 1486, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1487, 1488, and 1489, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1490, 1491, and 1492, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1493; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1494. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1493. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:1494. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1493, and a VL having an amino acid sequence of SEQ ID NO:1494. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1495. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:1496. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1495, and a light chain having an amino acid sequence of SEQ ID NO:1496. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1493. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95%

identity to an amino acid sequence of SEQ ID NO:1494. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1493, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1494. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1495. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1496. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1495, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1496.

[00241] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1497, 1498, and 1499, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1500, 1501, and 1502, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1503, 1504, and 1505, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1506, 1507, and 1508, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1509, 1510, and 1511, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1512, 1513, and 1514, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1515, 1516, and 1517, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1518, 1519, and 1520, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH

comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1521, 1522, and 1523, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1524, 1525, and 1526, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1527; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1528. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1527. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:1528. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1527, and a VL having an amino acid sequence of SEQ ID NO:1528. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1529. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:1530. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1529, and a light chain having an amino acid sequence of SEQ ID NO:1530. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1527. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1528. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1527, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1528. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1529. In one embodiment, the first antigen binding domain

that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1530. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1529, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1530.

[00242] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1531, 1532, and 1533, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1534, 1535, and 1536, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1537, 1538, and 1539, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1540, 1541, and 1542, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1543, 1544, and 1545, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1546, 1547, and 1548, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1549, 1550, and 1551, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1552, 1553, and 1554, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1555, 1556, and 1557, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1558, 1559, and 1560, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1561; and (ii) a VL comprising a VL CDR1, a VL CDR2,

and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1562. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1561. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:1562. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1561, and a VL having an amino acid sequence of SEQ ID NO:1562. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1563. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:1564. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1563, and a light chain having an amino acid sequence of SEQ ID NO:1564. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1561. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1562. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1561, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1562. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1563. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1564. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1563, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1564.

[00243] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1565, 1566, and 1567, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1568, 1569, and 1570, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1571, 1572, and 1573, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1574, 1575, and 1576, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1577, 1578, and 1579, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1580, 1581, and 1582, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1583, 1584, and 1585, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1586, 1587, and 1588, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1589, 1590, and 1591, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1592, 1593, and 1594, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1595; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1596. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1595. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:1596. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH

having an amino acid sequence of SEQ ID NO:1595, and a VL having an amino acid sequence of SEQ ID NO:1596. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1597. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:1598. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1597, and a light chain having an amino acid sequence of SEQ ID NO:1598. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1595. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1596. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1595, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1596. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1597. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1598. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1597, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1598.

[00244] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1599, 1600, and 1601, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1602, 1603, and 1604, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1605, 1606, and 1607, respectively, and

(ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1608, 1609, and 1610, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1611, 1612, and 1613, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1614, 1615, and 1616, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1617, 1618, and 1619, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1620, 1621, and 1622, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1623, 1624, and 1625, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1626, 1627, and 1628, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1629; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1630. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1629. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:1630. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1629, and a VL having an amino acid sequence of SEQ ID NO:1630. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1631. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:1632. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1631, and a light chain having an amino acid sequence of SEQ ID

NO:1632. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1629. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1630. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1629, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1630. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1631. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1632. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1631, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1632.

[00245] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1633, 1634, and 1635, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1636, 1637, and 1638, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1639, 1640, and 1641, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1642, 1643, and 1644, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1645, 1646, and 1647, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1648, 1649, and 1650, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH

CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1651, 1652, and 1653, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1654, 1655, and 1656, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1657, 1658, and 1659, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1660, 1661, and 1662, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1663; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1664. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1663. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:1664. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1663, and a VL having an amino acid sequence of SEQ ID NO:1664. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1665. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:1666. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1665, and a light chain having an amino acid sequence of SEQ ID NO:1666. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1663. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1664. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1663, and a VL having

an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1664. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1665. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1666. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1665, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1666.

[00246] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1667, 1668, and 1669, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1670, 1671, and 1672, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1673, 1674, and 1675, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1676, 1677, and 1678, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1679, 1680, and 1681, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1682, 1683, and 1684, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1685, 1686, and 1687, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1688, 1689, and 1690, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1691, 1692, and 1693, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1694, 1695, and 1696,

respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1697; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1698. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1697. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:1698. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1697, and a VL having an amino acid sequence of SEQ ID NO:1698. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1699. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:1700. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1699, and a light chain having an amino acid sequence of SEQ ID NO:1700. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1697. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1698. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1697, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1698. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1699. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1700. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino

acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1699, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1700.

[00247] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1701, 1702, and 1703, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1704, 1705, and 1706, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1707, 1708, and 1709, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1710, 1711, and 1712, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1713, 1714, and 1715, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1716, 1717, and 1718, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1719, 1720, and 1721, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1722, 1723, and 1724, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1725, 1726, and 1727, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1728, 1729, and 1730, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1731; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1732. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino

acid sequence of SEQ ID NO:1731. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:1732. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1731, and a VL having an amino acid sequence of SEQ ID NO:1732. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1733. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:1734. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1733, and a light chain having an amino acid sequence of SEQ ID NO:1734. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1731. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1732. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1731, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1732. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1733. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1734. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1733, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1734.

[00248] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1735, 1736, and 1737, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1738,

1739, and 1740, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1741, 1742, and 1743, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1744, 1745, and 1746, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1747, 1748, and 1749, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1750, 1751, and 1752, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1753, 1754, and 1755, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1756, 1757, and 1758, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1759, 1760, and 1761, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1762, 1763, and 1764, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1765; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1766. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1765. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:1766. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1765, and a VL having an amino acid sequence of SEQ ID NO:1766. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1767. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light

chain having an amino acid sequence of SEQ ID NO:1768. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1767, and a light chain having an amino acid sequence of SEQ ID NO:1768. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1765. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1766. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1765, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1766. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1767. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1768. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1767, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1768.

[00249] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1769, 1770, and 1771, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1772, 1773, and 1774, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1775, 1776, and 1777, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1778, 1779, and 1780, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1781, 1782, and 1783,

respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1784, 1785, and 1786, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1787, 1788, and 1789, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1790, 1791, and 1792, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1793, 1794, and 1795, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1796, 1797, and 1798, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1799; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1800. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1799. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:1800. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1799, and a VL having an amino acid sequence of SEQ ID NO:1800. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1801. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:1802. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1801, and a light chain having an amino acid sequence of SEQ ID NO:1802. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1799. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95%

identity to an amino acid sequence of SEQ ID NO:1800. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1799, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1800. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1801. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1802. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1801, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1802.

[00250] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1803, 1804, and 1805, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1806, 1807, and 1808, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1809, 1810, and 1811, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1812, 1813, and 1814, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1815, 1816, and 1817, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1818, 1819, and 1820, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1821, 1822, and 1823, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1824, 1825, and 1826, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH

comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1827, 1828, and 1829, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1830, 1831, and 1832, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1833; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1834. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1833. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:1834. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1833, and a VL having an amino acid sequence of SEQ ID NO:1834. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1835. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:1836. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1835, and a light chain having an amino acid sequence of SEQ ID NO:1836. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1833. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1834. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1833, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1834. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1835. In one embodiment, the first antigen binding domain

that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1836. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1835, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1836.

[00251] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1837, 1838, and 1839, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1840, 1841, and 1842, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1843, 1844, and 1845, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1846, 1847, and 1848, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1849, 1850, and 1851, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1852, 1853, and 1854, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1855, 1856, and 1857, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1858, 1859, and 1860, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1861, 1862, and 1863, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1864, 1865, and 1866, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1867; and (ii) a VL comprising a VL CDR1, a VL CDR2,

and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1868. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1867. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:1868. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1867, and a VL having an amino acid sequence of SEQ ID NO:1868. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1869. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:1870. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1869, and a light chain having an amino acid sequence of SEQ ID NO:1870. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1867. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1868. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1867, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1868. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1869. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1870. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1869, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1870.

[00252] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1871, 1872, and 1873, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1874, 1875, and 1876, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1877, 1878, and 1879, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1880, 1881, and 1882, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1883, 1884, and 1885, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1886, 1887, and 1888, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1889, 1890, and 1891, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1892, 1893, and 1894, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1895, 1896, and 1897, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1898, 1899, and 1900, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1901; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1902. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1901. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:1902. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH

having an amino acid sequence of SEQ ID NO:1901, and a VL having an amino acid sequence of SEQ ID NO:1902. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1903. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:1904. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1903, and a light chain having an amino acid sequence of SEQ ID NO:1904. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1901. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1902. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1901, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1902. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1903. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1904. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1903, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1904.

[00253] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1905, 1906, and 1907, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1908, 1909, and 1910, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1911, 1912, and 1913, respectively, and

(ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1914, 1915, and 1916, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1917, 1918, and 1919, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1920, 1921, and 1922, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1923, 1924, and 1925, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1926, 1927, and 1928, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1929, 1930, and 1931, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1932, 1933, and 1934, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1935; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1936. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1935. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:1936. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1935, and a VL having an amino acid sequence of SEQ ID NO:1936. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1937. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:1938. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1937, and a light chain having an amino acid sequence of SEQ ID

NO:1938. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1935. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1936. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1935, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1936. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1937. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1938. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1937, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1938.

[00254] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1939, 1940, and 1941, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1942, 1943, and 1944, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1945, 1946, and 1947, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1948, 1949, and 1950, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1951, 1952, and 1953, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1954, 1955, and 1956, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH

CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1957, 1958, and 1959, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1960, 1961, and 1962, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1963, 1964, and 1965, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1966, 1967, and 1968, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:1969; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:1970. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1969. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:1970. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:1969, and a VL having an amino acid sequence of SEQ ID NO:1970. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1971. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:1972. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:1971, and a light chain having an amino acid sequence of SEQ ID NO:1972. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1969. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1970. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1969, and a VL having

an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1970. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1971. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1972. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1971, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:1972.

[00255] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1973, 1974, and 1975, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1976, 1977, and 1978, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1979, 1980, and 1981, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1982, 1983, and 1984, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1985, 1986, and 1987, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1988, 1989, and 1990, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1991, 1992, and 1993, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:1994, 1995, and 1996, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:1997, 1998, and 1999, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:2000, 2001, and 2002,

respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:2003; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:2004. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:2003. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:2004. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:2003, and a VL having an amino acid sequence of SEQ ID NO:2004. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:2005. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:2006. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:2005, and a light chain having an amino acid sequence of SEQ ID NO:2006. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2003. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2004. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2003, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2004. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2005. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2006. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino

acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2005, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2006.

[00256] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:2007, 2008, and 2009, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:2010, 2011, and 2012, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:2013, 2014, and 2015, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:2016, 2017, and 2018, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:2019, 2020, and 2021, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:2022, 2023, and 2024, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:2025, 2026, and 2027, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:2028, 2029, and 2030, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:2031, 2032, and 2033, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:2034, 2035, and 2036, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:2037; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:2038. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino

acid sequence of SEQ ID NO:2037. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:2038. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:2037, and a VL having an amino acid sequence of SEQ ID NO:2038. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:2039. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:2040. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:2039, and a light chain having an amino acid sequence of SEQ ID NO:2040. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2037. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2038. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2037, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2038. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2039. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2040. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2039, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2040.

[00257] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:2041, 2042, and 2043, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:2044,

2045, and 2046, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:2047, 2048, and 2049, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:2050, 2051, and 2052, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:2053, 2054, and 2055, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:2056, 2057, and 2058, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:2059, 2060, and 2061, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:2062, 2063, and 2064, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:2065, 2066, and 2067, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:2068, 2069, and 2070, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:2071; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:2072. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:2071. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:2072. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:2071, and a VL having an amino acid sequence of SEQ ID NO:2072. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:2073. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light

chain having an amino acid sequence of SEQ ID NO:2074. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:2073, and a light chain having an amino acid sequence of SEQ ID NO:2074. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2071. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2072. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2071, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2072. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2073. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2074. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2073, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2074.

[00258] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:2075, 2076, and 2077, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:2078, 2079, and 2080, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:2081, 2082, and 2083, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:2084, 2085, and 2086, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:2087, 2088, and 2089,

respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:2090, 2091, and 2092, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:2093, 2094, and 2095, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:2096, 2097, and 2098, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:2099, 2100, and 2101, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:2102, 2103, and 2104, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:2105; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:2106. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:2105. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:2106. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:2105, and a VL having an amino acid sequence of SEQ ID NO:2106. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:2107. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:2108. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:2107, and a light chain having an amino acid sequence of SEQ ID NO:2108. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2105. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95%

identity to an amino acid sequence of SEQ ID NO:2106. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2105, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2106. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2107. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2108. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2107, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2108.

[00259] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:2109, 2110, and 2111, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:2112, 2113, and 2114, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:2115, 2116, and 2117, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:2118, 2119, and 2120, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:2121, 2122, and 2123, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:2124, 2125, and 2126, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:2127, 2128, and 2129, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:2130, 2131, and 2132, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH

comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:2133, 2134, and 2135, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:2136, 2137, and 2138, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:2139; and (ii) a VL comprising a VL CDR1, a VL CDR2, and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:2140. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:2139. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:2140. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:2139, and a VL having an amino acid sequence of SEQ ID NO:2140. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:2141. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:2142. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:2141, and a light chain having an amino acid sequence of SEQ ID NO:2142. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2139. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2140. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2139, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2140. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2141. In one embodiment, the first antigen binding domain

that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2142. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2141, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2142.

[00260] In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:2143, 2144, and 2145, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:2146, 2147, and 2148, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:2149, 2150, and 2151, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:2152, 2153, and 2154, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:2155, 2156, and 2157, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:2158, 2159, and 2160, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:2161, 2162, and 2163, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:2164, 2165, and 2166, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of SEQ ID NOs:2167, 2168, and 2169, respectively, and (ii) a VL comprising a VL CDR1, VL CDR2, and VL CDR3 having an amino acid sequence of SEQ ID NOs:2170, 2171, and 2172, respectively. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises: (i) a VH comprising a VH CDR1, a VH CDR2, and a VH CDR3 having an amino acid sequence of a VH CDR1, a VH CDR2, and a VH CDR3, respectively, of a VH having an amino acid sequence of SEQ ID NO:2173; and (ii) a VL comprising a VL CDR1, a VL CDR2,

and a VL CDR3 having an amino acid sequence of a VL CDR1, a VL CDR2, and a VL CDR3, respectively, of a VL having an amino acid sequence of SEQ ID NO:2174. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:2173. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence of SEQ ID NO:2174. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence of SEQ ID NO:2173, and a VL having an amino acid sequence of SEQ ID NO:2174. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:2175. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence of SEQ ID NO:2176. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence of SEQ ID NO:2175, and a light chain having an amino acid sequence of SEQ ID NO:2176. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2173. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2174. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a VH having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2173, and a VL having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2174. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2175. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2176. In one embodiment, the first antigen binding domain that specifically binds CD8, comprises a heavy chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2175, and a light chain having an amino acid sequence having at least 95% identity to an amino acid sequence of SEQ ID NO:2176.

[00261] In some embodiments, the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296.

[00262] In some embodiments, the second antigen binding domain that specifically binds CD3 comprises the VH of SEQ ID NO: 2297 and the VL of SEQ ID NO: 2298.

[00263] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds CD3 provided herein.

[00264] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds a third antigen. It is contemplated that an isolated molecule provided herein can comprise a first antigen binding domain that specifically binds CD8 provided herein, a second antigen binding domain that specifically binds CD3 provided herein, and a third antigen binding domain that specifically binds a third antigen provided herein.

[00265] In some embodiments, the third antigen comprises an antigen expressed by an undesired cell.

[00266] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds CD3 provided herein.

[00267] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds CD3 provided herein.

[00268] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of CD3 and CD8. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds CD3 provided herein.

[00269] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3 and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3 with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of CD3 and CD8. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds CD3 provided herein.

[00270] The disclosure also provides an isolated multispecific antibody, comprising: a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated multispecific antibody provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds CD3 provided herein.

[00271] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds a third antigen. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated multispecific antibody provided herein can comprise a first antigen binding domain that specifically binds CD8 provided herein, a second antigen binding domain that specifically binds CD3 provided herein, and a third antigen binding domain that specifically binds a third antigen provided herein.

[00272] In some embodiments, the third antigen comprises an antigen expressed by an undesired cell.

[00273] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated multispecific antibody provided herein can comprise a first antigen binding domain that specifically binds CD8 provided herein, a second antigen binding domain that specifically binds CD3 provided herein, and a third antigen binding domain that specifically binds a third antigen provided herein.

[00274] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated multispecific antibody provided herein can comprise a first antigen binding domain that specifically binds CD8 provided herein, a second antigen binding domain that specifically binds CD3 provided herein, and a third antigen binding domain that specifically binds a third antigen provided herein.

[00275] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8 and wherein the isolated multispecific antibody is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of CD3 and CD8. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated multispecific antibody provided herein can comprise a first antigen binding domain that specifically binds CD8 provided herein, a second antigen binding domain that specifically binds CD3 provided herein, and a third antigen binding domain that specifically binds a third antigen provided herein.

[00276] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen

binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3 with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of CD3 and CD8. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated multispecific antibody provided herein can comprise a first antigen binding domain that specifically binds CD8 provided herein, a second antigen binding domain that specifically binds CD3 provided herein, and a third antigen binding domain that specifically binds a third antigen provided herein.

[00277] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3, wherein the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00278] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds a third antigen, wherein the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00279] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the second antigen binding domain that specifically binds CD3

comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00280] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00281] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00282] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3 and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3 with affinities that result in activation or

recruitment of $CD8^+$ CTLs only upon co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00283] The disclosure also provides an isolated multispecific antibody, comprising: a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3, wherein the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00284] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds a third antigen, wherein the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00285] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the

second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00286] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00287] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8 and wherein the isolated multispecific antibody is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00288] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3 with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00289] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3, wherein the second antigen binding domain that specifically binds CD3 comprises the VH of SEQ ID NO: 2297 and the VL of SEQ ID NO: 2298. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00290] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds a third antigen, wherein the second antigen binding domain that specifically binds CD3 comprises the VH of SEQ ID NO: 2297 and the VL of SEQ ID NO: 2298. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00291] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an

undesired cell, wherein the second antigen binding domain that specifically binds CD3 comprises the VH of SEQ ID NO: 2297 and the VL of SEQ ID NO: 2298. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00292] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the VH of SEQ ID NO: 2297 and the VL of SEQ ID NO: 2298. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00293] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the VH of SEQ ID NO: 2297 and the VL of SEQ ID NO: 2298. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00294] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3 and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3 with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the VH of SEQ ID NO: 2297 and

the VL of SEQ ID NO: 2298. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00295] The disclosure also provides an isolated multispecific antibody, comprising: a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3, wherein the second antigen binding domain that specifically binds CD3 comprises the VH of SEQ ID NO: 2297 and the VL of SEQ ID NO: 2298. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00296] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds a third antigen, wherein the second antigen binding domain that specifically binds CD3 comprises the VH of SEQ ID NO: 2297 and the VL of SEQ ID NO: 2298. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00297] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the second antigen binding domain that specifically binds CD3 comprises the VH of SEQ ID NO: 2297 and the VL of SEQ ID NO: 2298. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00298] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically

binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the VH of SEQ ID NO: 2297 and the VL of SEQ ID NO: 2298. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00299] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8 and wherein the isolated multispecific antibody is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the VH of SEQ ID NO: 2297 and the VL of SEQ ID NO: 2298. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00300] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3 with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the VH of SEQ ID NO: 2297 and the VL of SEQ ID NO: 2298. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00301] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312.

[00302] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds a third antigen, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312.

[00303] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312.

[00304] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312.

[00305] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312.

[00306] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3 and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3 with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312.

[00307] The disclosure also provides an isolated multispecific antibody, comprising: a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312.

[00308] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically

binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds a third antigen, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312.

[00309] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312.

[00310] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312.

[00311] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the

isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8 and wherein the isolated multispecific antibody is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312.

[00312] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3 with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312.

[00313] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296.

[00314] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds a third antigen, wherein the

first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296.

[00315] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296.

[00316] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296.

[00317] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first

antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296.

[00318] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3 and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3 with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296.

[00319] The disclosure also provides an isolated multispecific antibody, comprising: a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and the second antigen binding domain that specifically binds CD3 comprises the

HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296.

[00320] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds a third antigen, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296.

[00321] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296.

[00322] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically

binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296.

[00323] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8 and wherein the isolated multispecific antibody is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296.

[00324] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first

antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3 with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296.

[00325] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, and wherein the antigen expressed by the undesired cell is BCMA. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds a TCR complex provided herein. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00326] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8, and wherein the antigen expressed by the undesired cell is BCMA. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds a TCR complex provided herein. In certain

embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00327] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8, and wherein the antigen expressed by the undesired cell is BCMA. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds a TCR complex provided herein. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00328] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds the TCR with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of the TCR complex and CD8, and wherein the antigen expressed by the undesired cell is BCMA. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds a TCR complex provided herein. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00329] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule

comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, and wherein the antigen expressed by the undesired cell is BCMA. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds a TCR complex provided herein. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00330] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8, and wherein the antigen expressed by the undesired cell is BCMA. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds a TCR complex provided herein. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00331] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and wherein the isolated multispecific antibody is unable to activate or

recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8, and wherein the antigen expressed by the undesired cell is BCMA. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds a TCR complex provided herein. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00332] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds the TCR complex with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of the TCR complex and CD8, and wherein the antigen expressed by the undesired cell is BCMA. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds a TCR complex provided herein. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00333] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, and wherein the antigen expressed by the undesired cell is BCMA. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain

specifically binds CD3 provided herein. In certain embodiments, the isolated moleculecomprises a first antigen binding domain that specifically binds CD8 provided herein.

[00334] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8, and wherein the antigen expressed by the undesired cell is BCMA. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds CD3 provided herein. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00335] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of CD3 and CD8, and wherein the antigen expressed by the undesired cell is BCMA. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds CD3 provided herein. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00336] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3 and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3 with affinities that result in activation or

recruitment of $CD8^+$ CTLs only upon co-engagement of CD3 and CD8, and wherein the antigen expressed by the undesired cell is BCMA. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds CD3 provided herein. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00337] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, and wherein the antigen expressed by the undesired cell is BCMA. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds CD3 provided herein. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00338] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8, and wherein the antigen expressed by the undesired cell is BCMA. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain

specifically binds CD3 provided herein. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00339] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8 and wherein the isolated multispecific antibody is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of CD3 and CD8, and wherein the antigen expressed by the undesired cell is BCMA. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds CD3 provided herein. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00340] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3 with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of CD3 and CD8, and wherein the antigen expressed by the undesired cell is BCMA. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds CD3 provided herein. In certain embodiments, the isolated

multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00341] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296, and wherein the antigen expressed by the undesired cell is BCMA. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00342] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296, and wherein the antigen expressed by the undesired cell is BCMA. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00343] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the

HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296, and wherein the antigen expressed by the undesired cell is BCMA. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00344] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3 and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3 with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296, and wherein the antigen expressed by the undesired cell is BCMA. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00345] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296, and wherein the antigen expressed by the undesired cell is BCMA. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00346] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first

antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296, and wherein the antigen expressed by the undesired cell is BCMA. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00347] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8 and wherein the isolated multispecific antibody is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296, and wherein the antigen expressed by the undesired cell is BCMA. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00348] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first

antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3 with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296, and wherein the antigen expressed by the undesired cell is BCMA. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00349] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the second antigen binding domain that specifically binds CD3 comprises the VH of SEQ ID NO: 2297 and the VL of SEQ ID NO: 2298, and wherein the antigen expressed by the undesired cell is BCMA. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00350] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the VH of SEQ ID NO: 2297 and the VL of SEQ ID NO: 2298, and wherein the antigen expressed by the undesired cell is BCMA. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00351] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-

engagement of CD3 and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the VH of SEQ ID NO: 2297 and the VL of SEQ ID NO: 2298, and wherein the antigen expressed by the undesired cell is BCMA. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00352] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3 and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3 with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the VH of SEQ ID NO: 2297 and the VL of SEQ ID NO: 2298, and wherein the antigen expressed by the undesired cell is BCMA. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00353] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the second antigen binding domain that specifically binds CD3 comprises the VH of SEQ ID NO: 2297 and the VL of SEQ ID NO: 2298, and wherein the antigen expressed by the undesired cell is BCMA. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00354] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically

binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the VH of SEQ ID NO: 2297 and the VL of SEQ ID NO: 2298, and wherein the antigen expressed by the undesired cell is BCMA. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00355] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8 and wherein the isolated multispecific antibody is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the VH of SEQ ID NO: 2297 and the VL of SEQ ID NO: 2298, and wherein the antigen expressed by the undesired cell is BCMA. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00356] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3 with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the VH of SEQ ID NO: 2297 and the VL of SEQ ID NO: 2298, and wherein the antigen expressed by the undesired cell is BCMA. In certain

embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00357] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and wherein the antigen expressed by the undesired cell is BCMA.

[00358] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and wherein the antigen expressed by the undesired cell is BCMA.

[00359] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and wherein the antigen expressed by the undesired cell is BCMA.

[00360] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3 and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3 with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and wherein the antigen expressed by the undesired cell is BCMA.

[00361] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and wherein the antigen expressed by the undesired cell is BCMA.

[00362] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO:

2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and wherein the antigen expressed by the undesired cell is BCMA.

[00363] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8 and wherein the isolated multispecific antibody is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and wherein the antigen expressed by the undesired cell is BCMA.

[00364] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3 with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and wherein the antigen expressed by the undesired cell is BCMA.

[00365] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically

binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296, and wherein the antigen expressed by the undesired cell is BCMA.

[00366] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296, and wherein the antigen expressed by the undesired cell is BCMA.

[00367] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO:

2311 and the LCDR3 of SEQ ID NO: 2312, and the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296, and wherein the antigen expressed by the undesired cell is BCMA.

[00368] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3 and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3 with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296, and wherein the antigen expressed by the undesired cell is BCMA.

[00369] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of

SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296, and wherein the antigen expressed by the undesired cell is BCMA.

[00370] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296, and wherein the antigen expressed by the undesired cell is BCMA.

[00371] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8 and wherein the isolated multispecific antibody is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO:

2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296, and wherein the antigen expressed by the undesired cell is BCMA.

[00372] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3 with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296, and wherein the antigen expressed by the undesired cell is BCMA.

[00373] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, and wherein the antigen expressed by the undesired cell is PSMA. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds aTCR complex provided herein. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00374] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first

antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8, and wherein the antigen expressed by the undesired cell is PSMA. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds aTCR complex provided herein. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00375] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8, and wherein the antigen expressed by the undesired cell is PSMA. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds aTCR complex provided herein. In certain embodiments, the isolated molecule antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00376] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds the TCR with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of the TCR complex and CD8, and wherein the antigen expressed by the undesired cell is PSMA. Exemplary first

antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds aTCR complex provided herein. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00377] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, and wherein the antigen expressed by the undesired cell is PSMA. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds aTCR complex provided herein. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00378] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8, and wherein the antigen expressed by the undesired cell is PSMA. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds aTCR complex provided herein. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00379] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and wherein the isolated multispecific antibody is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8, and wherein the antigen expressed by the undesired cell is PSMA. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds aTCR complex provided herein. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00380] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds the TCR complex with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of the TCR complex and CD8, and wherein the antigen expressed by the undesired cell is PSMA. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds aTCR complex provided herein. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00381] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, and wherein the antigen expressed by the undesired cell is PSMA. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds CD3 provided herein. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00382] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8, and wherein the antigen expressed by the undesired cell is PSMA. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds CD3 provided herein. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00383] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of CD3 and CD8, and wherein the antigen expressed by the undesired cell is PSMA. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen

binding domain specifically binds CD3 provided herein. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00384] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3 and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3 with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of CD3 and CD8, and wherein the antigen expressed by the undesired cell is PSMA. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds CD3 provided herein. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00385] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, and wherein the antigen expressed by the undesired cell is PSMA. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds CD3 provided herein. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00386] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically

binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8, and wherein the antigen expressed by the undesired cell is PSMA. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds CD3 provided herein. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00387] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8 and wherein the isolated multispecific antibody is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of CD3 and CD8, and wherein the antigen expressed by the undesired cell is PSMA. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds CD3 provided herein. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00388] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain

specifically binds CD3 with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of CD3 and CD8, and wherein the antigen expressed by the undesired cell is PSMA. Exemplary first antigen binding domains and second antigen binding domains are provided herein. It is contemplated that an isolated molecule provided herein can comprise any first antigen binding domain specifically binds CD8 provided herein, and any second antigen binding domain specifically binds CD3 provided herein. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00389] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296, and wherein the antigen expressed by the undesired cell is PSMA. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00390] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296, and wherein the antigen expressed by the undesired cell is PSMA. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00391] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first

antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296, and wherein the antigen expressed by the undesired cell is PSMA. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00392] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3 and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3 with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296, and wherein the antigen expressed by the undesired cell is PSMA. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00393] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of

SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296, and wherein the antigen expressed by the undesired cell is PSMA. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00394] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296, and wherein the antigen expressed by the undesired cell is PSMA. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00395] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8 and wherein the isolated multispecific antibody is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296, and wherein the antigen expressed by the undesired cell is PSMA. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00396] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3 with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296, and wherein the antigen expressed by the undesired cell is PSMA. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00397] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the second antigen binding domain that specifically binds CD3 comprises the VH of SEQ ID NO: 2297 and the VL of SEQ ID NO: 2298, and wherein the antigen expressed by the undesired cell is PSMA. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00398] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the VH of SEQ ID NO: 2297 and the VL of SEQ ID NO: 2298, and wherein the antigen expressed by the undesired cell is PSMA. In certain embodiments, the

isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00399] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the VH of SEQ ID NO: 2297 and the VL of SEQ ID NO: 2298, and wherein the antigen expressed by the undesired cell is PSMA. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00400] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3 and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3 with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the VH of SEQ ID NO: 2297 and the VL of SEQ ID NO: 2298, and wherein the antigen expressed by the undesired cell is PSMA. In certain embodiments, the isolated molecule comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00401] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the second antigen binding domain that specifically binds CD3 comprises the VH of SEQ ID NO:

2297 and the VL of SEQ ID NO: 2298, and wherein the antigen expressed by the undesired cell is PSMA. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00402] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the VH of SEQ ID NO: 2297 and the VL of SEQ ID NO: 2298, and wherein the antigen expressed by the undesired cell is PSMA. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00403] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8 and wherein the isolated multispecific antibody is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the VH of SEQ ID NO: 2297 and the VL of SEQ ID NO: 2298, and wherein the antigen expressed by the undesired cell is PSMA. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00404] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically

binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3 with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of CD3 and CD8, wherein the second antigen binding domain that specifically binds CD3 comprises the VH of SEQ ID NO: 2297 and the VL of SEQ ID NO: 2298, and wherein the antigen expressed by the undesired cell is PSMA. In certain embodiments, the isolated multispecific antibody comprises a first antigen binding domain that specifically binds CD8 provided herein.

[00405] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and wherein the antigen expressed by the undesired cell is PSMA.

[00406] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and wherein the antigen expressed by the undesired cell is PSMA.

[00407] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an

undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and wherein the antigen expressed by the undesired cell is PSMA.

[00408] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3 and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3 with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and wherein the antigen expressed by the undesired cell is PSMA.

[00409] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and wherein the antigen expressed by the undesired cell is PSMA.

[00410] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule

comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and wherein the antigen expressed by the undesired cell is PSMA.

[00411] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8 and wherein the isolated multispecific antibody is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and wherein the antigen expressed by the undesired cell is PSMA.

[00412] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3 with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID

NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and wherein the antigen expressed by the undesired cell is PSMA.

[00413] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296, and wherein the antigen expressed by the undesired cell is PSMA.

[00414] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296, and wherein the antigen expressed by the undesired cell is PSMA.

[00415] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically

binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296, and wherein the antigen expressed by the undesired cell is PSMA.

[00416] The disclosure also provides an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3 and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3 with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296, and wherein the antigen expressed by the undesired cell is PSMA.

[00417] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first

antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296, and wherein the antigen expressed by the undesired cell is PSMA.

[00418] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296, and wherein the antigen expressed by the undesired cell is PSMA.

[00419] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated multispecific antibody activates or recruits $CD8^+$ CTLs upon co-engagement of CD3 and CD8 and wherein the isolated multispecific antibody is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of CD3 and CD8, wherein the first antigen binding

domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296, and wherein the antigen expressed by the undesired cell is PSMA.

[00420] The disclosure also provides an isolated multispecific antibody, comprising: a first half molecule and a second half molecule, wherein the first half molecule comprises a first antigen binding domain and a second antigen binding domain and the second half molecule comprises a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds CD3, and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds CD3 with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of CD3 and CD8, wherein the first antigen binding domain that specifically binds CD8 comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312, and the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296, and wherein the antigen expressed by the undesired cell is PSMA.

[00421] The isolated molecule or the isolated multispecific antibody of the disclosure may be targeted to any undesired cell via the antigen binding domain that specifically binds an antigen expressed by the undesired cell. The isolated molecule or the multispecific antibody of the disclosure may be further engineered to comprise additional antigen binding domains which may, for example, bind a second antigen expressed by the undesired cell. In some embodiments, the undesired cell is a pathogenic cell. In some embodiments, the pathogenic cell is a cancer cell, a virus infected cell, an immune cell, an inflamed cell, a damaged cells, a

foreign cell, an apoptotic cell, a dysplastic cell, an immunogenic cell, a metaplastic cell or a mutant cell, or any combination thereof.

[00422] In some embodiments, the isolated molecule or the isolated multispecific antibody of the disclosure may bind an antigen that is inert in a system the antibody is used, such as a virus coat protein, such as RSV. The isolated molecule or the isolated multispecific antibody incorporating an inert arm may be used as a research tool as is known and described herein.

[00423] In some embodiments, the undesired cell is a cancer cell. In some embodiments, the cancer cell is a malignant cancer cell. In some embodiments, the cancer cell originates from a solid tumor. In some embodiments, the cancer cell originates from a hematological malignancy.

[00424] In some embodiments, the cancer cell originates from adenocarcinoma, anal cancer, basal cell carcinoma, biliary tract cancer, bladder cancer, bone cancer, breast cancer, cancer associated with infection, cancer of the adrenal gland, cancer of the endocrine system, cancer of the head or neck, cancer of the parathyroid gland, cancer of the penis, cancer of the thyroid gland, cancer of the urethra, cervical cancer, carcinoma of the breast, carcinoma of the fallopian tubes, carcinoma of the liver, carcinoma of the lung, carcinoma of the prostate, carcinoma of the renal pelvis, carcinoma of the vagina, carcinoma of the vulva, choriocarcinoma, clear cell carcinoma, colon cancer, colon carcinoma, colorectal cancer, connective tissue cancer, cutaneous or intraocular malignant melanoma, environmentally induced cancer, gastric cancer, gastrointestinal cancer, glioma, glioblastoma, endometrial cancer, epithelial cancer, esophageal cancer, eye cancer, larynx cancer, liver cancer, hepatocellular carcinoma, hormone refractory prostate adenocarcinoma, Kaposi's sarcoma, kidney cancer, lung cancer gastro-esophageal cancer, melanoma, mesothelioma, Merkel cell cancer, neuroblastoma, non-small cell lung cancer (NSCLC), osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, rectal cancer, renal cell carcinoma, retinoblastoma rhabdomyosarcoma, squamous cell cancer, soft tissue sarcoma, solid tumors of childhood, spinal axis tumor, stomach cancer, testicular cancer, thyroid cancer, uterine cancer, urothelial carcinoma or sarcomas, or any combination thereof.

[00425] In some embodiments, the cancer cell originates from B cell malignancies. In some embodiments, the cancer cell originates from T cell malignancies. In some embodiments, the cancer cell originates from NK cell malignancies. In some embodiments, the cancer cell originates from acute lymphoblastic leukemia, acute myeloid leukemia, anaplastic large-cell lymphoma, Burkitt's lymphoma, chronic lymphocytic leukemia, chronic myeloid leukemia,

diffuse large B-cell lymphoma, dendritic cell neoplasm, follicular lymphoma, hairy cell leukemia, Hodgkin's lymphoma, leukemia, B cell leukemia, T cell leukemia, light chain amyloidosis, lymphoma, B cell lymphoma, NK cell lymphoma, T cell lymphoma, mantle-cell lymphoma, marginal zone B-cell lymphoma, monoclonal gammopathy of undetermined significance, mucosa-associated lymphatic tissue lymphoma, multiple myeloma, myelodysplastic syndrome, non-Hodgkin's lymphoma, plasma cell leukemia, precursor B-cell lymphoblastic leukemia, smoldering multiple myeloma or Waldenstrom's macroglobulinemia.

[00426] In some embodiments, the undesired cell is an infected cell. In some embodiments, the undesired cell is infected with bacteria, virus, fungi, protozoa, parasite or prion. In some embodiments, the undesired cell is a bacterial infected cell. In some embodiments, the undesired cell is a virus infected cell.

[00427] In some embodiments, the virus infected cell is infected with adenovirus, arboviral encephalitis virus, coronavirus, coxsackie virus, cytomegalovirus (CMV), dengue virus, echovirus, Epstein Barr virus, flaviviruses, human immunodeficiency virus (HIV), hepatitis A virus, hepatitis B virus, hepatitis C virus, herpes virus, HTLV virus, influenza virus, JC virus, measles virus, molluscum virus, mumps virus, papillomavirus, parvovirus, poliovirus, rabies virus, respiratory syncytial virus, rhinovirus, rotavirus, rubella virus or vaccinia virus.

[00428] In some embodiments, the undesired cell is an immune cell. In some embodiments, the undesired cell is an activated immune cell. In some embodiments, the immune cell is a $CD4^+$ cell. $CD4^+$ expressing cells include Th1, Th2, Th9, Th17, T-follicular helper (Tfh), Treg, central memory (Tcm), effector memory (Tem), tissue resident memory (Trm), T peripheral helper (Tph) and memory stem cells (Tscm). In some embodiments, the immune cell is a Th1 cell. In some embodiments, the immune cell is a Th2 cell. In some embodiments, the immune cell is a Th9 cell. In some embodiments, the immune cell is a Th17 cell. In some embodiments, the immune cells is a Treg cell. In some embodiments, the immune cells is an antigen-presenting cell. In some embodiments, the immune cells is a macrophage. In some embodiments, the immune cells is a M1 macrophage. In some embodiments, the immune cells is a M2 macrophage. In some embodiments, the immune cells is a dendritic cell. In some embodiments, the immune cell is a B cell. In some embodiments, the immune cell is a natural killer (NK) cell. In some embodiments, the immune cells is a B regulatory (Breg) cell. In some embodiments, the immune cell is a myeloid derived suppressor cell (MDSC) cell. In some

embodiments, the immune cell is a neutrophil. In some embodiments, the immune cell is a mast cell. In some embodiments, the immune cell is a $CD8^+$ T cell that lacks expression of CD3. In some embodiments, the immune cell is an activated T cell. In some embodiments, the immune cell is a granulocyte.

[00429] In some embodiments, the undesired cell is a platelet. In some embodiments, the undesired cell is an endothelial cell. In some embodiments, the undesired cell is an epithelial cell.

[00430] In some embodiments, the undesired cell is a cell that contributes to pathogenesis of an immune-mediated disease, such as an inflammatory disease, an autoimmune disease or any condition resulting in tissue damage destruction, or any combination thereof.

[00431] In some embodiments, the undesired cell is a B cell that contributes to pathogenesis of multiple sclerosis, type 1 diabetes or rheumatoid arthritis.

[00432] In some embodiments, the undesired cell is a γδ T cell that contributes to pathogenesis of an autoimmune disease, such as rheumatoid arthritis or systemic lupus erythematosus (SLE).

[00433] In some embodiments, the undesired cell is a $PD\text{-}1^+CD4^+$ T cell, such as Tfh or Tph cell, that promotes B cell responses and antibody production and contribute to autoimmune diseases driven by autoantibody production, including rheumatoid arthritis, systemic lupus erythematosus, and Sjogren's Syndrome (see *e.g.,* US2019/0298850).

[00434] In some embodiments, the antigen expressed by an undesired cell is a tumor-associated antigens (TAAs) or tumor- specific antigens (TSAs). In some embodiments, the antigen expressed by an undesired cell comprises mesothelin, alpha-fetoprotein (ALP), BAGE, BCR-ABL, beta-catenin, beta-HCG, BrE3-antigen, BCA225, BCMA, BTAA, CA125, CA195, CA242, CA-50, CAM43, CAMEL, CAP-l, carbonic anhydrase IX, CA19-9, CA72-4, CAM 17.1, CASP-8, CCCL19, CCCL21, CD1, CD la, CD2, CD4, CD5, CD11A, CD14, CD15, CD16, CD18, CD19, CD20, CD21, CD22, CD23, CD25, CD29, CD30, CD32b, CD33, CD37, CD38, CD40, CD40L, CD44, CD45, CD46, CD47, CD52, CD54, CD55, CD59, CD64, CD66a-e, CD67, CD68, CD70, CD70L, CD74, CD79a, CD79b, CD80, CD83, CD95, CD123, CD126, CD132, CD133, CD138, CD147, CD154, CDC27, CDK4, CDK4m, CDKN2A, CO-029, CTLA4, CXCR4, CXCR7, CXCL12, HIF-la, colon- specific antigen-p (CSAp), CEACAM5) CEACAM6, c-Met, DAM, E2A-PRL, EGFR, EGFRvIII, EGP-l , EGP-2, ELF2-M, Ep-CAM,

FGF, FGF-5, Flt-l, Flt- 3, folate receptor, G250 antigen, Ga733VEpCAM, GAGE, gplOO, GRO-b, H4-RET, HLA-DR, HM1.24, human chorionic gonadotropin (HCG) HER2, HER3, HMGB-l, HIF-l, HSP70-2M, HST-2, HTgp-l75, la, IGF-1R, IFN-g, IFN-a, IFN-b, IFN- l, IL-4R, IL-6R, IL-13R, IL-15R, IL-17R, IL-18R, IL-2, IL-6, IL-8, IL-12, IL-15, IL-17, IL-18, IL-23, IL-25, insulin-like growth factor- 1 (IGF-l), KC4-antigen, KLK2, KSA, KS-l-antigen, KS1-4, LAGE-la, Le-Y, LDR/FUT, M344, MA-50, macrophage migration inhibitory factor (MIF), MAGE, MAGE-l, MAGE-3, MAGE-4, MAGE-5, MAGE-6, MART-l, MART-2, TRAG-3, MCP-l, MIP-1A, MIP-1B, MIF, MG7-Ag, MOV18, MUC1, MUC2, MUC3, MUC4, MUC5ac, MUC13, MUC16, MUM- 1/2, MUM-3, MYL-RAR, NB/70K, Nm23Hl, NuMA, NCA66, NCA95, NCA90, NY-ESO-l, pl5, pl6, pl85erbB2, pl80erbB3, PAM4 antigen, pancreatic cancer mucin, PD-l, PD-L1, PD-L2, PI5, placental growth factor, p53, PLAGL2, Pmell7 prostatic acid phosphatase, PSA, PRAME, PSMA, P1GF, ILGF, ILGF-1R, IL-6, IL-25, RCAS1, RS5, RAGE, RANTES, Ras, T101, SAGE, S100, SLAMF7, survivin, survivin-2B, SDDCAG16, TA-90\Mac2 binding protein, TAAL6, TAC, TAG-72, TLP, tenascin, TMEFF2, TRAIL receptors, TRP-l, TRP-2, TSP-180, VEGFR, ED-B fibronectin, WT-l, l7-lA-antigen, C3, C3a, C3b, C5a, C5, bcl-2, K-ras, tumor neoantigen or a viral antigen associated with cancer.

[00435] In some embodiments, the antigen expressed by an undesired cell is a viral antigen or a bacterial antigen. In some embodiments, the tumor antigen is a viral antigen derived from a virus associated with a human chronic disease or cancer (such as cervical cancer). For example, in some embodiments, the viral antigen is derived from Epstein-Barr virus (EBV), HPV antigens E6 and/or E7, hepatitis C virus (HCV), hepatitis B virus (HBV), or cytomegalovirus (CMV).

[00436] In some embodiments, the antigen expressed by an undesired cell is an antigen expressed by undesired immune cells. In some embodiments, the antigen expressed by undesired immune cells is CD19, CD20, CD38, BCMA, FcγRIIB, CD4, IL-12β2R, IL-18R, CD25, CTLA-4, CD40L, CD28, CD56, CD38, CD14, CD33, CD11c, CD123, CD66b, CD41, CD61, CD62, CD235a, CD146, CD326, CD23 or CD203c.

[00437] Exemplary cancers or tumors and specific tumor antigens associated with such tumors (but not exclusively), include acute lymphoblastic leukemia (etv6, amll, cyclophilin b), B cell lymphoma (Ig-idiotype), glioma (E-cadherin, a-catenin, b-catenin, g-catenin, pl20ctn), bladder cancer (p2lras), biliary cancer (p2lras), breast cancer (MUC family, HER2/neu, c-erbB-

2), cervical carcinoma (p53, p2lras), colon carcinoma (p2lras, HER2/neu, c-erbB-2, MUC family), colorectal cancer (Colorectal associated antigen (CRC)-COl7-lA/GA733, APC), choriocarcinoma (CEA), epithelial cell cancer (cyclophilin b), gastric cancer (HER2/neu, c-erbB- 2, ga733 glycoprotein), hepatocellular cancer (a-fetoprotein), Hodgkins lymphoma (Imp-l, EBNA-l), lung cancer (CEA, MAGE-3, NY-ESO-l), lymphoid cell-derived leukemia (cyclophilin b), melanoma (p5 protein, gp75, oncofetal antigen, GM2 and GD2 gangliosides, Melan-A/MART-l, cdc27, MAGE-3, p2lras, gplOO), myeloma (MUC family, p2lras), non-small cell lung carcinoma (HER2/neu, c-erbB-2), nasopharyngeal cancer (Imp-l, EBNA-l), ovarian cancer (MUC family, HER2/neu, c-erbB-2), prostate cancer (KLK2, Prostate Specific Antigen (PSA) and its antigenic epitopes PSA-l, PSA-2, and PSA-3, PSMA, HER2/neu, c-erbB-2, ga733 glycoprotein, TMEFF2), renal cancer (HER2/neu, c-erbB-2), squamous cell cancers of the cervix and esophagus, testicular cancer (NY-ESO-l), T cell leukemia (HTLV-l epitopes), and viral products or proteins, multiple myeloma (CD38, BCMA), AML (CD33, flt3), B cell malignancies (CD19, CD20, CD38), light chain amyloidosis (CD38).

[00438] Neoantigens presented on various tumor cells in the context of MHC may also be targeted using the isolated molecules or the multispecific antibodies of the disclosure. In these instances, the first antigen binding domain that specifically binds an antigen on undesired cells specifically binds a peptide/MHC complex expressed by the undesired cells. In these instances the isolated molecules or the multispecific antibodies of the disclosure may be used to target undesired cells harboring intracellular mutant, dysfunctional or foreign proteins. Exemplary neoantigens which may be targeted are disclosed for example in US10155031, US20180153975, US20190030147 and WO2017173321.

[00439] Exemplary antigens on undesired B cells comprise CD19, CD20, CD38, BCMA and FcγRII.

[00440] Exemplary antigens on undesired $CD4^+$ T cells comprise CD4, IL-12β2R and IL-18R.

[00441] Exemplary antigens on undesired activated T cells comprise CD25, CTLA-4 and CD40L.

[00442] Exemplary antigens on undesired T cells comprise CD28.

[00443] Exemplary antigens on undesired NK cells comprise CD56 and CD38.

[00444] Exemplary antigens on undesired macrophages comprise CD14 and CD33.

[00445] Exemplary antigens on undesired monocytes comprise CD14 and CD33.

[00446] Exemplary antigens on undesired dendritic cells comprise CD11c and CD123.

[00447] Exemplary antigens on undesired granulocytes comprise CD66b.

[00448] Exemplary antigens on undesired platelets comprise CD41, CD61 and CD62.

[00449] Exemplary antigens on undesired erythrocytes comprise CD235a.

[00450] Exemplary antigens on undesired endothelial cells comprise CD146.

[00451] Exemplary antigens on undesired epithelial cells comprise CD326.

[00452] Exemplary antigens on undesired mast cells comprise FcεR1, CD23 and CD203c.

[00453] Exemplary antigens on undesired Tfh or Tph cells comprise PD-1.

Methods Of Making Molecules Of The Disclosure

Antigen binding domains that specifically bind the TCR complex, CD8 or an antigen expressed by an undesired cell.

[00454] The antigen binding domains that specifically bind the TCR complex, CD8 or the antigen expressed by the undesired cell may be generated using known molecular biology technologies. The various antigen binding domains may be already known domains or they may be selected *de novo* using known methods.

[00455] Antigen binding domains of desired specificity may be selected from a phage, mammalian or *E. coli* libraries expressing human immunoglobulins or portions thereof such as Fabs, single chain antibodies (scFv), unpaired or paired antibody variable regions, camelid VHH domains or non-antibody scaffolds. The libraries may be screened for binding to the desired antigen and the obtained positive clones may be further characterized, re-engineered into various antigen binding domain formats as described herein and incorporated into the isolated molecules or isolated multispecific antibodies of the disclosure.

[00456] The hybridoma method of Kohler and Milstein may be used to identify VH/VL pairs from non-human species having the desired specificity.

[00457] Antigen binding domains of desired specificity may also be generated by immunizing non-human animals and subsequently humanized. Exemplary humanization techniques including selection of human acceptor frameworks include CDR grafting (U.S. Patent No. 5,225,539), SDR grafting (U.S. Patent No. 6,818,749), Resurfacing (Padlan, (1991) *Mol Immunol* 28:489-499), Specificity Determining Residues Resurfacing (U.S. Patent Publ. No. 2010/0261620), human framework adaptation (U.S. Patent No. 8,748,356) or

superhumanization (U.S. Patent No. 7,709, 226). In these methods, CDRs or a subset of CDR residues of parental antibodies are transferred onto human frameworks that may be selected based on their overall homology to the parental frameworks, based on similarity in CDR length, or canonical structure identity, or a combination thereof.

[00458] Transgenic animals, such as mice, rat or chicken carrying human immunoglobulin (Ig) loci in their genome may be used to generate antigen binding domains of desired specificity and are described in for example U.S. Patent No. 6,150,584, Int. Patent Publ. No. WO1999/45962, Int. Patent Publ. Nos. WO2002/066630, WO2002/43478, WO2002/043478 and WO1990/04036. The endogenous immunoglobulin loci in such animal may be disrupted or deleted, and at least one complete or partial human immunoglobulin locus may be inserted into the genome of the animal using homologous or non-homologous recombination, using transchromosomes, or using minigenes. Companies such as Regeneron (http://_www_regeneron_com), Harbour Antibodies (http://_www_harbourantibodies_com), Open Monoclonal Technology, Inc. (OMT) (http://_www_omtinc_net), KyMab (http://_www_kymab_com), Trianni (http://_www.trianni_com) and Ablexis (http://_www_ablexis_com) may be engaged to provide human antibodies directed against a selected antigen using technologies as described above.

[00459] Humanized antigen biding domains may be further optimized to improve their selectivity or affinity to a desired antigen by incorporating altered framework support residues to preserve binding affinity (backmutations) by techniques such as those described in Int. Patent Publ. Nos. WO1090/007861 and WO1992/22653, or by introducing variation at any of the CDRs for example to improve affinity of the antigen binding domain.

[00460] Preparation of antigens (*e.g.,* the TCR complex, CD8 and an antigen expressed by an undesired cell), their expression and production of antigen binding domains of the disclosure may be performed using any suitable technique, such as recombinant protein production. The antigens may be administered to an animal in the form of purified protein, or protein mixtures including whole cells or cell or tissue extracts, or the antigen may be formed *de novo* in the animal's body from nucleic acids encoding said antigen or a portion thereof.

[00461] Antigens presented on MCH, either class I or class II, may be prepared as recombinant antigen/MHC complexes using known methods, such as covalently coupling the antigen (*i.e.,* peptide) to the MHC, optionally using cleavable linkers and expressing the

complex as soluble molecules in a format such peptide-β2-α2-α1-β1 chain , peptide-α1-β1-α2-β2 or peptide- α1- α2-α3 as a heterodimer with β2 macroglobulin. Linkers which are at least 15 amino acids long may be used between the antigen and the MCH. Various additional expression formats are disclosed in US5976551, US5734023, US5820866, US7141656B2, US6270772B1 and US7074905B2.

Molecular formats

[00462] The molecules or the multispecific antibodies of the disclosure may be engineered into any multivalent format using any known or *de novo* identified antigen binding domain as long as molecules or the multispecific antibodies of the disclosure comprise the first antigen binding domain that specifically binds the undesired antigen, the second antigen binding domain that specifically binds the TCR complex and the third antigen binding domain that specifically binds CD8, and through selection of the first antigen binding domain and the second antigen binding domain, activate or recruit $CD8^+$ CTLs cells only upon co-engagement of the TCR complex and CD8. Exemplary formats are disclosed herein, and include molecules into which the antigen binding domains are engineered as scFv, Fab, Fv, VHH, dAb, VH, VL, Fab or as non-antibody scaffold as disclosed herein onto one or more Fc domains or fragment thereof, or optionally onto other scaffolds such as half-life extending moieties including albumin, transferrin or PEG. In the multispecific antibodies of the disclosure containing a first half molecule and a second half molecule, the second antigen binding domain that specifically binds the TCR complex and the third antigen binding domain that specifically binds CD8 may be engineered into the second half molecule and the antigen binding domain that specifically binds the antigen un undesired cells may be engineered into the first half molecule to provide spatial closeness of the second antigen binding domain and the third antigen binding domain to facilitate co-engagement. Exemplary formats that may be used (and their binding specificity) are:

[00463] Format 1:

[00464] 1st polypeptide: scFv(TCRcomplex)-VH(CD8)-CH1-hinge-CH2-CH3

[00465] 2nd polypeptide: VL(CD8)-CL

[00466] 3rd polypeptide: scFv(antigen on undesired cell)-Fc

[00467] Format 2:

[00468] 1st polypeptide: VH(CD8)-CH1-hinge-CH2-CH3

[00469] 2nd polypeptide: VL(CD8)-CL-scFv(TCRcomplex)

[00470] 3rd polypeptide: scFv(antigen on undesired cell)-Fc

[00471] Format 3:

[00472] 1st polypeptide: VH(CD8)-CH1-hinge-CH2-CH3-scFv(TCRcomplex)

[00473] 2nd polypeptide: VL(CD8)-CL

[00474] 3rd polypeptide: scFv(antigen on undesired cell)-Fc

[00475] Format 4:

[00476] 1st polypeptide: scFv(TCRcomplex)-VH(CD8)-CH1-hinge-CH2-CH3

[00477] 2nd polypeptide: VL(CD8)-CL

[00478] 3rd polypeptide: scFv(inert)-Fc

[00479] Format 5:

[00480] 1st polypeptide: VH(CD8)-CH1-hinge-CH2-CH3

[00481] 2nd polypeptide: VL(CD8)-CL-scFv(TCRcomplex)

[00482] 3rd polypeptide: scFv(inert)-Fc

[00483] Format 6:

[00484] 1st polypeptide: VH(CD8)-CH1-hinge-CH2-CH3-scFv(TCRcomplex)

[00485] 2nd polypeptide: VL(CD8)-CL

[00486] 3rd polypeptide: scFv(inert)-Fc

[00487] Fab used in the isolated molecules or in the multispecific antibodies of the disclosure may also be engineered by exchanging the VL and the VH domains for each other or exchanging the CH1 and LC domains for each other, as described in Int. Pat. Publ. No. WO2009/080251. Correct Fab pairing may also be promoted by introducing one or more amino acid substitutions in the CH1, CL, VH or VL domains of the Fab. The amino acids that are modified are typically part of the VH:VL and CH1:CL interface such that the Fab components preferentially pair with each other rather than with components of other Fabs. The amino acid substitutions may be made at the conserved framework residues of the VH/VL and CH1/CL domains. The modifications introduced in the VH and CH1 and/or VL and CL domains may be complementary to each other and may be achieved on the basis of steric and hydrophobic contacts, electrostatic/charge interactions or a combination of the variety of interactions. The complementarity between protein surfaces is broadly described in the literature in terms of lock and key fit, knob into hole, protrusion and cavity, donor and acceptor etc., all implying the

nature of structural and chemical match between the two interacting surfaces. Exemplary substitutions are described in WO2014/150973 and WO2014/082179, and include a T192E substitution in the CH1 domain and S114A and N137K substitutions in the CL domain, which introduces a salt-bridge between the CH1 and CL domains (see, Golay et al., 2016, J Immunol 196:3199-211). Alternatively, the Fab domain may comprise a 143Q and 188V substitutions in the CH1 domain and 113T and 176V substitutions in the CL domain, which serves to swap hydrophobic and polar regions of contact between the CH1 and CL domain (see, Golay et al., 2016, J Immunol 196:3199-211).

[00488] Fabs may also be engineered into a single chain Fab fragment, which is a polypeptide consisting of VH-CH1-VL-CL and an optional linker between the various domains. Exemplary single chain Fab fragments that may be used in the isolated molecules or in the multispecific antibodies of the disclosure include formats in N-to C-terminal order: VH-CH1-linker-VL-CL, VL-CL- linker-VH-CH1 , VH-CL-linker-VL-CH1 or VL-CH1-linker-VH-CL. The linker may be a polypeptide of at least 30 amino acids, such as between about 32 and about 50 amino acids. The single chain Fab domains may be stabilized via the natural disulfide bond between the CL domain and the CH1 domain or alternatively, via an engineered disulfide bond between the VH and the VL between following positions: VH position 44 to VL position 100, VH position n105 to VL position 43, or VH position 101 to VL position 100 (numbering according to the EU index.

[00489] scFvs may be incorporated into the isolated molecules or into the multispecific antibodies of the disclosure in either order, *e.g.,* from N- to C-terminus in the order VH-linker-VL or VL-linker-VH. scFvs incorporated into the molecules of the disclosure may be stabilized by engineering interdomain disulfide bonds between the VH and the VL. The disulfide bond may be engineered for example between the VH position H44 and the VL position L100, between the VH position H46 and the VL position L98, between the VH position H101 and the VL position L44, between the VH position H103 and the VL position L42, or between the VH position H103 and the VL position L43 (see. *e.g., Zhao et al., Int J Mol Sci* 12: 1-11, 2011).

[00490] VHH domains from *Camelidae* family, such as camels, llamas and alpacas, as well as other single domain antibodies may also be incorporated as antigen binding domains into the isolated molecules or in the multispecific antibodies of the disclosure. The VHH domains may be further engineered at hallmark residues, such as residues 11, 37, 44, 45 and 47 (residue

numbering according to Kabat) (Muyldermans, Reviews Mol Biotech 74:277-302 (2001), US9156905).

[00491] Non-antibody scaffolds may also be used as antigen binding domains and incorporated into the molecules or the multispecific antibodies of the disclosure. Such scaffolds are typically derived from repeat proteins and include ankyrin repeat proteins (DARPins), Avimers (short for avidity multimers; domain A of LDL receptor), Anticalin/Lipocalins, Kunitz domains, Affibodies, Adnexins, Affilins, Affitins (also known as Nanofitins), Knottins, Pronectins, Versabodies, Duocalins, and Fynomers and fibronectin type III (Fn3) repeat based scaffold such as Centyrins. Non-antibody scaffolds that can be used include those described in Mintz and Crea, 2013, Bioprocess International 11(2):40-48).

[00492] Additional formats that incorporate the desired multispecificity into the molecules or the multispecific antibodies of the disclosure that may be used include those described in Int. Pat. Publ. WO2019/195535. For example, a Fab, Fv, scFv or non-antibody scaffolds (*e.g.*, non-immunoglobulin based domains) may be attached to one or two Fc domains or fragments thereof or to a light chain or fragment thereof, either N- or C-terminally, to generate trispecific molecules. Antigen binding domains may also be conjugated head-to-tail into one Fc or fragment thereof or into one light chain or fragment thereof. Additional trispecific formats that may be used are formats disclosed in WO2014/145806; WO2017/124002; Liu et al., Front Immunol. 8:38, 2017; Brinkmann & Kontermann, 2017, mAbs 9:2, 182-212; US2016/0355600; Klein et al., 2016, MAbs 8(6):1010- 20; and US2017/0145116, or formats further engineered by incorporating one or more additional antigen binding domains into the formats disclosed in any of the references.

[00493] The isolated molecules or the multispecific antibodies of the disclosure comprising a first half molecule and a second half molecule, or two Fc domains or fragments thereof, may be engineered to promote preferred association of the first half molecule and the second half molecule or the two Fc domains or fragments thereof by engineering mutations into the CH3 domains which promote heterodimerization of the first half molecule and the second half molecule or the two Fc domains or fragments thereof (instead of homodimerization) Exemplary CH3 mutations that may be used in the first half molecule and in the second half molecule include technologies such as Duobody® mutations (Genmab), Knob-in-Hole mutations (Genentech), electrostatically-matched mutations (Chugai, Amgen, NovoNordisk, Oncomed),

the Strand Exchange Engineered Domain body (SEEDbody) (EMD Serono), and other asymmetric mutations (*e.g.*, Zymeworks). Duobody® mutations (Genmab) are disclosed for example in US9150663 and US2014/0303356 and include mutations F405L/K409R, wild-type/F405L_R409K, T350I_K370T_F405L/K409R, K370W/K409R, D399AFGHILMNRSTVWY/K409R, T366ADEFGHILMQVY/K409R, L368ADEGHNRSTVQ/K409AGRH, D399FHKRQ/K409AGRH, F405IKLSTVW/K409AGRH and Y407LWQ/K409AGRH. Knob-in-hole mutations are disclosed for example in WO1996/027011 and include mutations on the interface of CH3 region in which an amino acid with a small side chain (hole) is introduced into the first CH3 region and an amino acid with a large side chain (knob) is introduced into the second CH3 region, resulting in preferential interaction between the first CH3 region and the second CH3 region. Exemplary CH3 region mutations forming a knob and a hole are T366Y/F405A, T366W/F405W, F405W/Y407A, T394W/Y407T, T394S/Y407A, T366W/T394S, F405W/T394S and T366W/T366S_L368A_Y407V. Heterodimer formation may be promoted by using electrostatic interactions by substituting positively charged residues on the first CH3 region and negatively charged residues on the second CH3 region as described in US2010/0015133, US2009/0182127, US2010/028637 or US2011/0123532. Other asymmetric mutations that may be used to promote heavy chain heterodimerization are L351Y_F405A_Y407V/T394W, T366I_K392M_T394W/F405A_Y407V, T366L_K392M_T394W/F405A_Y407V, L351Y_Y407A/T366A_K409F, L351Y_Y407A/T366V_K409F, Y407A/T366A_K409F, or T350V_L351Y_F405A_Y407V/T350V_T366L_K392L_T394W as described in US2012/0149876 or US2013/0195849. SEEDbody mutations involve substituting select IgG residues with IgA residues to promote heterodimerization as described in US20070287170. Other exemplary mutations that may be used are R409D_K370E/D399K_E357K, S354C_T366W/Y349C_ T366S_L368A_Y407V, Y349C_T366W/S354C_T366S_L368A_Y407V, T366K/L351D, L351K/Y349E, L351K/Y349D, L351K/L368E, L351Y_Y407A/T366A_K409F, L351Y_Y407A/T366V_K409F, K392D/D399K, K392D/ E356K, K253E_D282K_K322D/D239K_E240K_K292D, K392D_K409D/D356K_D399K as described

in WO2007/147901, WO 2011/143545, WO2013157954, WO2013096291 and US2018/0118849.

Linkers

[00494] The isolated molecules or the multispecific antibodies of the disclosure may also comprise linkers connecting one or more antigen binding domains to the VH, the VL, the CH1 domain, the CL domain, the CH2 domain, the CH3 domain, the Fc region or fragments thereof, albumin, PEG, transferrin, or to one another. Various linkers may be used, including synthetic sequences or sequences from native immunoglobulin hinge regions or fragments thereof, or modified hinge regions. Hinge regions may be derived from human or any other species, such as mouse, rat, rabbit, camel, llama, shark, goat or dog. Hinge regions may be of different isotype than the HC or Fc region that is used in the particular molecule of the disclosure. The hinge regions or fragments thereof may be modified by one or more substitution, such as substitutions that increase or decrease the number of cysteine residues in the hinge. Modified hinge regions are those disclosed for example in U.S. Pat. No. 5,677,425, W09915549, W02005003170, W02005003169, W02005003170, W09825971 and W02005003171. Exemplary hinge regions or fragments thereof or modified hinge regions are shown in **Table 1**.

Table 1.

Hinge region name	Amino acid sequence	SEQ ID
H1 Human lgA1	VPSTPPTPSPSTPPTPSPS	2183
H2 Human lgA2	VPPPPP	2184
H3 Human IgD	ESPKAQASSVPTAQPQAEGSLAKATTAPATTRN TGRGGEEKKKEKEKEEQEERETKTP	2185
H4 Human lgG1	EPKSCDKTHTCPPCP	2186
H5 Human lgG2	ERKCCVECPPCP	2187
H6 Human lgG3	ELKTPLGDTTHTCPRCPEPKSCDTPPPCPRCPE PKSCDTPPPCPRCPEPKSCDTPPPCPRCP	2188
H7 Human lgG4	ESKYGPPCPSCP	2189
H8 Human lgG4(P)	ESKYGPPCPPCP	2190
H9 Engineered hinge v1	CPPC	2191
H10 Engineered hinge v2	CPSC	2192
H11 Engineered hinge v3	CPRC	2193
H12 Engineered hinge v4	SPPC	2194
H13 Engineered hinge v5	CPPS	2195
H14 Engineered hinge v6	SPPS	2196
H15 Engineered hinge v7	DKTHTCAA	2197
H16 Engineered hinge v8	DKTHTCPPCPA	2198
H17 Engineered hinge v9	DKTHTCPPCPATCPPCPA	2199

Hinge region name	Amino acid sequence	SEQ ID
H18 Engineered hinge	DKTHTCPPCPATCPPCPATCPPCPA	2200
H19 Engineered hinge	DKTHTCPPCPAGKPTLYNSLVMSDTAGTCY	2201
H20 Engineered hinge	DKTHTCPPCPAGKPTHVNVSVVMAEVDGTCY	2202
H21 Engineered hinge	DKTHTCCVECPPCPA	2203
H22 Engineered hinge	DKTHTCPRCPEPKSCDTPPPCPRCPA	2204
H23 Engineered hinge	DKTHTCPSCPA	2205

[00495] Synthetic linkers that may be used to connect the antigen binding domains to one another or the VH, the VL, the CH1 domain, the CL domain, the CH2 domain, the CH3 domain or the Fc region or fragments thereof include flexible and/or charged peptide linkers of varying length, such as linkers between from about 2 to about 60 amino acids. Synthetic linkers that may be used include those disclosed by Chen et al., 2013, Adv Drug Deliv Rev. 65(10): 1357-1369 and Klein et al., 2014, Protein Engineering, Design & Selection 27(10): 325-330. Exemplary suitable synthetic linkers are shown in **Table 2**.

Table 2.

Linker name	Linker amino acid sequence	SEQ
L1	ADAAP	2206
L2	ADAAPTVSIFP	2207
L3	ADAAPTVSIFPP	2208
L4	AKTTAP	2209
L5	AKTTAPSVYPLAP	2210
L6	AKTTPKLEEGEFSEARV	2211
L7	AKTTPKLGG	2212
L8	AKTTPP	2213
L9	AKTTPPSVTPLAP	2214
L10	ASTKGP	2215
L11	ASTKGPSVFPLAP	2216
L12	ASTKGPSVFPLAPASTKGPSVFPLAP	2217
L13	EGKSSGSGSESKST	2218
L14	GEGESGEGESGEGES	2219
L15	GEGESGEGESGEGESGEGES	2220
L16	GEGGSGEGGSGEGGS	2221
L17	GENKVEYAPALMALS	2222
L18	GGEGSGGEGSGGEGS	2223
L19	GGGESGGEGSGEGGS	2224
L20	GGGESGGGESGGGES	2225
L21	GGGGSGGGGS	2226
L22	GGGGSGGGGSGGGGS	2227
L23	GGGGSGGGGSGGGGSGGGGS	2228

Linker name	Linker amino acid sequence	SEQ
L24	GGGKSGGGKSGGGKS	2229
L25	GGGKSGGKGSGKGGS	2230
L26	GGKGSGGKGSGGKGS	2231
L27	GGSGG	2232
L28	GGSGGGGSGGGGS	2233
L29	GHEAAAVMQVQYPAS	2234
L30	GKGGSGKGGSGKGGS	2235
L31	GKGKSGKGKSGKGKS	2236
L32	GKGKSGKGKSGKGKSGKGKS	2237
L33	GKPGSGKPGSGKPGS	2238
L34	GKPGSGKPGSGKPGSGKPGS	2239
L35	GPAKELTPLKEAKVS	2240
L36	GSAGSAAGSGEF	2241
L37	IRPRAIGGSKPRVA	2242
L38	KESGSVSSEQLAQFRSLD	2243
L39	KTTPKLEEGEFSEAR	2244
L40	QPKAAP	2245
L41	QPKAAPSVTLFPP	2246
L42	RADAAAAGGPGS	2247
L43	RADAAP	2248
L44	RADAAPTVS	2249
L45	SAKTTP	2250
L46	SAKTTPKLEEGEFSEARV	2251
L47	SAKTTPKLGG	2252
L48	STAGDTHLGGEDFD	2253
L49	TVAAP	2254
L50	TVAAPSVFIFPP	2255
L51	TVAAPSVFIFPPTVAAPSVFIFPP	2256
L52	RADAAAA(G4S)4	2257
L53	GGSEGKSSGSGSESKSTGGS	2258
L54	GGGSGGGS	2259
L55	GGGSGGGSGGGS	2260
L56	GGGSGGGSGGGSGGGS	2261
L57	GGGSGGGSGGGSGGGSGGGS	2262
L58	GGGGSGGGGSGGGGS	2263
L59	GGGGSGGGGSGGGGSGGGGS	2264
L60	GGGGSGGGGSGGGGSGGGGSGGGGS	2265
L61	GSTSGSGKPGSGEGSTKG	2266
L62	IRPRAIGGSKPRVA	2267
L63	GKGGSGKGGSGKGGS	2268
L64	GGKGSGGKGSGGKGS	2269
L65	GGGKSGGGKSGGGKS	2270
L66	GKGKSGKGKSGKGKS	2271

Linker name	Linker amino acid sequence	SEQ
L67	GGGKSGGKGSGKGGS	2272
L68	GKPGSGKPGSGKPGS	2273
L69	GKPGSGKPGSGKPGSGKPGS	2274
L70	GKGKSGKGKSGKGKSGKGKS	2275
L71	STAGDTHLGGEDFD	2276
L72	GEGGSGEGGSGEGGS	2277
L73	GGEGSGGEGSGGEGS	2278
L74	GEGESGEGESGEGES	2279
L75	GGGESGGEGSGEGGS	2280
L76	GEGESGEGESGEGESGEGES	2281
L77	GSTSGSGKPGSGEGSTKG	2282
L78	PRGASKSGSASQTGSAPGS	2283
L79	GTAAAGAGAAGGAAAGAAG	2284
L80	GTSGSSGSGSGGSGSGGGG	2285
L81	GKPGSGKPGSGKPGSGKPGS	2286
L82	GSGS	2287
L83	APAPAPAPAP	2288
L84	APAPAPAPAPAPAPAPAPAP	2289
L85	AEAAAKEAAAKEAAAAKEAAAAKEAAAAKAAA	2290

Isotypes, allotypes and Fc engineering

[00496] The isolated molecules or the isolated multispecific antibodies of the disclosure may be of any isotype or allotype in instances when a portion of a full heavy chain is present in the molecules or in the multispecific antibodies.

[00497] It is expected that allotype has no influence on properties of isolated molecules or the isolated multispecific antibodies of the disclosure, such as specific binding to an antigen or Fc-mediated effector functions or half-life. Allotype is related to amino acid sequence variations at specific locations in the constant region sequences of a heavy chain of an immunoglobulin. **Table 3** shows select IgG1, IgG2 and IgG4 allotypes.

Table 3.

Allotype	Amino acid residue at position of diversity (residue numbering: EU Index)							
	IgG2		IgG4		IgG1			
	189	282	309	422	214	356	358	431
G2m(n)	T	M						
G2m(n-)	P	V						
G2m(n)/(n-	T	V						
nG4m(a)			L	R				
G1m(17)					K	E	M	A
G1m(17,1)					K	D	L	A

[00498] When present, C-terminal lysine may be removed from the isolated molecules or the isolated multispecific antibodies of the disclosure by endogenous circulating carboxypeptidases in the blood stream (Cai *et al.*, (2011) *Biotechnol Bioeng* 108:404-412). During manufacturing, CTL removal may be controlled to less than the maximum level by control of concentration of extracellular Zn^{2+}, EDTA or EDTA – Fe^{3+} as described in U.S. Patent Publ. No. US20140273092. C-terminal lysine content of proteins may be measured using known methods. In some embodiments, the isolated molecule or the isolated multispecific antibody of the disclosure has a C-terminal lysine content from about 10% to about 90%. In some embodiments, the C-terminal lysine content is from about 20% to about 80%. In some embodiments, the C-terminal lysine content is from about 40% to about 70%. In some embodiments, the C-terminal lysine content is from about 55% to about 70%. In some embodiments, the C-terminal lysine content is about 60%.

[00499] The Fc region (Fc), when present in the isolated molecules or the isolated multispecific antibodies of the disclosure, may comprise at least one substitution in the Fc region which modulates Fc-mediated effector functions CDC, ACC, ADCP by modulating binding to activating or inhibitory FcγR or FcRn, or which modulates protein A binding to facilitate purification. Fc positions that may be substituted to reduce binding of the isolated molecule or the isolated multispecific antibody of the disclosure to the activating FcγR and subsequently to reduce effector function include positions 214, 233, 234, 235, 236, 237, 238, 265, 267, 268, 270, 295, 297, 309, 327, 328, 329, 330, 331 and 365. Exemplary substitutions that may be made singularly or in combination are substitutions K214T, E233P, L234V, L234A, deletion of G236, V234A, F234A, L235A, G237A, P238A, P238S, D265A, S267E, H268A, H268Q, Q268A, N297A, A327Q, P329A, D270A, Q295A, V309L, A327S, L328F, A330S and P331S in IgG1, IgG2, IgG3 or IgG4.

[00500] Exemplary combination substitutions that may be made to reduce ADCC are mutations L234A/L235A on IgG1, L234A/L235A/D265S on IgG1, V234A/G237A/ P238S/H268A/V309L/A330S/P331S on IgG2, F234A/L235A on IgG4, S228P/F234A/ L235A on IgG4, N297A on all Ig isotypes, V234A/G237A on IgG2, K214T/E233P/ L234V/L235A/G236-deleted/A327G/P331A/D365E/L358M on IgG1, H268Q/V309L/A330S/P331S on IgG2, S267E/L328F on IgG1, L234F/L235E/D265A on IgG1, L234A/L235A/G237A/P238S/H268A/A330S/P331S on IgG1,

S228P/F234A/L235A/G237A/P238S on IgG4, and S228P/F234A/L235A/G236-deleted/G237A/P238S on IgG4. Hybrid IgG2/4 Fc domains may also be used, such as Fc with residues 117-260 from IgG2 and residues 261-447 from IgG4.

[00501] Exemplary substitution that may be used to reduce CDC is a K322A mutation.

[00502] Fc positions that may be substituted to enhance binding of the isolated molecule or the isolated multispecific antibody of the disclosure to the activating FcγR and/or enhance Fc effector functions include positions 236, 239, 243, 256,290,292, 298, 300, 305, 312, 326, 330, 332, 333, 334, 345, 360, 339, 378, 396 or 430 (residue numbering according to the EU index). Exemplary mutations that may be made singularly or in combination are G236A, S239D, F243L, T256A, K290A, R292P, S298A, Y300L, V305L, K326A, A330K, I332E, E333A, K334A, A339T and P396L. Exemplary combination substitutions that may be made to enhance ADCC or ADCP are S239D/I332E, S298A/E333A/K334A, F243L/R292P/Y300L, F243L/R292P/Y300L/P396L, F243L/R292P/Y300L/V305I/P396L or G236A/S239D/I332E. Fc positions that may be substituted to enhance CDC include positions 267, 268, 324, 326, 333, 345 and 430. Exemplary substitutions that may be made singularly or in combination are S267E, F1268F, S324T, K326A, K326W, E333A, E345K, E345Q, E345R, E345Y, E430S, E430F and E430T. Exemplary combination substitutions that may be made to enhance CDC are K326A/E333A, K326W/E333A, H268F/S324T, S267E/H268F, S267E/S324T and S267E/H268F/S324T.

[00503] In some embodiments, the FcγR is FcγRI, FcγRIIA, FcγRIIB or FcγRIII, or any combination thereof.

[00504] Fc positions that may be substituted to modulate half-life (*e.g.,* binding to FcRn) include positions 250, 252, 253, 254, 256, 257, 307, 376, 380, 428, 434 and 435. Exemplary substitutions that may be made singularly or in combination are mutations T250Q, M252Y, I253A, S254T, T256E, P257I, T307A, D376V, E380A, M428L, H433K, N434S, N434A, N434H, N434F, H435A and H435R. Exemplary singular or combination substitutions that may be made to increase the half-life are substitutions M428L/N434S, M252Y/S254T/T256E, T250Q/M428L, N434A and T307A/E380A/N434A. M252Y/S254T/T256E is particularly useful. Exemplary singular or combination substitutions that may be made to reduce the half-life are mutations H435A, P257I/N434H, D376V/N434H, M252Y/S254T/T256E/H433K/N434F, T308P/N434A and H435R.

[00505] The specific substitutions described herein are substitutions when compared to the wild-type IgG1, wild-type IgG2 and wild-type IgG4 amino acid sequences of SEQ ID NOs: 2315, 2316 and 2317, respectively.

[00506] Exemplary substitutions that may be used in molecules that comprise two Fc regions are: L235A_L235A_D265S_T350V_L351Y_F405A_Y407V in the first Fc region and L235A_L235A_D265S_T350V_T366L_K392L_T394W in the second Fc region; or L235A_L235A_D265S_T350V_T366L_K392L_T394W in the first Fc region and L235A_L235A_D265S_T350V_L351Y_F405A_Y407V in the second Fc region.

[00507] SEQ ID NO: 2315 (wild-type IgG1)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS
SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG
GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

[00508] SEQ ID NO: 2316 (wild-type IgG2)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
GLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSV
FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNS
TFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREE
MTKNQVSLTCLVKGFYPSDISVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKS
RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

[00509] SEQ ID NO: 2317 (wild-type IgG4)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPS
VFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQE
EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKS
RWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

[00510] Binding of the molecule or the multispecific antibody of the disclosure to FcγR or FcRn may be assessed on cells engineered to express each receptor using flow cytometry. In an

exemplary binding assay, $2x10^5$ cells per well are seeded in 96-well plate and blocked in BSA Stain Buffer (BD Biosciences, San Jose, USA) for 30 min at 4°C. Cells are incubated with a test molecule on ice for 1.5 hour at 4°C. After being washed twice with BSA stain buffer, the cells are incubated with R-PE labeled anti-human IgG secondary antibody (Jackson Immunoresearch Laboratories) for 45 min at 4°C. The cells are washed twice in stain buffer and then resuspended in 150 μL of Stain Buffer containing 1:200 diluted DRAQ7 live/dead stain (Cell Signaling Technology, Danvers, USA). PE and DRAQ7 signals of the stained cells are detected by Miltenyi MACSQuant flow cytometer (Miltenyi Biotec, Auburn, USA) using B2 and B4 channel respectively. Live cells are gated on DRAQ7 exclusion and the geometric mean fluorescence signals are determined for at least 10,000 live events collected. FlowJo software (Tree Star) is used for analysis. Data is plotted as the logarithm of antibody concentration versus mean fluorescence signals. Nonlinear regression analysis is performed.

[00511] "**Antibody-dependent cellular cytotoxicity**", "antibody-dependent cell-mediated cytotoxicity" or (ADCC) is a mechanism for inducing cell death that depends upon the interaction of antibody-coated target cells with effector cells possessing lytic activity, such as natural killer cells (NK), monocytes, macrophages and neutrophils via Fc gamma receptors (FcγR) expressed on effector cells. For example, NK cells express FcγRIIIa, whereas monocytes express FcγRI, FcγRII and FcγRIIIa. ADCC activity of the antibodies may be assessed using an *in vitro* assay using cells expressing the antigen the molecule or the multispecific antibody of the disclosure specifically binds to and NK cells as effector cells. Cytolysis may be detected by the release of label (*e.g.*, radioactive substrates, fluorescent dyes or natural intracellular proteins) from the lysed cells. In an exemplary assay, target cells are used with a ratio of 1 target cell to 4 effector cells. Target cells are pre-labeled with BATDA and combined with effector cells and the test antibody. The samples are incubated for 2 hours and cell lysis measured by measuring released BATDA into the supernatant. Data is normalized to maximal cytotoxicity with 0.67% Triton X-100 (Sigma Aldrich) and minimal control determined by spontaneous release of BATDA from target cells in the absence of any antibody.

[00512] "**Antibody-dependent cellular phagocytosis**" (ADCP) refers to a mechanism of elimination of antibody-coated target cells by internalization by phagocytic cells, such as macrophages or dendritic cells. ADCP may be evaluated by using monocyte-derived macrophages as effector cells and cells expressing the antigen the molecule or the multispecific

antibody of the disclosure specifically binds to as target cells also engineered to express GFP or another labeled molecule. In an exemplary assay, effector:target cell ratio may be for example 4:1. Effector cells may be incubated with target cells for 4 hours with or without the antibody of the invention. After incubation, cells may be detached using accutase. Macrophages may be identified with anti-CD11b and anti-CD14 antibodies coupled to a fluorescent label, and percent phagocytosis may be determined based on % GFP fluorescence in the $CD11^{+}CD14^{+}$ macrophages using standard methods.

[00513] "**Complement-dependent cytotoxicity**", (CDC), refers to a mechanism for inducing cell death in which the Fc effector domain of a target-bound antibody binds and activates complement component C1q which in turn activates the complement cascade leading to target cell death. Activation of complement may also result in deposition of complement components on the target cell surface that facilitate CDC by binding complement receptors (*e.g.*, CR3) on leukocytes. CDC of cells may be measured for example by plating cells expressing the antigen the molecule or the multispecific antibody of the disclosure specifically binds to at 1×10^{5} cells/well (50 μL/well) in RPMI-B (RPMI supplemented with 1% BSA), adding 50 μL of test molecule to the wells at final concentration between 0-100 μg/mL, incubating the reaction for 15 min at room temperature, adding 11 μL of pooled human serum to the wells, and incubation the reaction for 45 min at 37° C. Percentage (%) lysed cells may be detected as % propidium iodide stained cells in FACS assay using standard methods.

[00514] The Fc engineered molecules or the multispecific antibodies of the disclosure may be assessed for their functionality using several known assays and those described herein. Soluble forms of the receptors, such as the FcγRI, FcγRII, FcγRIII or FcRn receptors may be used, or alternatively cell-based assays may be used.

[00515] Protein A binding may be modulated using substitutions 435R and/or 436F as described in US9982013 or Q311R, Q311K, T307P/L309Q, T307P/V309Q, T307P/L309Q/Q311R or T307P/V309Q/Q311R as described in Int. Pat. Publ. No. WO2018/224951. Typically substations modulating protein A binding are engineered in asymmetric fashion to facilitate purification of the desired end product from intermediate or parental products.

Half-life extension

[00516] Various additional approaches in addition to incorporating Fc region and introducing FcRn modulating substitutions into the Fc may be taken to modulate half-life of the molecules of the disclosures. The molecules of the disclosure may be pegylated, conjugated to albumin, albumin binding proteins transferring and fragments or analogues thereof, or XTEN polypeptide sequences (Int Pat. Publ. No. WO2010/091122) using known methods.

[00517] Additional half-life extending moieties that may be conjugated to molecules of the disclosure include polyethylene glycol (PEG) molecules, such as PEG5000 or PEG20,000, fatty acids and fatty acid esters of different chain lengths, for example laurate, myristate, stearate, arachidate, behenate, oleate, arachidonate, octanedioic acid, tetradecanedioic acid, octadecanedioic acid, docosanedioic acid, and the like, polylysine, octane, carbohydrates (dextran, cellulose, oligo- or polysaccharides) for desired properties. These moieties may be direct fusions with the molecules of the disclosure and may be generated by standard cloning and expression techniques. Alternatively, well known chemical coupling methods may be used to attach the moieties to recombinantly produced antigen binding domains that bind hK2 of the disclosure.

[00518] A pegyl moiety may for example be conjugated to the antigen binding domain by incorporating a cysteine residue to the C-terminus of the antigen binding domain, or engineering cysteines into residue positions that face away from the antigen binding site and attaching a pegyl group to the cysteine using well known methods.

Glycoengineering

[00519] The isolated molecules or the isolated multispecific antibodies of the disclosure may be glycoengineered for the purpose of for example to facilitate manufacturing or to provide additional functionality. This can be accomplished for example by deleting or introducing N-glycosylation and/or O-glycosylation sites. Fc region containing molecules or the isolated multispecific antibodies may be converted to aglycosyl variants by N297A or N297Q substitution. Aglycosyl Fc variants may provide improved manufacturability in terms of more homogenous batches and also demonstrated reduced FcyR binding and hence reduced Fc-mediated effector functions.

[00520] Further, the isolated molecules or the isolated multispecific antibodies of the disclosure may also be expressed utilizing conditions that result in molecules having reduced

amount of fucosyl residues or increased bisecting GlcNac structures. Such altered glycosylation patterns have been demonstrated to potentiate ADCC. These carbohydrate modifications may be accomplished by, for example, expressing the isolated molecules or the isolated multispecific antibodies of the disclosure in a cell with altered glycosylation machinery. Cells with altered glycosylation machinery have been described in the art and can be used as host cells in which to express the molecules of the disclosure to thereby produce molecules with altered glycosylation. For example, EP 1,176,195 describes a cell line with a functionally disrupted FUT8 gene, which encodes a fucosyl transferase, such that molecules expressed in such a cell line exhibit hypofucosylation. PCT Publication WO 03/03583 describes a variant CHO cell line, Lecl3 cells, with reduced ability to attach fucose to Asn(297)-linked carbohydrates, also resulting in hypofucosylation of molecules expressed in that host cell (see also Shields et ai, 2002, J. Biol. Chem. 277:26733-26740). PCT Publication WO 99/54342 by Umana et al. describes cell lines engineered to express glycoprotein modifying glycosyl transferases (*e.g.*, beta(1 ,4)-N acetylglucosaminyltransferase III (GnTIII)) such that molecules expressed in the engineered cell lines exhibit increased bisecting GlcNac structures which results in increased ADCC activity of the molecules (see also Umana et ai, Nat. Biotech. 17:176-180, 1999). Additionally, relatively high defucosylated molecules bearing the biantennary complex-type of Fc oligosaccharides may be generated by controlling culture osmolality (Konno *et al.,* Cytotechnology 64(:249-65, 2012), application of a variant CHO line EB66 as the host cell line (Olivier *et al., MAbs*;2(4): 405-415, 2010; PMID:20562582), application of a rat hybridoma cell line YB2/0 as the host cell line (Shinkawa *et al., J Biol Chem* 278:3466-3473, 2003), introduction of small interfering RNA specifically against the a 1,6-fucosyltrasferase (*FUT8)* gene (Mori *et al., Biotechnol Bioeng* 88:901-908, 2004), or co-expression of β-1,4-*N*-acetylglucosaminyltransferase III and Golgi α-mannosidase II or a potent alpha-mannosidase I inhibitor, kifunensine (Ferrara *et al., J Biol Chem* 281:5032-5036, 2006, Ferrara *et al., Biotechnol Bioeng* 93:851-861, 2006; Xhou *et al., Biotechnol Bioeng* 99:652-65, 2008).

Co-engagement of the TCR complex and CD8

[00521] The isolated molecules or the multispecific antibodies of the disclosure are generated in a manner that results in $CD8^+$ CTL activation only upon co-engagement of the TCR complex and CD8. Co-engagement and subsequent $CD8^+$ CTL cell activation is controlled by choosing sufficiently low affinity CD8 and TCR complex antigen binding domains to be incorporated

into the molecules or the multispecific antibodies. Using the low affinity binding domains, activation of $CD8^+$ CTLs does not occur in molecules in which only either the low affinity CD8 binding domain or the low affinity TCR complex binding domain is present. The concept was successfully demonstrated herein as shown in Example 2. Molecules incorporating a low affinity CD3 binding domain without CD8 binding domains were unable to mediate tumor cell death or T cell activation, however incorporation of a CD8 binding domain into these molecules resulted in robust tumor cell death and T cell activation. On the contrary, molecules incorporating high affinity CD3 binding domains were able to mediate tumor cell killing in the absence of CD8 biding domains in the molecules.

[00522] The affinities of the antigen binding domains that specifically bind CD8 and the antigen binding domains that specifically bind the TCR complex that can be incorporated into the molecules or the multispecific antibodies of the disclosure may be in the range of about 50 nM or higher for an antigen binding domain that binds the TCR complex and about 0.5 nM or higher for an antigen binding domain that binds CD8. However, higher affinity antigen binding domains may also be used as long as they do not alone activate T cells.

[00523] Affinity of the antigen binding domains that bind CD8 or TCR complex or molecules comprising the antigen binding domains that specifically bind CD8 or TCR complex may be measured using known methods. The binding may be measured using Biacore 8K SPR. In an exemplary method, Biacore 8K SPR assay format is to capture the test molecule (*e.g.*, the antigen binding domain or the molecule comprising the antigen binding domain) using a high density anti-human Fc surface, then inject antigen concentration titration using a single cycle kinetics method. Goat anti-human Fc IgG (Jackson Immunoresearch, Cat# 109-005-098) is directly immobilized via amine coupling at 30 µg/mL in 10mM acetate buffer, pH 4.5 on flow cells 1 and 2, on CM5 Sensor Chip (GE) with a flow rate of 30 µL/min in HBSP (GE) buffer. The test molecules are captured on the anti-human Fc IgG surface at 0.5 µg/ml (~200-300 RU) on flow cell 2. The running buffer is then changed to HBSP + 100ug/ml BSA. Antigen at 30nM concentration in 3-fold dilution series is injected from low to high concentration using single cycle kinetics method. The off-rate is monitored 30 minutes after the last or highest concentration injection and then the surface is regenerated using 0.8% phosphoric acid (Bio-Rad). A buffer blank run, capturing the same test molecule and using the same conditions of sample run is also completed. The raw data is processed by subtracting two sets of reference

data from the response data: 1) reference flow cell 1 subtracted from sample flow cell 2 and 2) buffer blank run from experimental run. The processed data at all concentrations for each test molecule is globally fit to a 1:1 simple Langmuir binding model to extract estimates of the kinetic (kon, koff) and affinity (KD) constants.

[00524] The affinity of the third antigen binding domain that specifically binds an antigen expressed by an undesired cell may be determined using methods described herein. The affinity of the third antigen binding domain may range substantially and typically may be about $1x10^{-8}$ or less.

[00525] The effect of the molecule or the multispecific antibody on T cell activation may be assessed for example evaluating T cell proliferation in an assay in which human Pan T cell are isolated from healthy human donor PBMCs using for example EasySep™ Human T Cell Enrichment Kit, culturing the isolated T cells in a 1:1 Effector:Target ratio (10,000 T cells:10,000 target cells) at varying test molecule concentrations starting from 500ng/ml, with 3-fold serial dilution. Suitable target cells are for example H929 cells. T cells ware labeled with CellTrace™ Violet (CTV) Cell Proliferation dye Kit (ThermoFisher) prior to co-culture. After 72hrs, samples are harvested, labeled with anti-CD3 and anti-CD8 antibody and analyzed for CTV dye dilution. Cells are gated for FSC/SSC, live cells and CD3+ CD8+ or CD3+ CD8- cells. Alternatively, CD25 may be used as surrogate for T cell activation.

Conjugates with cytotoxic agents, drugs, detectable labels, and the like

[00526] The isolated molecules or the multispecific molecules of the disclosure may be conjugated to a cytotoxic agent, therapeutic agent, detectable labels and the like. These molecules are referred herein to immunoconjugates. The immunoconjugates comprising the isolated molecules or the multispecific molecules of the disclosure may be used to detect, deliver payload or kill cells the undesired cells the molecules or the multispecific molecules of the disclosure bind to. Alternatively, the immunoconjugates comprising the isolated molecules or the multispecific molecules of the disclosure may be used to detect, deliver payload or kill the $CD8^+$ CTLs in instances when the molecules or the multispecific molecules of the disclosure do not comprise the thirds antigen binding domain that binds an antigen expressed by an undesired cell, *e.g.,* bispecific CD3xCD8 molecules.

[00527] In some embodiments, the immunoconjugate comprises a detectable label.

[00528] In some embodiments, the immunoconjugate comprises a cytotoxic agent.

[00529] In some embodiments, the immunoconjugate comprises a therapeutic.

[00530] A detectable label includes compositions that can be visualized via spectroscopic, photochemical, biochemical, immunochemical, or chemical means. Detectable labels may also include cytotoxic agents, cytotoxic agents may include detectable labels.

[00531] Exemplary detectable labels include radioactive isotopes, magnetic beads, metallic beads, colloidal particles, fluorescent dyes, electron-dense reagents, enzymes (for example, as commonly used in an ELISA), biotin, digoxigenin, haptens, luminescent molecules, chemiluminescent molecules, fluorochromes, fluorophores, fluorescent quenching agents, colored molecules, radioactive isotopes, scintillates, avidin, streptavidin, protein A, protein G, antibodies or fragments thereof, polyhistidine, Ni^{2+}, Flag tags, myc tags, heavy metals, enzymes, alkaline phosphatase, peroxidase, luciferase, electron donors/acceptors, acridinium esters, and colorimetric substrates.

[00532] A detectable label may emit a signal spontaneously, such as when the detectable label is a radioactive isotope. In other cases, the detectable label emits a signal as a result of being stimulated by an external field.

[00533] Exemplary radioactive isotopes may be γ-emitting, Auger-emitting, β-emitting, an alpha-emitting or positron-emitting radioactive isotope. Exemplary radioactive isotopes include ^{3}H, ^{11}C, ^{13}C, ^{15}N, ^{18}F, ^{19}F, ^{55}Co, ^{57}Co, ^{60}Co, ^{61}Cu, ^{62}Cu, ^{64}Cu, ^{67}Cu, ^{68}Ga, ^{72}As, ^{75}Br, ^{86}Y, ^{89}Zr, ^{90}Sr, ^{94m}Tc, ^{99m}Tc, ^{115}In, $^{123}1$, $^{124}1$, ^{125}I, $^{131}1$, ^{211}At, ^{212}Bi, ^{213}Bi, ^{223}Ra, ^{226}Ra, ^{225}Ac and ^{227}Ac.

[00534] Exemplary metal atoms are metals with an atomic number greater than 20, such as calcium atoms, scandium atoms, titanium atoms, vanadium atoms, chromium atoms, manganese atoms, iron atoms, cobalt atoms, nickel atoms, copper atoms, zinc atoms, gallium atoms, germanium atoms, arsenic atoms, selenium atoms, bromine atoms, krypton atoms, rubidium atoms, strontium atoms, yttrium atoms, zirconium atoms, niobium atoms, molybdenum atoms, technetium atoms, ruthenium atoms, rhodium atoms, palladium atoms, silver atoms, cadmium atoms, indium atoms, tin atoms, antimony atoms, tellurium atoms, iodine atoms, xenon atoms, cesium atoms, barium atoms, lanthanum atoms, hafnium atoms, tantalum atoms, tungsten atoms, rhenium atoms, osmium atoms, iridium atoms, platinum atoms, gold atoms, mercury atoms, thallium atoms, lead atoms, bismuth atoms, francium atoms, radium atoms, actinium atoms, cerium atoms, praseodymium atoms, neodymium atoms, promethium atoms, samarium atoms, europium atoms, gadolinium atoms, terbium atoms, dysprosium atoms, holmium atoms,

erbium atoms, thulium atoms, ytterbium atoms, lutetium atoms, thorium atoms, protactinium atoms, uranium atoms, neptunium atoms, plutonium atoms, americium atoms, curium atoms, berkelium atoms, californium atoms, einsteinium atoms, fermium atoms, mendelevium atoms, nobelium atoms, or lawrencium atoms.

[00535] In some embodiments, the metal atoms may be alkaline earth metals with an atomic number greater than twenty. In some embodiments, the metal atoms may be lanthanides. In some embodiments, the metal atoms may be actinides. In some embodiments, the metal atoms may be transition metals. In some embodiments, the metal atoms may be poor metals. In some embodiments, the metal atoms may be gold atoms, bismuth atoms, tantalum atoms, and gadolinium atoms. In some embodiments, the metal atoms may be metals with an atomic number of 53 (*i.e.*, iodine) to 83 (*i.e.*, bismuth).

[00536] In some embodiments, the metal atoms may be atoms suitable for magnetic resonance imaging.

[00537] The metal atoms may be metal ions in the form of +1, +2, or +3 oxidation states, such as Ba^{2+}, Bi^{3+}, Cs^{+}, Ca^{2+}, Cr^{2+}, Cr^{3+}, Cr^{6+}, Co^{2+}, Co^{3+}, Cu^{+}, Cu^{2+}, Cu^{3+}, Ga^{3+}, Gd^{3+}, Au^{+}, Au^{3+}, Fe^{2+}, Fe^{3+}, F^{3+}, Pb^{2+}, Mn^{2+}, Mn^{3+}, Mn^{4+}, Mn^{7+}, Hg^{2+}, Ni^{2+}, Ni^{3+}, Ag^{+}, Sr^{2+}, Sn^{2+}, Sn^{4+}, and Zn^{2+}. The metal atoms may comprise a metal oxide, such as iron oxide, manganese oxide, or gadolinium oxide.

[00538] Suitable dyes include any commercially available dyes such as, for example, 5(6)-carboxyfluorescein, IRDye 680RD maleimide or IRDye 800CW, ruthenium polypyridyl dyes, and the like.

[00539] Suitable fluorophores are fluorescein isothiocyanate (FITC), fluorescein thiosemicarbazide, rhodamine, Texas Red, CyDyes (*e.g.*, Cy3, Cy5, Cy5.5), Alexa Fluors (*e.g.*, Alexa488, Alexa555, Alexa594; Alexa647), near infrared (NIR) (700-900 nm) fluorescent dyes, and carbocyanine and aminostyryl dyes.

[00540] The immunoconjugates comprising a detectable label may be used as an imaging agent.

[00541] In some embodiments, the cytotoxic agent is a chemotherapeutic agent, a drug, a growth inhibitory agent, a toxin (*e.g.*, an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (*i.e.*, a radioconjugate).

[00542] In some embodiments, the cytotoxic agent is daunomycin, doxorubicin, methotrexate, vindesine, bacterial toxins such as diphtheria toxin, ricin, geldanamycin, maytansinoids or calicheamicin. The cytotoxic agent may elicit their cytotoxic and cytostatic effects by mechanisms including tubulin binding, DNA binding, or topoisomerase inhibition.

[00543] In some embodiments, the cytotoxic agent is an enzymatically active toxin such as diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, *Aleurites fordii* proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, PAPII, and PAP-S), *momordica charantia* inhibitor, curcin, crotin, *sapaonaria officinalis* inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes.

[00544] In some embodiments, the cytotoxic agent is a radionuclide, such as ^{212}Bi, ^{131}I, ^{131}In, ^{90}Y, and ^{186}Re.

[00545] In some embodiments, the cytotoxic agent is dolastatins or dolostatin peptidic analogs and derivatives, auristatin or monomethyl auristatin phenylalanine. Exemplary molecules are disclosed in U.S. Pat No. 5,635,483 and 5,780,588. Dolastatins and auristatins have been shown to interfere with microtubule dynamics, GTP hydrolysis, and nuclear and cellular division (Woyke et al (2001) Antimicrob Agents and Chemother. 45(12):3580-3584) and have anticancer and antifungal activity. The dolastatin or auristatin drug moiety may be attached to the antibody of the invention through the N (amino) terminus or the C (carboxyl) terminus of the peptidic drug moiety (WO02/088172), or via any cysteine engineered into the antibody.

[00546] The immunoconjugates may be made using known methods.

[00547] In some embodiments, the detectable label is complexed with a chelating agent.

[00548] The detectable label, cytotoxic agent or therapeutic may be linked directly, or indirectly via a linker, to the polypeptides, the heterologous polypeptides or the proteinaceous molecules that bind the polypeptides or the heterologous polypeptides. Suitable linkers are known in the art and include, for example, prosthetic groups, non-phenolic linkers (derivatives of N-succimidyl-benzoates; dodecaborate), chelating moieties of both macrocyclics and acyclic chelators, such as derivatives of 1,4,7,10-tetraazacyclododecane-1,4,7,10,tetraacetic acid (DOTA), derivatives of diethylenetriaminepentaacetic avid (DTPA), derivatives of S-2-(4-Isothiocyanatobenzyl)-1,4,7-triazacyclononane-1,4,7-triacetic acid (NOTA) and derivatives of

1,4,8,11-tetraazacyclodocedan-1,4,8,11-tetraacetic acid (TETA), N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCl), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis(p-azidobenzoyl)hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as toluene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene) and other chelating moieties. Suitable peptide linkers are well known.

Kits

[00549] The disclosure also provides a kit comprising one or more isolated molecules or isolated multispecific antibodies of the disclosure. The kit may be used for therapeutic uses or as diagnostic kits.

[00550] In some embodiments, the kit comprises the isolated molecule or the isolated multispecific antibody of the disclosure and reagents for detecting the isolated molecule or the isolated multispecific antibody. The kit can include one or more other elements including: instructions for use; other reagents, *e.g.*, a label, a therapeutic agent, or an agent useful for chelating, or otherwise coupling, an antibody to a label or therapeutic agent, or a radioprotective composition; devices or other materials for preparing the isolated molecule or the isolated multispecific antibody for administration; pharmaceutically acceptable carriers; and devices or other materials for administration to a subject.

Pharmaceutical compositions

[00551] The disclosure also provides a pharmaceutical composition comprising the isolated molecule or the isolated multispecific antibody of the disclosure and a pharmaceutically acceptable carrier. For therapeutic use, the isolated molecule or the isolated multispecific antibody of the disclosure may be prepared as pharmaceutical compositions containing an effective amount of the isolated molecule or the isolated multispecific antibody of the disclosure as an active ingredient in a pharmaceutically acceptable carrier. "Carrier" refers to a diluent, adjuvant, excipient, or vehicle with which the antibody of the invention is administered. Such vehicles may be liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. For example, 0.4% saline and 0.3% glycine may be used. These solutions are sterile and generally free of particulate matter. They may be sterilized by conventional, well-known sterilization

techniques (*e.g.*, filtration). The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, stabilizing, thickening, lubricating and coloring agents, etc. The concentration of the antibodies of the invention in such pharmaceutical formulation may vary, from less than about 0.5%, usually to at least about 1% to as much as 15 or 20% by weight and may be selected primarily based on required dose, fluid volumes, viscosities, etc., according to the mode of administration selected. Suitable vehicles and formulations, inclusive of other human proteins, *e.g.*, human serum albumin, are described, for example, in *e.g.*, Remington: The Science and Practice of Pharmacy, 21st Edition, Troy, D.B. ed., Lipincott Williams and Wilkins, Philadelphia, PA 2006, Part 5, Pharmaceutical Manufacturing pp 691-1092, See especially pp. 958-989.

Methods and Uses

[00552] The isolated molecules and the multispecific antibodies of the disclosure have broad applicability in therapeutic or research setting, as therapeutics, diagnostics, research tools, imaging agents and capture agents. The isolated molecules and the multispecific antibodies of the disclosure provide an improvement to the state of art by providing selective activation or recruitment of $CD8^+$ CTLs and are thereby expected to provide more safe and effective treatment with a broader therapeutic index. The isolated molecules and the multispecific antibodies of the disclosure can be used to treat any diseases in which depletion or reduction in a number of undesired cells is desired. The isolated molecules and the multispecific antibodies of the disclosure may have a potential to treat patients without large naïve repertoire, such as elderly patients or any patients whose immune system is compromised.

[00553] The disclosure provides a method of targeting $CD8^+$ CTLs to an undesired cell in a subject, comprising administering to the subject an isolated molecule comprising a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[00554] The disclosure also provides a method of targeting $CD8^+$ CTLs to an undesired cell in a subject, comprising administering to the subject an isolated molecule comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a second antigen binding domain comprising a scFv that specifically binds a TCR complex, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain; the second polypeptide comprises, from N- to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[00555] The disclosure also provides a method of targeting $CD8^+$ CTLs to an undesired cell in a subject, comprising administering to the subject an isolated molecule comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain; the second polypeptide comprises, from N- to C-terminus, a VL that is capable of specifically binding CD8, a CL domain and a second antigen binding domain comprising a scFv that specifically binds a TCR complex; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[00556] The disclosure also provides a method of targeting $CD8^+$ CTLs to an undesired cell in a subject, comprising administering to the subject an isolated molecule comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a VH that is capable of specifically CD8, a CH1 domain, a hinge, a CH2 domain, a CH3 domain and a second antigen binding domain comprising a scFv that specifically binds a TCR complex; the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and the third

polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[00557] The disclosure also provides a method of treating a cancer in a subject, comprising: administering to the subject an isolated molecule comprising a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[00558] The disclosure also provides a method of treating a cancer in a subject, comprising administering to the subject an isolated molecule comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a second antigen binding domain comprising a scFv that specifically binds a TCR complex, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain; the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[00559] The disclosure also provides a method of treating a cancer in a subject, comprising administering to the subject an isolated molecule comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain; the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8, a CL domain and a second antigen binding domain

comprising a scFv that specifically binds a TCR complex; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[00560] The disclosure also provides a method of treating a cancer in a subject, comprising administering to the subject an isolated molecule comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a VH that is capable of specifically CD8, a CH1 domain, a hinge, a CH2 domain, a CH3 domain and a second antigen binding domain comprising a scFv that specifically binds a TCR complex; the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[00561] The disclosure also provides a method of enhancing a $CD8^+$ CTL response against an undesired cell in a subject, comprising: administering to the subject an isolated molecule comprising a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds TCR complex and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[00562] The disclosure also provides a method of enhancing a $CD8^+$ CTL response against an undesired cell in a subject, comprising administering to the subject an isolated molecule comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a second antigen binding domain comprising a

scFv that specifically binds a TCR complex, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain; the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[00563] The disclosure also provides a method of enhancing a $CD8^+$ CTL response against an undesired cell in a subject, comprising administering to the subject an isolated molecule comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain; the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8, a CL domain and a second antigen binding domain comprising a scFv that specifically binds a TCR complex; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[00564] The disclosure also provides a method of enhancing a $CD8^+$ CTL response against an undesired cell in a subject, comprising administering to the subject an isolated molecule comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a VH that is capable of specifically CD8, a CH1 domain, a hinge, a CH2 domain, a CH3 domain and a second antigen binding domain comprising a scFv that specifically binds a TCR complex; the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs

upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[00565] The disclosure also provides a method of enhancing a $CD8^+$ CTL response against a cancer in a subject, comprising: administering to the subject an isolated molecule comprising a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[00566] The disclosure also provides a method of enhancing a $CD8^+$ CTL response against a cancer in a subject, comprising administering to the subject an isolated molecule comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a second antigen binding domain comprising a scFv that specifically binds a TCR complex, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain; the second polypeptide comprises, from N- to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[00567] The disclosure also provides a method of enhancing a $CD8^+$ CTL response against a cancer in a subject, comprising administering to the subject an isolated molecule comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain; the second polypeptide comprises, from N- to C-terminus, a VL that is capable of specifically binding CD8, a CL domain and a second antigen binding domain comprising a scFv that specifically binds a TCR complex; and third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a

scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[00568] The disclosure also provides a method of enhancing a $CD8^+$ CTL response against a cancer in a subject, comprising administering to the subject an isolated molecule comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a VH that is capable of specifically CD8, a CH1 domain, a hinge, a CH2 domain, a CH3 domain and a second antigen binding domain comprising a scFv that specifically binds a TCR complex; the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[00569] The disclosure also provides a method of providing an improved T cell redirection therapy to a subject in need thereof, comprising: administering to the subject an isolated molecule comprising a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[00570] The disclosure also provides a method of providing an improved T cell redirection therapy to a subject in need thereof, comprising: administering to the subject an isolated molecule comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a second antigen binding domain comprising a scFv that specifically binds a TCR complex, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain; the second

polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[00571] The disclosure also provides a method of providing an improved T cell redirection therapy to a subject in need thereof, comprising: administering to the subject an isolated molecule comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain; the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8, a CL domain and a second antigen binding domain comprising a scFv that specifically binds a TCR complex; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[00572] The disclosure also provides a method of providing an improved T cell redirection therapy to a subject in need thereof, comprising: administering to the subject an isolated molecule comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a VH that is capable of specifically CD8, a CH1 domain, a hinge, a CH2 domain, a CH3 domain and a second antigen binding domain comprising a scFv that specifically binds a TCR complex; the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[00573] The disclosure also provides a method of selectively activating or recruiting $CD8^+$ CTLs towards an undesired cell, comprising: contacting a population of lymphocytes with an isolated molecule, comprising: a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[00574] The disclosure also provides a method of selectively activating or recruiting $CD8^+$ CTLs towards an undesired cell, comprising: contacting a population of lymphocytes with an isolated molecule comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a second antigen binding domain comprising a scFv that specifically binds a TCR complex, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain; the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[00575] The disclosure also provides a method of selectively activating or recruiting $CD8^+$ CTLs towards an undesired cell, comprising: contacting a population of lymphocytes with an isolated molecule comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain; the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8, a CL domain and a second antigen binding domain comprising a scFv that specifically binds a TCR complex; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed

by an undesired cell and a Fc or a fragment of the Fc, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[00576] The disclosure also provides a method of selectively activating or recruiting $CD8^+$ CTLs towards an undesired cell, comprising: contacting a population of lymphocytes with an isolated molecule comprising a first polypeptide, a second polypeptide and a third polypeptide, wherein the first polypeptide comprises, from N- to C-terminus, a VH that is capable of specifically CD8, a CH1 domain, a hinge, a CH2 domain, a CH3 domain and a second antigen binding domain comprising a scFv that specifically binds a TCR complex; the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[00577] In some embodiments, the selective activation or recruitment of $CD8^+$ CTLs comprises *in vitro* selective activation or recruitment of $CD8^+$ CTLs.

[00578] In some embodiments, the selective activation or recruitment of $CD8^+$ CTLs comprises *ex vivo* selective activation or recruitment of $CD8^+$ CTLs.

[00579] In some embodiments, the selective activation or recruitment of $CD8^+$ CTLs comprises *in vivo* selective activation or recruitment of $CD8^+$ CTLs.

[00580] The disclosure also provides a method of selectively activating or recruiting $CD8^+$ CTLs towards an undesired cell in a subject, comprising: administering to the subject an isolated molecule comprising a first antigen binding domain, a second antigen binding domain and a third antigen binding domain, wherein the first antigen binding domain specifically binds CD8, the second antigen binding domain specifically binds a TCR complex and the third antigen binding domain specifically binds an antigen expressed by an undesired cell, wherein the isolated molecule selectively activates or recruits $CD8^+$ CTLs upon co-engagement of the TCR complex and CD8 and is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.

[00581] In some embodiments, the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds the TCR complex with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of the TCR complex and CD8.

[00582] In some embodiments, the first antigen binding domain, the second antigen binding domain or the third antigen binding domain comprises a scFv, a Fab, a Fab', a $F(ab')_2$, a Fd, a Fv, a domain antibody (dAb), a VHH, a VH, a LV, a non-antibody scaffold, or fragments thereof.

[00583] In some embodiments, the first antigen binding domain comprises the Fab In some embodiments, the second antigen binding domain comprises the scFv. In some embodiments, the third antigen binding domain comprises the scFv.

[00584] In some embodiments, the isolated molecule comprises: a first polypeptide comprising, from N- to C-terminus, the second antigen binding domain comprising the scFv, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain; a second polypeptide comprising, from N- to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and a third polypeptide comprising, from N- to C-terminus, the third antigen binding domain comprising the scFv and a Fc or a fragment of the Fc.

[00585] In some embodiments, the isolated molecule comprises: a first polypeptide comprising, from N- to C-terminus, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain; a second polypeptide comprising, from N- to C-terminus, a VL that is capable of specifically binding CD8, a CL domain and the second antigen binding domain comprising the scFv; and a third polypeptide comprising, from N- to C-terminus, the third antigen binding domain comprising the scFv and a Fc or a fragment of the Fc.

[00586] In some embodiments, the isolated molecule comprises: a first polypeptide comprising, from N- to C-terminus, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain, a CH3 domain and the second antigen binding domain comprising the scFv; a second polypeptide comprising, from N- to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and a third polypeptide comprising, from

N- to C-terminus, the third antigen binding domain comprising the scFv and a Fc or a fragment of the Fc.

[00587] In some embodiments, the first antigen binding domain comprising the Fab, the second antigen binding domain comprising the scFv or the third antigen binding domain comprising the scFv is conjugated to the Fc or the fragment of the Fc, to the VH that is capable of specifically biding CD8, to the CL domain or to the CH3 domain via a linker.

[00588] In some embodiments, the linker comprises a polypeptide of SEQ ID NOs: 2183-2290.

[00589] In some embodiments, the fragment of the Fc comprises a CH2 domain and a CH3 domain.

[00590] In some embodiments, the CH3 domain comprises one or more substitutions when compared to a wild-type CH3 domain.

[00591] In some embodiments, the one or more substitutions comprise T350V, L351Y, F405A,Y407V, T366Y, T366W, F405W, T394W, T394S, Y407T, Y407A, T366S/L368A/Y407V, L351Y/F405A/Y407V, T366I/K392M/T394W, F405A/Y407V, T366L/K392M/T394W, L351Y/Y407A, T366A/K409F, L351Y/Y407A, T366V/K409F, T366A/K409F, T350V/L351Y/F405A/Y407V or T350V/T366L/K392L/T394W, wherein residue numbering is according to the EU index.

[00592] In some embodiments, the first antigen binding domain comprising the Fab, the second antigen binding domain comprising the scFv or the third antigen binding domain comprising the scFv is conjugated to the Fc or the fragment of the Fc, to the VH that is capable of specifically biding CD8, to the CL domain or to the CH3 domain via a linker.

[00593] In some embodiments, the linker comprises a polypeptide of SEQ ID NOs: 2183-2290.

[00594] In some embodiments, the first polypeptide comprises a CH3 domain comprising one or more substitutions when compared to a wild-type CH3 domain which promote heterodimerization of the first polypeptide with the third polypeptide; the third polypeptide comprises a CH3 domain comprising one or more substitutions when compared to the wild-type CH3 domain which promote heterodimerization of the third polypeptide with the first polypeptide; or the first polypeptide comprises the CH3 domain comprising one or more substitutions when compared to the wild-type CH3 which promote heterodimerization of the

first polypeptide with the third polypeptide and the third polypeptide comprises the CH3 domain comprising one or more substitutions when compared to the wild-type CH3 which promote heterodimerization of the third polypeptide with the first polypeptide.

[00595] In some embodiments, the one or more substitutions comprise T350V, L351Y, F405A,Y407V, T366Y, T366W, F405W, T394W, T394S, Y407T, Y407A, T366S/L368A/Y407V, L351Y/F405A/Y407V, T366I/K392M/T394W, F405A/Y407V, T366L/K392M/T394W, L351Y/Y407A, T366A/K409F, L351Y/Y407A, T366V/K409F, T366A/K409F, T350V/L351Y/F405A/Y407V or T350V/T366L/K392L/T394W, wherein residue numbering is according to the EU index.

[00596] In some embodiments, the Fc, the CH2 domain or the CH3 domain is an IgG1, IgG2, IgG3 or IgG4 isotype.

[00597] In some embodiments, the second antigen binding domain specifically binds CD3, TCRα chain, TCRβ chain, TCRγ chain or TCRδ chain, or any combination thereof.

[00598] In some embodiments, the TCRβ chain comprises TCRVB17.

[00599] In some embodiments, CD3 comprises CD3ε, CD3γ, CD3δ or CD3ζ.

[00600] In some embodiments, the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296.

[00601] In some embodiments, the second antigen binding domain that specifically binds CD3 comprises the VH of SEQ ID NO: 2297 and the VL of SEQ ID NO: 2298.

[00602] In some embodiments, the first antigen binding domain comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312.

[00603] In some embodiments, the first antigen binding domain comprises the VH of SEQ ID NO: 2313 and the VL of SEQ ID NO: 2314.

[00604] In some embodiments, the undesired cell is a pathogenic cell.

[00605] In some embodiments, the undesired cell is a cancer cell, an infected cell, a virus infected cell, a bacterial infected cell, an immune cell, an inflamed cell, a damaged cells, a

foreign cell, an apoptotic cell, a dysplastic cell, an immunogenic cell, a metaplastic cell or a mutant cell, or any combination thereof.

[00606] In some embodiments, the subject has a cancer, a viral infection, or an immune-mediated disease.

[00607] In some embodiments, the cancer is a hematological malignancy or a solid tumor.

[00608] In some embodiments, the hematological malignancy comprises acute lymphoblastic leukemia, acute myeloid leukemia, anaplastic large-cell lymphoma, Burkitt's lymphoma, chronic lymphocytic leukemia, chronic myeloid leukemia, diffuse large B-cell lymphoma, dendritic cell neoplasm, follicular lymphoma, hairy cell leukemia, Hodgkin's lymphoma, leukemia, B cell leukemia, T cell leukemia, light chain amyloidosis, lymphoma, B cell lymphoma, NK cell lymphoma, T cell lymphoma, mantle-cell lymphoma, marginal zone B-cell lymphoma, monoclonal gammopathy of undetermined significance, mucosa-associated lymphatic tissue lymphoma, multiple myeloma, myelodysplastic syndrome, non-Hodgkin's lymphoma, plasma cell leukemia, precursor B-cell lymphoblastic leukemia, smoldering multiple myeloma or Waldenstrom's macroglobulinemia, or any combination thereof. In some embodiments, hematological malignancy comprises B cell malignancies. In some embodiments, hematological malignancy comprises T cell malignancies. In some embodiments, hematological malignancy comprises NK cell malignancies.

[00609] Exemplary B-cell non-Hodgkin's lymphomas are a lymphomatoid granulomatosis, a primary effusion lymphoma, an intravascular large B-cell lymphoma, a mediastinal large B-cell lymphoma, heavy chain diseases (including γ, μ, and a disease), lymphomas induced by therapy with immunosuppressive agents, such as cyclosporine-induced lymphoma, and methotrexate-induced lymphoma.

[00610] In some embodiments, the solid tumor comprises adenocarcinoma, anal cancer, basal cell carcinoma, biliary tract cancer, bladder cancer, bone cancer, breast cancer, cancer associated with infection, cancer of the adrenal gland, cancer of the endocrine system, cancer of the head or neck, cancer of the parathyroid gland, cancer of the penis, cancer of the thyroid gland, cancer of the urethra, cervical cancer, carcinoma of the breast, carcinoma of the fallopian tubes, carcinoma of the liver, carcinoma of the lung, carcinoma of the prostate, carcinoma of the renal pelvis, carcinoma of the vagina, carcinoma of the vulva, choriocarcinoma, clear cell carcinoma, colon cancer, colon carcinoma, colorectal cancer, connective tissue cancer,

cutaneous or intraocular malignant melanoma, environmentally induced cancer, gastric cancer, gastrointestinal cancer, glioma, glioblastoma, endometrial cancer, epithelial cancer, esophageal cancer, eye cancer, larynx cancer, liver cancer, hepatocellular carcinoma, hormone refractory prostate adenocarcinoma, Kaposi's sarcoma, kidney cancer, lung cancer gastro-esophageal cancer, melanoma, mesothelioma, Merkel cell cancer, neuroblastoma, non-small cell lung cancer (NSCLC), osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, rectal cancer, renal cell carcinoma, retinoblastoma rhabdomyosarcoma, squamous cell cancer, soft tissue sarcoma, solid tumors of childhood, spinal axis tumor, stomach cancer, testicular cancer, thyroid cancer, uterine cancer, urothelial carcinoma or sarcomas, or any combination thereof.

[00611] In some embodiments, the cancer is a relapsed cancer. In some embodiments, the cancer is a refractor cancer. In some embodiments, the subject is treatment naïve.

[00612] In some embodiments, the viral infection is infection with adenovirus, arboviral encephalitis virus, coronavirus, coxsackie virus, cytomegalovirus (CMV), dengue virus, echovirus, Epstein Barr virus, flaviviruses, human immunodeficiency virus (HIV), hepatitis A virus, hepatitis B virus, hepatitis C virus, herpes virus, HTLV virus, influenza virus, JC virus, measles virus, molluscum virus, mumps virus, papillomavirus, parvovirus, poliovirus, rabies virus, respiratory syncytial virus, rhinovirus, rotavirus, rubella virus or vaccinia virus, bacteria, virus, fungi, protozoa, parasite or prion, or any combination thereof.

[00613] In some embodiments, the immune-mediated disease is an autoimmune disease or an inflammatory disease. In some embodiments, the autoimmune disease comprises systemic lupus erythematosus (SLE), ankylosing spondylitis, Chagas disease, chronic obstructive pulmonary disease, Crohn's Disease, dermatomyositis, diabetes mellitus type 1, endometriosis, Goodpasture's syndrome, Graves' disease, Guillain-Barre syndrome (GBS), Hashimoto's disease, hidradenitis suppurativa, Kawasaki disease, IgA nephropathy, idiopathic thrombocytopenic purpura, interstitial cystitis, mixed connective tissue disease, morphea, multiple sclerosis, myasthenia gravis, narcolepsy, neuromyotonia, pemphigus vulgaris, pernicious anaemia, psoriasis, psoriatic arthritis, polymyositis, primary biliary cirrhosis, relapsing polychondritis, rheumatoid arthritis (RA), sarcoidosis, schizophrenia, scleroderma, Sjogren's syndrome, temporal arteritis, ulcerative colitis, vasculitis, vitiligo, Wegener's granulomatosis, IgG4-related disease, anti-synthetase syndrome, and autoimmunity associated with immunodeficiency including chronic variable immunodeficiency, Wiskott-Aldrich

syndrome, Good syndrome, IgA deficiency, Hyper IgM syndrome, and complement disorders. In some embodiments, the subject to has or likely to develop allograft rejection.

[00614] In some embodiments, subjects have an autoantibody-associated condition. In some embodiments, the an autoantibody-associated condition comprises seropositive RA, SLE, postmyocardial infarction syndrome, subacute bacterial endocarditis, anti-glomerular basement membrane nephritis, autoimmune hepatitis, primary biliary cirrhosis, alopecia areata, bullous pemphigoid, cicatricial pemphigoid, dermatitis herpetiformis, gestational pemphigoid, pemphigus vulgaris, systemic scleroderma, Addison's disease, autoimmune polyendocrine syndrome type 2, autoimmune pancreatitis, diabetes mellitus type 1, autoimmune thyroiditis, Graves' disease, Sjogren's syndrome, celiac disease, antiphospholipid syndrome, autoimmune thrombocytopenic purpura, cold agglutinin disease, pernicious anemia, thrombocytopenia, adult onset Still's disease, CREST syndrome, drug-induced lupus, enthesitis-related arthritis, juvenile arthritis, mixed connective tissue disease, palindromic rheumatism, Parry Romberg syndrome, rheumatic fever, undifferentiated connective tissue disease, dermatomysitis, myasthenia gravis, neuromyotonia, paraneoplastic cerebellar degeneration, polymyositis, Bickerstaff's encephalitis, chronic inflammatory demyelinating polyneuropathy, Guillain-Barre syndrome, Hashimoto's encephalopathy, Lambert-Eaton myasthenic syndrome, multiple sclerosis, progressive inflammatory neuropathy, Stiff person syndrome, autoimmune uveitis, neuromyelitis optica, symphathetic ophthalmia, Meniere's disease, anti-neutrophil cytoplasmic antibody-associated vasculitis, Churg-Strauss syndrome, Henoch-Schonlein purpura, microscopic polyangiitis, urticarial vasculitis, and vasculitis. Examples of autoantibody-associated autoimmune conditions include gastritis and POEMS syndrome. Examples of autoantibody-associated (non-autoimmune) diseases include agammaglobulinemia, amyotrophic lateral sclerosis, Castleman's disease, cutaneous leukocytoclastic angiitis, eczema, eosinophilic gastroenteritis, erythroblastosis fetalis, fibrodysplasia ossificans progressive, hypogammaglobulinemia, idiopathic pulmonary fibrosis, IgA nephropathy, Majeed syndrome, narcolepsy, Rasmussen's encephalitis, spondyloarthropathy or Sweet's syndrome.

[00615] In some embodiments, the antigen expressed by the undesired cell comprises mesothelin, alpha-fetoprotein (ALP), BAGE, BCR-ABL, beta-catenin, beta-HCG, BrE3-antigen, BCA225, BCMA, BTAA, CA125, CA195, CA242, CA-50, CAM43, CAMEL, CAP-l, carbonic anhydrase IX, CA19-9, CA72-4, CAM 17.1, CASP-8, CCCL19, CCCL21, CD1, CD

la, CD2, CD4, CD5, CD11A, CD14, CD15, CD16, CD18, CD19, CD20, CD21, CD22, CD23, CD25, CD29, CD30, CD32b, CD33, CD37, CD38, CD40, CD40L, CD44, CD45, CD46, CD47, CD52, CD54, CD55, CD59, CD64, CD66a-e, CD67, CD68, CD70, CD70L, CD74, CD79a, CD79b, CD80, CD83, CD95, CD123, CD126, CD132, CD133, CD138, CD147, CD154, CDC27, CDK4, CDK4m, CDKN2A, CO-029, CTLA4, CXCR4, CXCR7, CXCL12, HIF-la, colon- specific antigen-p (CSAp), CEACAM5) CEACAM6, c-Met, DAM, E2A-PRL, EGFR, EGFRvIII, EGP-l , EGP-2, ELF2-M, Ep-CAM, FGF, FGF-5, Flt-l, Flt- 3, folate receptor, G250 antigen, Ga733VEpCAM, GAGE, gplOO, GRO-b, H4-RET, HLA-DR, HM1.24, human chorionic gonadotropin (HCG) HER2, HER3, HMGB-l, HIF-l, HSP70-2M, HST-2, HTgp-l75, la, IGF-1R, IFN-g, IFN-a, IFN-b, IFN- l, IL-4R, IL-6R, IL-13R, IL-15R, IL-17R, IL-18R, IL-2, IL-6, IL-8, IL-12, IL-15, IL-17, IL-18, IL-23, IL-25, insulin-like growth factor- 1 (IGF-l), KC4-antigen, KLK2, KSA, KS-l-antigen, KS1-4, LAGE-la, Le-Y, LDR/FUT, M344, MA-50, macrophage migration inhibitory factor (MIF), MAGE, MAGE-l, MAGE-3, MAGE-4, MAGE-5, MAGE-6, MART-l, MART-2, TRAG-3, MCP-l, MIP-1A, MIP-1B, MIF, MG7-Ag, MOV18, MUC1, MUC2, MUC3, MUC4, MUC5ac, MUC13, MUC16, MUM- 1/2, MUM-3, MYL-RAR, NB/70K, Nm23Hl, NuMA, NCA66, NCA95, NCA90, NY-ESO-l, pl5, pl6, pl85erbB2, pl80erbB3, PAM4 antigen, pancreatic cancer mucin, PD-l, PD-L1, PD-L2, PI5, placental growth factor, p53, PLAGL2, Pmell7 prostatic acid phosphatase, PSA, PRAME, PSMA, P1GF, ILGF, ILGF-1R, IL-6, IL-25, RCAS1, RS5, RAGE, RANTES, Ras, T101, SAGE, S100, SLAMF7, survivin, survivin-2B, SDDCAG16, TA-90\Mac2 binding protein, TAAL6, TAC, TAG-72, TLP, tenascin, TMEFF2, TRAIL receptors, TRP-l, TRP-2, TSP-180, VEGFR, ED-B fibronectin, WT-l, l7-lA-antigen, C3, C3a, C3b, C5a, C5, bcl-2, K-ras, tumor neoantigen, a viral antigen associated with cancer, FcγRIIB, IL-12β2R, CD28, CD56, CD11c, CD66b, CD41, CD61, CD62, CD235a, CD146, CD326, or CD203c, or any combination thereof.

[00616] In some embodiments, the antigen expressed by the undesired cell is BCMA. In some embodiments, the antigen expressed by the undesired cell is PSMA.

[00617] In some embodiments, the isolated molecule is an antibody or a non-antibody molecule.

[00618] In some embodiments, the antibody comprises a first half molecule and a second half molecule, wherein the first half molecule comprises the first antigen binding domain and the

second antigen binding domain and the second half molecule comprises the third antigen binding domain.

[00619] The isolated molecules and multispecific molecules comprising an antigen binding domain that specifically binds BCMA disclosed herein may be used in the treatment of multiple myeloma (MM).

[00620] In some embodiments, the multiple myeloma is a newly diagnosed multiple myeloma.

[00621] In some embodiments, the multiple myeloma is a relapsed or a refractory multiple myeloma.

[00622] In some embodiments, the multiple myeloma is a high-risk multiple myeloma. Subjects with high-risk multiple myeloma are known to relapse early and have poor prognosis and outcome. Subjects can be classified as having high-risk multiple myeloma is they have one or more of the following cytogenetic abnormalities: t(4;14)(p16;q32), t(14;16)(q32;q23), del17p, 1qAmp, t(4;14)(p16;q32) and t(14;16)(q32;q23), t(4;14)(p16;q32) and del17p, t(14;16)(q32;q23) and del17p, or t(4;14)(p16;q32), t(14;16)(q32;q23) and del17p.

[00623] In some embodiments, the subject having the high-risk multiple myeloma has one or more chromosomal abnormalities comprising: t(4;14)(p16;q32), t(14;16)(q32;q23), del17p, 1qAmp, t(4;14)(p16;q32) and t(14;16)(q32;q23), t(4;14)(p16;q32) and del17p, t(14;16)(q32;q23) and del17p; or t(4;14)(p16;q32), t(14;16)(q32;q23) and del17p, or any combination thereof.

[00624] Various qualitative and/or quantitative methods may be used to determine relapse or refractory nature of the disease. Symptoms that may be associated are for example a decline or plateau of the well-being of the patient or re-establishment or worsening of various symptoms associated with solid tumors, and/or the spread of cancerous cells in the body from one location to other organs, tissues or cells.

[00625] The cytogenetic abnormalities can be detected for example by fluorescent in situ hybridization (FISH). In chromosomal translocations, an oncogene is translocated to the IgH region on chromosome 14q32, resulting in dysregulation of these genes. t(4;14)(p16;q32) involves translocation of fibroblast growth factor receptor 3 (FGFR3) and multiple myeloma SET domain containing protein (MMSET) (also called WHSC1/NSD2), and t(14;16)(q32;q23)

involves translocation of the MAF transcription factor C-MAF. Deletion of 17p (del17p) involves loss of the p53 gene locus.

[00626] In some embodiments, the multiple myeloma is relapsed or refractory to treatment with the anti-CD38 antibody, lenalinomide, bortezomib, pomalidomide, carfilzomib, elotozumab, ixazomib, melphalan or thalidomide, or any combination thereof.

[00627] In some embodiments, the multiple myeloma is relapsed or refractory to treatment with the anti-CD38 antibody. In some embodiments, the multiple myeloma is relapsed or refractory to treatment with lenalinomide. In some embodiments, the multiple myeloma is relapsed or refractory to treatment with bortezomib. In some embodiments, the multiple myeloma is relapsed or refractory to treatment with pomalidomide. In some embodiments, the multiple myeloma is relapsed or refractory to treatment with carfilzomib. In some embodiments, the multiple myeloma is relapsed or refractory to treatment with elotozumab. In some embodiments, the multiple myeloma is relapsed or refractory to treatment with ixazomib. In some embodiments, the multiple myeloma is relapsed or refractory to treatment with melphalan. In some embodiments, the multiple myeloma is relapsed or refractory to treatment with or thalidomide.

[00628] The isolated molecules and multispecific molecules comprising an antigen binding domain that specifically binds PSMA disclosed herein may be used in the treatment of prostate cancer.

[00629] "**Prostate cancer**" is meant to include all types of cancerous growths within prostate or oncogenic processes, metastatic tissues or malignantly transformed cells, tissues, or organs, irrespective of histopathology type or stage of invasiveness.

[00630] In some embodiments, the prostate cancer is an adenocarcinoma.

[00631] In some embodiments, the prostate cancer is a metastatic prostate cancer. In some embodiments, the prostate cancer has metastasized to rectum, lymph node or bone, or any combination thereof.

[00632] In some embodiments, the prostate cancer is a relapsed or a refractory prostate cancer.

[00633] In some embodiments, the prostate cancer is a castration resistant prostate cancer.

[00634] In some embodiments, the prostate cancer is sensitive to an androgen deprivation therapy.

[00635] In some embodiments, the prostate cancer is insensitive to the androgen deprivation therapy.

[00636] In some embodiments, the subject is treatment naïve.

[00637] In some embodiments, the subject has received androgen deprivation therapy.

[00638] In some embodiments, the subject has an elevated level of prostate specific antigen (PSA). PSA is elevated in a subject when the level is typically about ≥4.0 ng/mL. In some instances, elevated PSA may refer to level off ≥ 3.0 ng/mL. PSA levels may also be compared to post-androgen deprivation therapy levels.

[00639] Androgen deprivation therapies include abiraterone, ketoconazole, enzalutamide, galeterone, ARN-509 and orteronel (TAK-700), or prostatectomy.

Enrichment and detection methods

[00640] The isolated molecules or the isolated multispecific antibodies of the disclosure can be used to selectively enrich, isolate, separate, purify, sort, select, capture or detect $CD8^+$ CTLs. The isolated molecules or the isolated multispecific antibodies of the disclosure may be utilized in a bispecific format, *e.g.,* containing a first antigen binding domain that specifically binds CD8 and a second antigen binding domain that specifically binds the TCR complex, or they may be utilized in a format that incorporates the third antigen binding domain that specifically binds a third antigen. In some embodiments, the third antigen is an inert antigen.

[00641] The disclosure provides a method of enriching, isolating, separating, purifying, sorting, selecting, capturing or detecting a CD8+ CTL comprising:
providing a sample comprising the $CD8^+$ CTL;
contacting the sample with an isolated molecule comprising a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds a TCR complex; and
enriching, isolating, separating, purifying, sorting, selecting, capturing or detecting the $CD8^+$ CTL bound to the isolated molecule.

[00642] The disclosure provides a method of enriching a CD8+ CTL comprising:
providing a sample comprising the $CD8^+$ CTL;
contacting the sample with an isolated molecule comprising a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds a TCR complex; and

enriching the $CD8^+$ CTL bound to the isolated molecule.

[00643] The disclosure provides a method of isolating a CD8+ CTL comprising:

providing a sample comprising the $CD8^+$ CTL;

contacting the sample with an isolated molecule comprising a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds a TCR complex; and

isolating the $CD8^+$ CTL bound to the isolated molecule.

[00644] The disclosure provides a method of separating a CD8+ CTL comprising:

providing a sample comprising the $CD8^+$ CTL;

contacting the sample with an isolated molecule comprising a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds a TCR complex; and

separating the $CD8^+$ CTL bound to the isolated molecule.

[00645] The disclosure provides a method of purifying a CD8+ CTL comprising:

providing a sample comprising the $CD8^+$ CTL;

contacting the sample with an isolated molecule comprising a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds a TCR complex; and

purifying the $CD8^+$ CTL bound to the isolated molecule.

[00646] The disclosure provides a method of sorting a CD8+ CTL comprising:

providing a sample comprising the $CD8^+$ CTL;

contacting the sample with an isolated molecule comprising a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds a TCR complex; and

sorting the $CD8^+$ CTL bound to the isolated molecule.

[00647] The disclosure provides a method of selecting a CD8+ CTL comprising:

providing a sample comprising the $CD8^+$ CTL;

contacting the sample with an isolated molecule comprising a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds a TCR complex; and

selecting the $CD8^+$ CTL bound to the isolated molecule.

[00648] The disclosure provides a method of capturing a CD8+ CTL comprising:
providing a sample comprising the $CD8^+$ CTL;
contacting the sample with an isolated molecule comprising a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds a TCR complex; and
capturing the $CD8^+$ CTL bound to the isolated molecule.

[00649] The disclosure provides a method of detecting a CD8+ CTL comprising:
providing a sample comprising the $CD8^+$ CTL;
contacting the sample with an isolated molecule comprising a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds a TCR complex; and
detecting the $CD8^+$ CTL bound to the isolated molecule.

[00650] The disclosure also provides a method of enriching, isolating, separating, purifying, sorting, selecting, capturing or detecting a $CD8^+$ CTL, comprising:
contacting the $CD8^+$ CTL with an isolated molecule comprising a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds a TCR complex; and
enriching, isolating, separating, purifying, sorting, selecting, capturing or detecting the $CD8^+$ CTL based on binding of the $CD8^+$ CTL to the isolated molecule.

[00651] The disclosure also provides a method of enriching a $CD8^+$ CTL, comprising:
contacting the $CD8^+$ CTL with an isolated molecule comprising a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds a TCR complex; and
enriching the $CD8^+$ CTL based on binding of the $CD8^+$ CTL to the isolated molecule.

[00652] The disclosure also provides a method of isolating a $CD8^+$ CTL, comprising: \
contacting the $CD8^+$ CTL with an isolated molecule comprising a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds a TCR complex; and
isolating the $CD8^+$ CTL based on binding of the $CD8^+$ CTL to the isolated molecule.

[00653] The disclosure also provides a method of separating a $CD8^+$ CTL, comprising:

contacting the $CD8^+$ CTL with an isolated molecule comprising a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds a TCR complex; and separating the $CD8^+$ CTL based on binding of the $CD8^+$ CTL to the isolated molecule.

[00654] The disclosure also provides a method of purifying or detecting a $CD8^+$ CTL, comprising:

contacting the $CD8^+$ CTL with an isolated molecule comprising a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds a TCR complex; and purifying the $CD8^+$ CTL based on binding of the $CD8^+$ CTL to the isolated molecule.

[00655] The disclosure also provides a method of a $CD8^+$ CTL, comprising:

contacting the $CD8^+$ CTL with an isolated molecule comprising a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds a TCR complex; and sorting the $CD8^+$ CTL based on binding of the $CD8^+$ CTL to the isolated molecule.

[00656] The disclosure also provides a method of selecting a $CD8^+$ CTL, comprising:

contacting the $CD8^+$ CTL with an isolated molecule comprising a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds a TCR complex; and selecting the $CD8^+$ CTL based on binding of the $CD8^+$ CTL to the isolated molecule.

[00657] The disclosure also provides a method of capturing a $CD8^+$ CTL, comprising:

contacting the $CD8^+$ CTL with an isolated molecule comprising a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds a TCR complex; and capturing the $CD8^+$ CTL based on binding of the $CD8^+$ CTL to the isolated molecule.

[00658] The disclosure also provides a method of detecting a $CD8^+$ CTL, comprising:

contacting the $CD8^+$ CTL with an isolated molecule comprising a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds a TCR complex; and detecting the $CD8^+$ CTL based on binding of the $CD8^+$ CTL to the isolated molecule.

[00659] In some embodiments, the sample is a blood sample or a tissue sample.

[00660] In some embodiments, the method is conducted in suspension or on a solid support.

[00661] In some embodiments, the method is conducted using beads, microfluidics, fluorescent cell sorting, chips, columns or surfaces.

[00662] In some embodiments, the isolated molecule further comprises a third antigen binding domain that specifically binds a third antigen.

[00663] In some embodiments, the first antigen binding domain, the second antigen binding domain or the third antigen binding domain comprises a scFv, a Fab, a Fab', a $F(ab')_2$, a Fd, a Fv, a dAb, a VHH, a VH, a VL, a non-antibody scaffold, or fragments thereof.

[00664] In some embodiments, the isolated molecule comprises: a first polypeptide comprising, from N- to C-terminus, the second antigen binding domain comprising the scFv, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain; a second polypeptide comprising, from N- to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and a third polypeptide comprising, from N- to C-terminus, the third antigen binding domain comprising the scFv and a Fc or a fragment of the Fc.

[00665] In some embodiments, the isolated molecule comprises: a first polypeptide comprising, from N- to C-terminus, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain; a second polypeptide comprising, from N- to C-terminus, a VL that is capable of specifically binding CD8, a CL domain and the second antigen binding domain comprising the scFv; and a third polypeptide comprising, from N- to C-terminus, the third antigen binding domain comprising the scFv and a Fc or a fragment of the Fc.

[00666] In some embodiments, the isolated molecule comprises: a first polypeptide comprising, from N- to C-terminus, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain, a CH3 domain and the second antigen binding domain comprising the scFv; a second polypeptide comprising, from N- to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and a third polypeptide comprising, from N- to C-terminus, the third antigen binding domain comprising the scFv and a Fc or a fragment of the Fc.

[00667] In some embodiments, the first antigen binding domain comprising the Fab, the second antigen binding domain comprising the scFv or the third antigen binding domain

comprising the scFv is conjugated to the Fc or the fragment of the Fc, to the VH that is capable of specifically biding CD8, to the CL domain or to the CH3 domain via a linker.

[00668] In some embodiments, the linker comprises a polypeptide of SEQ ID NOs: 2183-2290.

[00669] In some embodiments, the fragment of the Fc comprises a CH2 domain and a CH3 domain.

[00670] In some embodiments, the Fc, the CH2 domain or the CH3 domain is an IgG1, IgG2, IgG3 or IgG4 isotype.

[00671] In some embodiments, the second antigen binding domain specifically binds CD3, TCRα chain, TCRβ chain, TCRγ chain or TCRδ chain, or any combination thereof.

[00672] In some embodiments, the TCRβ chain comprises TCRVB17.

[00673] In some embodiments, CD3 comprises CD3ε, CD3γ, CD3δ or CD3ζ.

[00674] In some embodiments, the second antigen binding domain that specifically binds CD3 comprises the HCDR1 of SEQ ID NO: 2291, the HCDR2 of SEQ ID NO: 2292, the HCDR3 of SEQ ID NO: 2293, the LCDR1 of SEQ ID NO: 2294, the LCDR2 of SEQ ID NO: 2295 and the LCDR3 of SEQ ID NO: 2296.

[00675] In some embodiments, the second antigen binding domain that specifically binds CD3 comprises the VH of SEQ ID NO: 2297 and the VL of SEQ ID NO: 2298.

[00676] In some embodiments, the first antigen binding domain comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312.

[00677] In some embodiments, the first antigen binding domain comprises the VH of SEQ ID NO: 2313 and the VL of SEQ ID NO: 2314.

[00678] In some embodiments, the isolated molecule is an antibody or a non-antibody molecule.

[00679] In some embodiments, the antibody comprises a first half molecule and a second half molecule, wherein the first half molecule comprises the first antigen binding domain and the second antigen binding domain and the second half molecule comprises the third antigen binding domain.

[00680] Enrichment, isolation, separation, purification, sorting, selecting, capturing or detecting, or any combination thereof can be done using known technologies such as bead, microfluidics, solid support, columns etc. In general the isolated molecule of the disclosure, when bound to the $CD8^+$ CTL may be separated or visualized using known methods.

[00681] The following examples are provided to further describe some of the embodiments disclosed herein. The examples are intended to illustrate, not to limit, the disclosed embodiments.

EXAMPLES

EXAMPLE 1: DESIGN AND GENERATION OF TRISPECIFIC MOLECULES SPECIFICALLY ENGAGING $CD8^+$ CTLS

[00682] The approach to specifically engage $CD8^+$ CTLs was to design and test multispecific molecules having a CD3 binding domain of various affinities, an agonistic CD8+ binding domain and a tumor associated antigen (TAA) binding domain and tailor the binding affinities within the range that would result in $CD8^+$ T cell activation and tumor cell killing only in instances when co-engagement of CD3 and CD8 occurred. Towards that end, CD3 binding domains CD2B219 and CD3B450 were incorporated into a trispecific antibody together with OKT8, an agonistic CD8 binding antibody and a domain that binds the TAA. BCMA and PSMA binding domains were used to target the trispecific molecules to tumors. **FIG. 1**, **FIG. 2** and **FIG. 3** show the designed protein formats used in the study. In the Protein Format 1 (**FIG. 1**), the TAA binding arm was incorporated as a scFv coupled to a Fc (HC1_scFv), the CD8 binding arm was incorporated as a HC/LC chain (HC2 N-term and LC2 2^{nd} N-term), and the CD3 binding arm was incorporated as a scFv attached to the N-terminus of the CD8 binding HC (LC2 1^{st} N-term). In the Protein Format 2 (**FIG. 2**), the TAA binding arm was incorporated as a scFv coupled to the Fc (HC1_scFv), the CD8 binding arm was incorporated as a HC/LC chain (HC2 N-term and LC2 1^{st} N-term), and the CD3 binding arm was incorporated as a scFv attached to the C-terminus of the CD8 binding LC (LC2 C-term). In the Protein Format 3 (**FIG. 3**), the TAA binding arm was incorporated as a scFv coupled to the Fc (HC1_scFv), the CD8 binding arm was incorporated as a HC/LC chain (HC2 N-term and LC1 1^{st} N-term), and the CD3 binding arm was incorporated as a scFv attached to the C-terminus of the CD8 binding HC (HC2 C-term). To evaluate differences resulting from engagement of either CD3 or CD8 alone or co-engagement of CD3 and CD8, corresponding constructs were generated in which either

the CD3 or the CD8 binding domain was replaced by the inert arm (RSV binding domain B21M) or not included at all (null). In some constructs, the TAA binding domain was excluded from the design.

[00683] The CD3 binding domain used were the VH/VL domains of CD3B219 or CD3B450 and the CD8 binding domain used were the VH/VL domain of OKT8. The amino acid sequences of the various domains are shown in **Table 4**. CD3B219 is considered a high affinity (low K_D) binder and CD3B450 is considered a low affinity (high K_D) binder. The K_D of CD3B219 was about 8 mM and the K_D of CD3B450 was about 80 nM for binding to CD3. The CD8 binding domain used were the VL/VL domains of OKT8. The amino acid sequences of OKT8 CDRs and VH/VL domains are shown in **Table 5.**

[00684] The trispecific molecules were cloned, expressed and purified using standard methods. To promote HC/HC heterodimerization, knob-in-hole mutations were introduced in the heavy chains.

Table 4.

CD3 binding domain	Region	Amino acid sequence	SEQ ID NO:
CD3B450	HCDR1	NNNAAWS	2291
	HCDR2	RTYYRSKWLYDYAVSVKS	2292
	HCDR3	GYSSSFDY	2293
	LCDR1	TGTSSNIGTYKFVS	2294
	LCDR2	EVSKRPS	2295
	LCDR3	VSYAGSGTLL	2296
	VH	QVQLQQSGPGLVKPSQTLSLTCAISGDSVFNNNAAWSWIRQSPSRGLEWLGRTYYRSKWLYDYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCARGYSSSFDYWGQGTLVTVSS	2297
	VL	QSALTQPASVSGSPGQSITISCTGTSSNIGTYKFVSWYQQHPGKAPKVMIYEVSKRPSGVSNRFSGSKSGNTAS	2298

CD3 binding domain	Region	Amino acid sequence	SEQ ID NO:
		LTISGLQAEDEADYYCVSYAGSGT LLFGGGTKLTVL	
CD3B219	HCDR1	TYAMN	2299
	HCDR2	RIRSKYNNYATYYAASVKG	2300
	HCDR3	HGNFGNSYVSWFAY	2301
	LCDR1	RSSTGAVTTSNYAN	2302
	LCDR2	GTNKRAP	2303
	LCDR3	ALWYSNLWV	2304
	VH	EVQLVESGGGLVQPGGSLRLSCAA SGFTFNTYAMNWVRQAPGKGLE WVARIRSKYNNYATYYAASVKGR FTISRDDSKNSLYLQMNSLKTEDT AVYYCARHGNFGNSYVSWFAYW GQGTLVTVSS	2305
	VL	QTVVTQEPSLTVSPGGTVTLTCRSS TGAVTTSNYANWVQQKPGQAPRG LIGGTNKRAPGTPARFSGSLLGGK AALTLSGVQPEDEAEYYCALWYS NLWVFGGGTKLTVL	2306

Table 5.

CD8 binding domain	Region	Amino acid sequence	SEQ ID NO:
OKT8	HCDR1	DTYIH	2307
	HCDR2	RIDPANDNTLYASKFQG	2308
	HCDR3	GYGYYVFDH	2309
	LCDR1	RTSRSISQYLA	2310
	LCDR2	SGSGS	2311

CD8 binding domain	Region	Amino acid sequence	SEQ ID NO:
	LCDR3	QQHNENPLT	2312
	VH	EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIH FVRQRPEQGLEWIGRIDPANDNTLYASKFQGKATI TADTSSNTAYMHLCSLTSGDTAVYYCGRGYGYY VFDHWGQGTTLTVSS	2313
	VL	DVQINQSPSFLAASPGETITINCRTSRSISQYLAWY QEKPGKTNKLLIYSGSTLQSGIPSRFSGSGSGTDFT LTISGLEPEDFAMYYCQQHNENPLTFGAGTKLEL R	2314

[00685] The specific constructs generated incorporating CD3, CD8 and BCMA binding domains are shown in **Table 6.** **Table 6** constructs 1-12 were engineered as Protein Format 1, constructs 13-17 and 31-36 were engineered as Protein Format 2, and constructs 19-30 were engineered as Protein Format 3. The specific constructs generated incorporating CD3, CD8 and PSMA binding domains are shown in **Table 7**. **Table 7** constructs P3-P5, P15-P17, P21-P23 and P33-P35 were engineered as Protein Format 1, constructs P6-P8, P12-P14, P24-P26 and P30-P32 were engineered as Protein Format 2, and constructs P1, P2, P9-P11, P18-P20, P270P29 and P36 were engineered as Protein Format 3.

Table 6.

Construct number	HC1_scFv	HC2 (N-term)	HC2 (C-term)	LC2 (1st N-term)	LC2 (2nd N-term)	LC2 (C-term)
1	BCMA-scFv	OKT8-Fab-RF	n/a	CD3B450-LH-scFv	OKT8-LC	n/a
2	BCMA-scFv	OKT8-Fab-RF	n/a	CD3B219-LH-scFv	OKT8-LC	n/a
3	BCMA-scFv	OKT8-Fab-RF	n/a	null-scFv	OKT8-LC	n/a

Construct number	HC1_scFv	HC2 (N-term)	HC2 (C-term)	LC2 (1st N-term)	LC2 (2nd N-term)	LC2 (C-term)
4	BCMA-scFv	B21M-Fab-RF	n/a	CD3B450-LH-scFv	B21M-LC	n/a
5	BCMA-scFv	B21M-Fab-RF	n/a	CD3B219-LH-scFv	B21M-LC	n/a
6	BCMA-scFv	B21M-Fab-RF	n/a	null-scFv	B21M-LC	n/a
7	null-scFv	OKT8-Fab-RF	n/a	CD3B450-LH-scFv	OKT8-LC	n/a
8	null-scFv	OKT8-Fab-RF	n/a	CD3B219-LH-scFv	OKT8-LC	n/a
9	null-scFv	OKT8-Fab-RF	n/a	null-scFv	OKT8-LC	n/a
10	null-scFv	B21M-Fab-RF	n/a	CD3B450-LH-scFv	B21M-LC	n/a
11	null-scFv	B21M-Fab-RF	n/a	CD3B219-LH-scFv	B21M-LC	n/a
12	null-scFv	B21M-Fab-RF	n/a	null-scFv	B21M-LC	n/a
13	BCMA-scFv	OKT8-Fab-RF	n/a	OKT8-LC	n/a	CD3B450-LH-scFv
14	BCMA-scFv	OKT8-Fab-RF	n/a	OKT8-LC	n/a	CD3B219-LH-scFv
15	BCMA-scFv	OKT8-Fab-RF	n/a	OKT8-LC	n/a	null-scFv
16	BCMA-scFv	B21M-Fab-RF	n/a	B21M-LC	n/a	CD3B450-LH-scFv
17	BCMA-scFv	B21M-Fab-RF	n/a	B21M-LC	n/a	CD3B219-LH-scFv

Construct number	HC1_scFv	HC2 (N-term)	HC2 (C-term)	LC2 (1st N-term)	LC2 (2nd N-term)	LC2 (C-term)
18	BCMA-scFv	B21M-Fab-RF	n/a	B21M-LC	n/a	null-scFv
34	null-scFv	OKT8-Fab-RF	n/a	OKT8-LC	n/a	CD3B450-LH-scFv
35	null-scFv	OKT8-Fab-RF	n/a	OKT8-LC	n/a	CD3B219-LH-scFv
36	null-scFv	OKT8-Fab-RF	n/a	OKT8-LC	n/a	null-scFv
31	null-scFv	B21M-Fab-RF	n/a	B21M-LC	n/a	CD3B450-LH-scFv
32	null-scFv	B21M-Fab-RF	n/a	B21M-LC	n/a	CD3B219-LH-scFv
33	null-scFv	B21M-Fab-RF	n/a	B21M-LC	n/a	null-scFv
19	BCMA-scFv	OKT8-Fab-RF	CD3B450-LH-scFv	OKT8-LC	n/a	n/a
20	BCMA-scFv	OKT8-Fab-RF	CD3B219-LH-scFv	OKT8-LC	n/a	n/a
21	BCMA-scFv	OKT8-Fab-RF	null-scFv	OKT8-LC	n/a	n/a
22	BCMA-scFv	B21M-Fab-RF	CD3B450-LH-scFv	B21M-LC	n/a	n/a
23	BCMA-scFv	B21M-Fab-RF	CD3B219-LH-scFv	B21M-LC	n/a	n/a
24	BCMA-scFv	B21M-Fab-RF	null-scFv	B21M-LC	n/a	n/a
25	null-scFv	OKT8-Fab-RF	CD3B450-LH-scFv	OKT8-LC	n/a	n/a

Construct number	HC1_scFv	HC2 (N-term)	HC2 (C-term)	LC2 (1st N-term)	LC2 (2nd N-term)	LC2 (C-term)
26	null-scFv	OKT8-Fab-RF	CD3B219-LH-scFv	OKT8-LC	n/a	n/a
27	null-scFv	OKT8-Fab-RF	null-scFv	OKT8-LC	n/a	n/a
28	null-scFv	B21M-Fab-RF	CD3B450-LH-scFv	B21M-LC	n/a	n/a
29	null-scFv	B21M-Fab-RF	CD3B219-LH-scFv	B21M-LC	n/a	n/a
30	null-scFv	B21M-Fab-RF	null-scFv	B21M-LC	n/a	n/a

Table 7.

Construct number	HC1_scFv	HC2 (N-term)	HC2 (C-term)	LC2 (1st N-term)	LC2 (2nd N-term)	LC2 (C-term)
P4	PSMA-scFv	OKT8-Fab-RF	n/a	CD3B450-LH-scFv	OKT8-LC	n/a
P3	PSMA-scFv	OKT8-Fab-RF	n/a	CD3B219-LH-scFv	OKT8-LC	n/a
P5	PSMA-scFv	OKT8-Fab-RF	n/a	null-scFv	OKT8-LC	n/a
P16	PSMA-scFv	B21M-Fab-RF	n/a	CD3B450-LH-scFv	B21M-LC	n/a
P15	PSMA-scFv	B21M-Fab-RF	n/a	CD3B219-LH-scFv	B21M-LC	n/a
P17	PSMA-scFv	B21M-Fab-RF	n/a	null-scFv	B21M-LC	n/a
P22	null-scFv	OKT8-Fab-RF	n/a	CD3B450-LH-scFv	OKT8-LC	n/a

Construct number	HC1_scFv	HC2 (N-term)	HC2 (C-term)	LC2 (1st N-term)	LC2 (2nd N-term)	LC2 (C-term)
P21	null-scFv	OKT8-Fab-RF	n/a	CD3B219-LH-scFv	OKT8-LC	n/a
P23	null-scFv	OKT8-Fab-RF	n/a	null-scFv	OKT8-LC	n/a
P34	null-scFv	B21M-Fab-RF	n/a	CD3B450-LH-scFv	B21M-LC	n/a
P33	null-scFv	B21M-Fab-RF	n/a	CD3B219-LH-scFv	B21M-LC	n/a
P35	null-scFv	B21M-Fab-RF	n/a	null-scFv	B21M-LC	n/a
P7	PSMA-scFv	OKT8-Fab-RF	n/a	OKT8-LC	n/a	CD3B450-LH-scFv
P6	PSMA-scFv	OKT8-Fab-RF	n/a	OKT8-LC	n/a	CD3B219-LH-scFv
P8	PSMA-scFv	OKT8-Fab-RF	n/a	OKT8-LC	n/a	null-scFv
P12	PSMA-scFv	B21M-Fab-RF	n/a	B21M-LC	n/a	CD3B450-LH-scFv
P13	PSMA-scFv	B21M-Fab-RF	n/a	B21M-LC	n/a	CD3B219-LH-scFv
P14	PSMA-scFv	B21M-Fab-RF	n/a	B21M-LC	n/a	null-scFv
P25	null-scFv	OKT8-Fab-RF	n/a	OKT8-LC	n/a	CD3B450-LH-scFv
P24	null-scFv	OKT8-Fab-RF	n/a	OKT8-LC	n/a	CD3B219-LH-scFv
P26	null-scFv	OKT8-Fab-RF	n/a	OKT8-LC	n/a	null-scFv

Construct number	HC1_scFv	HC2 (N-term)	HC2 (C-term)	LC2 (1st N-term)	LC2 (2nd N-term)	LC2 (C-term)
P30	null-scFv	B21M-Fab-RF	n/a	B21M-LC	n/a	CD3B450-LH-scFv
P31	null-scFv	B21M-Fab-RF	n/a	B21M-LC	n/a	CD3B219-LH-scFv
P32	null-scFv	B21M-Fab-RF	n/a	B21M-LC	n/a	null-scFv
P2	PSMA-scFv	OKT8-Fab-RF	CD3B450-LH-scFv	OKT8-LC	n/a	n/a
P1	PSMA-scFv	OKT8-Fab-RF	CD3B219-LH-scFv	OKT8-LC	n/a	n/a
P9	PSMA-scFv	OKT8-Fab-RF	null-scFv	OKT8-LC	n/a	n/a
P11	PSMA-scFv	B21M-Fab-RF	CD3B450-LH-scFv	B21M-LC	n/a	n/a
P10	PSMA-scFv	B21M-Fab-RF	CD3B219-LH-scFv	B21M-LC	n/a	n/a
P18	PSMA-scFv	B21M-Fab-RF	null-scFv	B21M-LC	n/a	n/a
P20	null-scFv	OKT8-Fab-RF	CD3B450-LH-scFv	OKT8-LC	n/a	n/a
P19	null-scFv	OKT8-Fab-RF	CD3B219-LH-scFv	OKT8-LC	n/a	n/a
P27	null-scFv	OKT8-Fab-RF	null-scFv	OKT8-LC	n/a	n/a
P29	null-scFv	B21M-Fab-RF	CD3B450-LH-scFv	B21M-LC	n/a	n/a
P28	null-scFv	B21M-Fab-RF	CD3B219-LH-scFv	B21M-LC	n/a	n/a

Construct number	HC1_scFv	HC2 (N-term)	HC2 (C-term)	LC2 (1st N-term)	LC2 (2nd N-term)	LC2 (C-term)
P36	null-scFv	B21M-Fab-RF	null-scFv	B21M-LC	n/a	n/a

EXAMPLE 2: CO-ENGAGEMENT OF CD3 AND CD8 RESULTS IN TUMOR CELL DEATH AND ACTIVATION OF T CELLS

[00686] All constructs were tested for their ability to mediate tumor cell death and to activate T cells using known methods.

[00687] **Table 8** shows the results of % tumor cell death and % T cell activation (as assessed by % $CD25^+$ live T cells) of trispecific BCMAxCD3xCD8 antibodies and controls. **Table 9** shows the results of % tumor cell death and % T cell activation of trispecific PSMAxCD3xCD8 antibodies and controls. As is shown in **Table 8**, constructs with low affinity CD3 binding domain mediated tumor cell death and T cell activation only via co-engagement with CD8 in the context of multispecific CD3xCD8xBCMA antibodies (construct number 1,13, 19). Constructs with high affinity CD3 binding domain mediated tumor cell death and T cell activation without co-engagement with CD8 (constructs 15, 17, 23). Further, constructs with high affinity CD3 binding domain and CD8 binding domain without TAA binding domain were able to mediate tumor cell killing and to activate T cells (**Table 8**, construct 8, 35 and **Table 9**, constructs P21 and P24). Similarly, as is shown in **Table 9**, trispecific antibodies binding PSMA with high affinity CD3 domains were able to mediate tumor cell killing and T cell activation only in the presence of CD8 co-engagement. **Table 10** and **Table 11** shows cytokine production by T cells contacted with BCMAxCD3xCD8 trispecific antibodies or controls and **Table 12** and **Table 13** show cytokine production by T cells contacted with PSMAxCD3xCD8 trispecifc antibodies or controls as shown in the Tables. In general, cytokine release, tumor killing and T-cell activation by T cells appeared comparable. Overall data indicated that the trispecific constructs with CD8 antibody plus high affinity CD3 binding domain CD3B450 appeared to be weaker in releasing IFNγ than the constructs with CD8 antibody and the high affinity CD3 binding domain CD3B219. The null controls with no TAA but with CD8 and CD3 domains appeared to show

some very weak cytokine activity. Overall IFNγ, IL-10 and TNFα levels appeared to be released at higher levels than the rest of the cytokines from the panel.

[00688] Cytotoxicity was measured in a real-time cell analyzer xCELLigence (Roche) using adherent tumor cell lines as target cells. All experiments were performed using the respective target cell culturing media. Fifty microliters of medium was added to E-Plates 96 (Roche, Grenzach-Wyhlen, Germany) for measurement of background values. Target cells used in the experiments include C4-2B, LnCap MM1R, H929 tumor cell lines. Target cells were seeded in an additional 100 µl medium at a density of around 10,000 cells per well. Suitable cell densities were determined by previous titration experiments. Cell attachment was monitored using the RTCA SP (Roche) instrument and the RTCA software Version 1.1 (Roche) until the plateau phase was reached. T cells were added at variant dosages of trispecific antibodies. Upon addition of effector cells, impedance measurements were performed every 15 min for up to 81 h. All experiments were performed in triplicates. Changes in electrical impedance were expressed as a dimensionless cell index (CI) value, which derives from relative impedance changes corresponding to cellular coverage of the electrode sensors, normalized to baseline impedance values with medium only. To analyze the acquired data, CI values were exported, and percentage of lysis was calculated in relation to the control cells lacking any effector T cells. The percentage of cytolysis is readily calculated using a simple formula: Percentage of cytolysis = ((Cell Index no effector – Cell Index effector)/Cell Index no effector) X 100. Cytotoxicity of the T cells was also tested by using the IncuCyte zoom living cell imaging system. Co-culture was set up the same as the above in xCELLigence assay. images were taken every 30min and the number of dead cells was quantified.

[00689] The Intellicyt human T cell activation and cytokine profiling kit was applied for T cell activation and cytokine profile. Briefly, T cells were cocultured with prostate tumor cells at an effector to target cells ratio (E:T ratio) of 1 to 1 in 96-well round bottom plate in 200ul RPMI complete media. The trispecific antibodies were co-cultured and 24 hr later, T cell activation was assessed by the TCA kit from a 30ul cell/supernatant mixture sample following the protocol. Samples were acquired on the Intellicyt iQue Screener PLUS. Standard curves to quantitate the levels of secreted cytokines. Data were analyzed with ForeCyt software.

Table 8.

Construct number	Protein Format	Domains present			% Tumor cell death		% CD25 +ve Live T-cells	
		TAA	CD3	CD8	nM EC_{50}	Max. Activity	nM EC_{50}	Max. Activity
Control					0.08	57.63	0.18	71.83
1	1	BCMA	LA	P	0.44	73.94	0.8	72.85
13	2	BCMA	LA	P	0.4	70.64	1.54	71.09
19	3	BCMA	LA	P	0.08	69.59	0.4	72.25
4	1	BCMA	LA	A	>10.00	50.38	6.99	54.74
16	2	BCMA	LA	A	>10.00	0.89	>10.00	3.88
22	3	BCMA	LA	A	7.42	52.49	5.02	56.05
3	1	BCMA	A	P	>10.00	-0.31	>10.00	4.18
15	2	BCMA	A	P	>10.00	1.18	>10.00	4.33
21	3	BCMA	A	P	>10.00	10.21	>10.00	17.4
6	1	BCMA	A	A	>10.00	-1.25	>10.00	4.39
18	2	BCMA	A	A	>10.00	-0.25	>10.00	3.78
24	3	BCMA	A	A	>10.00	0.96	>10.00	3.74
7	1	none	LA	P	>10.00	19.52	3.92	33.77

34	2	none	LA	P	>10.00	15.57	>10.00	21.75
25	3	none	LA	P	>10.00	7.24	>10.00	13.07
10	1	none	LA	A	>10.00	-0.04	>10.00	4.35
31	2	none	LA	A	>10.00	3.96	>10.00	3.25
28	3	none	LA	A	>10.00	1.09	>10.00	4.48
2	1	BCMA	HA	P	0.04	72.26	0.09	80.34
14	2	BCMA	HA	P	0.02	74.38	0.19	84.94
20	3	BCMA	HA	P	0.02	71.62	0.11	81.04
5	1	BCMA	HA	A	0.58	68.37	0.64	66.49
17	2	BCMA	HA	A	0.84	59.12	1.16	68.07
23	3	BCMA	HA	A	0.89	65.04	1.03	64.55
8	1	none	HA	P	3.22	22.71	0.17	44.81
35	2	none	HA	P	5.76	29.18	0.77	48.62
26	3	none	HA	P	>10.00	6.45	>10.00	22.41
11	1	none	HA	A	>10.00	8.93	>10.00	16.37
32	2	none	HA	A	>10.00	1.47	>10.00	4.51
29	3	none	HA	A	>10.00	0.24	>10.00	4.07
9	1	none	A	P	>10.00	-0.54	>10.00	4.38

36	2	none	A	P	>10.00	14.79	>10.00	13.6
27	3	none	A	P	>10.00	0.84	>10.00	4.03
12	1	none	A	A	>10.00	12.1	>10.00	16.4
33	2	none	A	A	>10.00	-0.55	>10.00	3.02
30	3	none	A	A	>10.00	0.92	>10.00	4.76
Positive control					0.08	57.6	0.18	71.8
Negative control (HC3B1.007)					>10.00	6.8	>10.00	4.47
	LA: low affinity (high K_D); HA: high affinity (low K_D), A: absent; P: present							

Table 9.

Construct number	Protein format	Domains present			% Tumor cell death		% CD25 +ve Live T-cells	
		TAA	CD3	CD8	nM EC50	Max. Activity	nM EC50	Max. Activity
P4	1	PSMA	LA	P	1.9	67.7	9.2	70.6
P7	2	PSMA	LA	P	0.7	80.1	2.5	68.2
P2	3	PSMA	LA	P	0.9	73.8	2.9	26.8
P16	1	PSMA	LA	A	>10.00	6.7	>10.00	3.3
P12	2	PSMA	LA	A	>10.00	3.8	>10.00	2.8
P11	3	PSMA	LA	A	>10.00	9.8	>10.00	3.2

P5	1	PSMA	A	P	>10.00	4.7	>10.00	3.9
P8	2	PSMA	A	P	>10.00	9.8	>10.00	4.8
P9	3	PSMA	A	P	>10.00	13.7	>10.00	3.3
P17	1	PSMA	A	A	>10.00	7.5	>10.00	5.1
P14	2	PSMA	A	A	>10.00	4.7	>10.00	3.8
P18	3	PSMA	A	A	>10.00	7.9	>10.00	3.5
P22	1	none	LA	P	>10.00	8.9	>10.00	25.4
P25	2	none	LA	P	>10.00	67.9	>10.00	45.7
P20	3	none	LA	P	>10.00	9.9	>10.00	3.8
P34	1	none	LA	A	>10.00	9.4	>10.00	3.7
P30	2	none	LA	A	>10.00	9.5	>10.00	6.3
P29	3	none	LA	A	>10.00	7.9	>10.00	3.3
P3	1	PSMA	HA	P	0.2	72.4	0.3	82.1
P6	2	PSMA	HA	P	0.03	83.1	0.3	76.7
P1	3	PSMA	HA	P	0.6	84.6	>10.00	47.5
P15	1	PSMA	HA	A	>10.00	14.5	6.6	15.2
P13	2	PSMA	HA	A	>10.00	79.1	>10.00	19.0
P10	3	PSMA	HA	A	>10.00	14.2	>10.00	5.3
P21	1	none	HA	P	0.2	67.5	0.2	60.2
P24	2	none	HA	P	1.5	59.7	1.9	64.7
P19	3	none	HA	P	>10.00	7.6	>10.00	4.7
P33	1	none	HA	A	>10.00	8.6	>10.00	3.1
P31	2	none	HA	A	>10.00	13.5	>10.00	7.9
P28	3	none	HA	A	>10.00	5.2	>10.00	2.8
P23	1	none	A	P	>10.00	5.4	>10.00	3.1
P26	2	none	A	P	>10.00	14.3	>10.00	3.7
P27	3	none	A	P	>10.00	7.0	>10.00	3.2
P35	1	none	A	A	>10.00	2.8	>10.00	4.7
P32	2	none	A	A	>10.00	6.1	>10.00	2.9

P36	3	none	A	A	>10.00	7.7	0.4	7.7
Positive control					0.6	80.2	1.2	75.1
Negative control					>10.00	14.5	>10.00	3.5
LA: low affinity (high K_D); HA: high affinity (low K_D), A: absent; P: present								

Table 10.

Construct number	Protein Format	Domains present			IFNγ	IL-1b	IL-2	IL-4
		TAA	CD3	CD8				
1	1	BCMA	LA	P	1.049	0.986	10.000	1.056
13	2	BCMA	LA	P	0.834	10.000	1.244	10.000
19	3	BCMA	LA	P	0.195	10.000	10.000	0.354
4	1	BCMA	LA	A	10.000	10.000	10.000	10.000
16	2	BCMA	LA	A	10.000	10.000	10.000	10.000
22	3	BCMA	LA	A	10.000	10.000	10.000	3.158
3	1	BCMA	A	P	10.000	10.000	10.000	10.000
15	2	BCMA	A	P	10.000	10.000	10.000	3.333
21	3	BCMA	A	P	10.000	10.000	10.000	10.000
6	1	BCMA	A	A	10.000	10.000	10.000	10.000
18	2	BCMA	A	A	10.000	10.000	10.000	10.000
24	3	BCMA	A	A	10.000	10.000	10.000	10.000
7	1	none	LA	P	10.000	10.000	10.000	10.000
34	2	none	LA	P	10.000	10.000	10.000	10.000
25	3	none	LA	P	10.000	0.001	10.000	10.000
10	1	none	LA	A	10.000	10.000	10.000	10.000
31	2	none	LA	A	10.000	0.004	10.000	1.111
28	3	none	LA	A	10.000	10.000	10.000	10.000

2	1	BCMA	HA	P	0.324	0.158	6.757	0.043
14	2	BCMA	HA	P	0.042	0.037	10.000	10.000
20	3	BCMA	HA	P	0.060	10.000	10.000	0.000
5	1	BCMA	HA	A	0.958	4.737	2.491	0.973
17	2	BCMA	HA	A	1.108	10.000	2.842	9.057
23	3	BCMA	HA	A	1.697	10.000	2.659	1.114
8	1	none	HA	P	10.000	10.000	10.000	0.551
35	2	none	HA	P	0.992	0.400	10.000	10.000
26	3	none	HA	P	10.000	10.000	10.000	10.000
11	1	none	HA	A	10.000	10.000	10.000	10.000
32	2	none	HA	A	10.000		10.000	10.000
29	3	none	HA	A	10.000	10.000	10.000	10.000
9	1	none	A	P	10.000	10.000	10.000	10.000
36	2	none	A	P	10.000	10.000	10.000	10.000
27	3	none	A	P	10.000		10.000	10.000
12	1	none	A	A	10.000	10.000	10.000	10.000
33	2	none	A	A	10.000	10.000	10.000	10.000
30	3	none	A	A	10.000	10.000	10.000	10.000
Positive Control					0.248	0.002	0.374	0.129
HC3B1.007					10.000	10.000	10.000	10.000
LA: low affinity (high K_D); HA: high affinity (low K_D), A: absent; P: present								

Table 11.

Construct number	Protein Format	Domains present			IL-6	IL-8	IL-10	IL-13	TNFα
		TAA	CD3	CD8					
1	1	BCMA	LA	P	0.864	10.000	2.594	10.000	1.450
13	2	BCMA	LA	P	0.649	0.416	7.071	10.000	1.585

19	3	BCMA	LA	P	0.057	0.000	1.498	10.000	1.380
4	1	BCMA	LA	A	10.000	2.987	10.000	10.000	10.000
16	2	BCMA	LA	A	10.000	9.776	10.000	10.000	10.000
22	3	BCMA	LA	A	10.000	4.399	10.000	10.000	10.000
3	1	BCMA	A	P	10.000	10.000	10.000	10.000	10.000
15	2	BCMA	A	P	10.000	10.000	10.000	10.000	10.000
21	3	BCMA	A	P	10.000	10.000	10.000	10.000	10.000
6	1	BCMA	A	A	10.000	10.000	10.000	10.000	10.000
18	2	BCMA	A	A	10.000	10.000	10.000	10.000	10.000
24	3	BCMA	A	A	10.000	10.000	10.000	10.000	10.000
7	1	none	LA	P	10.000	10.000	10.000	10.000	10.000
34	2	none	LA	P	10.000	10.000	10.000	10.000	10.000
25	3	none	LA	P	10.000	10.000	10.000	10.000	10.000
10	1	none	LA	A	10.000	10.000	10.000	10.000	10.000
31	2	none	LA	A	10.000	10.000	10.000	10.000	10.000
28	3	none	LA	A	10.000	10.000	10.000	10.000	10.000
2	1	BCMA	HA	P	0.115	0.065	0.474	0.000	0.807
14	2	BCMA	HA	P	0.041	0.739	10.000	10.000	10.000
20	3	BCMA	HA	P	0.056	0.000	1.104	0.095	0.695
5	1	BCMA	HA	A	0.643	10.000	0.443	10.000	1.113
17	2	BCMA	HA	A	0.773	0.672	1.089	10.000	10.000
23	3	BCMA	HA	A	1.271	0.000	1.122	10.000	1.219
8	1	none	HA	P	5.135	0.561	1.404	10.000	0.994
35	2	none	HA	P	10.000	1.070	2.992	10.000	6.925
26	3	none	HA	P	10.000	10.000	10.000	10.000	10.000
11	1	none	HA	A	10.000	10.000	10.000	10.000	10.000
32	2	none	HA	A	10.000	10.000	10.000	10.000	10.000
29	3	none	HA	A	10.000	10.000	10.000	10.000	10.000
9	1	none	A	P	10.000	10.000	10.000	10.000	10.000

36	2	none	A	P	10.000	10.000	10.000	10.000	10.000
27	3	none	A	P	10.000	10.000	10.000	10.000	10.000
12	1	none	A	A	10.000	10.000	10.000	0.008	10.000
33	2	none	A	A	10.000	10.000	10.000		
30	3	none	A	A	10.000	10.000	10.000	10.000	10.000
Positive Control					0.074	0.002	0.123	0.116	0.327
Negative control (HC3B1.007)					10.000	10.000	10.000	10.000	10.000
LA: low affinity (high K_D); HA: high affinity (low K_D), A: absent; P: present									

Table 12.

Construct number	Protein format	TAA	CD3	CD8	IFNγ	IL-1B	IL2	IL4
P4	1	PSMA	LA	P	5.672	5.350	10.000	10.000
P7	2	PSMA	LA	P	4.622	1.670	10.000	10.000
P2	3	PSMA	LA	P	10.000	1.537	10.000	10.000
P16	1	PSMA	LA	A	10.000	10.000	10.000	10.000
P12	2	PSMA	LA	A	10.000	10.000	10.000	0.041
P11	3	PSMA	LA	A	10.000	10.000	10.000	10.000
P5	1	PSMA	A	P	10.000	10.000	10.000	10.000
P8	2	PSMA	A	P	10.000	10.000	10.000	10.000
P9	3	PSMA	A	P	10.000	10.000	10.000	10.000
P17	1	PSMA	A	A	10.000	10.000	10.000	0.370
P14	2	PSMA	A	A	10.000	10.000	10.000	10.000
P18	3	PSMA	A	A	10.000	10.000	10.000	3.333
P22	1	none	LA	P	9.984	10.000	10.000	10.000
P25	2	none	LA	P	8.333	9.076	10.000	10.000
P20	3	none	LA	P	10.000	10.000	10.000	3.333

P34	1	none	LA	A	10.000	10.000	10.000	10.000
P30	2	none	LA	A	10.000	10.000	10.000	0.370
P29	3	none	LA	A	10.000	10.000	9.299	0.370
P3	1	PSMA	HA	P	0.489	0.267	10.000	10.000
P6	2	PSMA	HA	P	0.867	0.085	10.000	10.000
P1	3	PSMA	HA	P	9.596	0.263	10.000	10.000
P15	1	PSMA	HA	A	10.000	10.000	10.000	0.370
P13	2	PSMA	HA	A	10.000	10.000	10.000	10.000
P10	3	PSMA	HA	A	10.000	10.000	10.000	10.000
P21	1	none	HA	P	0.316	0.285	10.000	10.000
P24	2	none	HA	P	8.126	5.372	10.000	10.000
P19	3	none	HA	P	10.000	10.000	10.000	3.333
P33	1	none	HA	A	10.000	10.000	10.000	10.000
P31	2	none	HA	A	1.111	10.000	0.000	0.005
P28	3	none	HA	A	1.111	10.000	10.000	0.370
P23	1	none	A	P	10.000	10.000	10.000	10.000
P26	2	none	A	P	1.111	0.001	10.000	10.000
P27	3	none	A	P	10.000	10.000	10.000	1.111
P35	1	none	A	A	10.000	10.000	10.000	10.000
P32	2	none	A	A	3.333	10.000	10.000	0.370
P36	3	none	A	A	10.000	10.000	10.000	0.123
Negative control					10.000	10.000	10.000	10.000
Positive control					10.000	1.104	10.000	10.000
LA: low affinity (high K_D); HA: high affinity (low K_D), A: absent; P: present								

Table 13.

Construct number	Protein format	TAA	CD3	CD8	IL6	IL8	IL10	IL13	TNFα
P4	1	PSMA	LA	P	10.000	5.061	8.295	3.861	8.710
P7	2	PSMA	LA	P	0.996	0.441	5.187	1.230	8.490
P2	3	PSMA	LA	P	10.000	1.145	10.000	0.960	10.000
P16	1	PSMA	LA	A	10.000	10.000	10.000	10.000	10.000
P12	2	PSMA	LA	A	10.000	10.000	10.000	10.000	10.000
P11	3	PSMA	LA	A	10.000	10.000	10.000	10.000	0.123
P5	1	PSMA	A	P	10.000	10.000	10.000	10.000	10.000
P8	2	PSMA	A	P	0.002	10.000	10.000	0.002	10.000
P9	3	PSMA	A	P	10.000	10.000	10.000	10.000	0.000
P17	1	PSMA	A	A	3.333	10.000	10.000	10.000	3.333
P14	2	PSMA	A	A	10.000	10.000	10.000	10.000	0.123
P18	3	PSMA	A	A	3.333	10.000	3.333	1.111	0.000
P22	1	none	LA	P	10.000	8.820	10.000	10.000	10.000
P25	2	none	LA	P	10.000	3.333	8.925	10.000	10.000
P20	3	none	LA	P	10.000	0.000	10.000	1.111	0.000
P34	1	none	LA	A	10.000	10.000	10.000	10.000	10.000
P30	2	none	LA	A	10.000	10.000	10.000	0.466	10.000
P29	3	none	LA	A	10.000	10.000	10.000	10.000	10.000
P3	1	PSMA	HA	P	1.151	0.000	0.502	0.000	0.700
P6	2	PSMA	HA	P	0.888	0.000	2.192	0.050	1.453
P1	3	PSMA	HA	P	10.000	0.000	10.000	0.177	10.000
P15	1	PSMA	HA	A	10.000	7.143	10.000	10.000	10.000
P13	2	PSMA	HA	A	10.000	3.498	10.000	10.000	10.000

P10	3	PSMA	HA	A	10.000	10.000	10.000	10.000	10.000
P21	1	none	HA	P	0.373	0.030	0.385	0.260	1.395
P24	2	none	HA	P	10.000	1.093	10.000	1.633	10.000
P19	3	none	HA	P	10.000	10.000	10.000	10.000	10.000
P33	1	none	HA	A	10.000	10.000	10.000	0.000	10.000
P31	2	none	HA	A	3.333	0.000	3.333	10.000	10.000
P28	3	none	HA	A	10.000	10.000	10.000	10.000	0.370
P23	1	none	A	P	10.000	10.000	10.000	10.000	10.000
P26	2	none	A	P	10.000	10.000	10.000	10.000	1.111
P27	3	none	A	P	10.000	10.000	3.333	3.333	0.000
P35	1	none	A	A	10.000	10.000	10.000	10.000	10.000
P32	2	none	A	A	3.333	10.000	0.370	10.000	10.000
P36	3	none	A	A	10.000	10.000	10.000	10.000	0.370
Negative control					10.000	3.333	10.000	4.617	10.000
Positive control					1.793	0.370	3.440	0.528	2.967
LA: low affinity (high K_D); HA: high affinity (low K_D), A: absent; P: present									

EXAMPLE 3: LOW AFFINITY CD3 MULTISPECIFICS PAIRED WITH CD8 BINDERS SHOW SELECTIVE ACTIVATION OF CD8 T CELLS AND REDUCED ANTI-INFLAMMATORY CYTOKINE RELEASE

[00690] Trispecific PSMAxCD3xCD8 antibodies were constructed as shown in **FIG. 4A**. Pan T cells were isolated from the peripheral blood mononuclear cells (PBMCs) of healthy volunteers and stained with the test multispecifics at room temperature for 30min followed by detection using an anti-human IgG antibody and staining with anti-human CD3, CD4 and CD8 antibodies. Binding affinity was determined using the secondary antibody-stained samples as negative controls. As shown in **FIG.4B** and Table 14, low affinity CD3 multispecifics paired with CD8 binders show higher selective binding to CD8 T cells compared to the controls.

[00691] Low affinity CD3 multispecifics paired with CD8 binders demonstrated superior effects in cytotoxicity assays on C4-2B cells (target) and PBMCs (effector) (see **FIG. 5A and FIG. 5B**).

[00692] Low affinity CD3 multispecifics paired with CD8 binders were tested for potent cytotoxicity against target cell lines in a CD8 T cell dependent manner. PBMCs of healthy volunteers were either depleted of CD8 T cells or used as such. CD8 depleted and non depleted PBMCs were cocultured with C4-2B target cells as a 1:1 effector to target ratio (CD3 to target cells) for 72hrs in the presence of the test multispecifics. Cytotoxicity was monitored using the Incucyte automated live cell analysis system and EC50 values were calculated after normalizing to no multispecific containing wells. As shown in **FIG. 6**, C4-2B target cells liability is high in the CD8 T cells depletion group indicating that low affinity CD3 multispecifics paired with CD8 binders show potent cytotoxicity against target cell lines in a CD8 T cell dependent manner.

[00693] PBMCs were cocultured with C4-2B target cells as a 1:1 effector to target ratio (CD3 to target cells) for the indicated time points in the presence of the test multispecifics. At each time point, cells were harvested and CD3, CD4 and CD8 T cells were analyzed for the presence of the indicated activation and exhaustion markers. As shown in **FIG. 7**, results indicate low affinity CD3 multispecifics paired with CD8 binders specifically and potently activate only CD8 T cells.

[00694] PBMCs were cocultured with C4-2B target cells as a 1:1 effector to target ratio (CD3 to target cells) for the indicated time points in the presence of the test multispecifics. At each time point, supernatants were harvested and analyzed for the indicated cytokines using a multiplex Luminex analysis system. The results indicate that low affinity CD3 multispecifics paired with CD8 binders show reduced anti-inflammatory cytokine release (see **FIG. 8**).

Table 14.

Antibody	**combination**	**CD3 arm**	**Affinity**
CD8B573.001	CD3xCD8xPSMA	CD3B450	Ultra low
CD8B574.001	CD8xPSMA	NA	
CD8B155.003	CD3xPSMA	CD3B450	Ultra low
CD8B52	PSMB410scFv x CD3B376-Fab	CD3B376	Medium (40-60nM)
VB19	CD3B220xPSMB365	CD3B220	high

EXAMPLE 4: PRODUCTION OF ANTIBODIES THAT BIND CD8

4.1: GENERATION CD8α ANTIBODIES, CD8β ANTIBODIES, AND CD8αβ ANTIBODIES

[00695] ***Immunogen.*** Recombinant human CD8alpha/beta heterodimer protein (cat # 9358-CD) was obtained from R&D Systems, Inc. The amino acid sequence of the heterodimeric protein is listed in **Table 15**.

Table 15. Amino acid sequence of recombinant human CD8α/β heterodimer protein

Name	Protein ID	Sequence	SEQ ID NO
Recombinant human CD8α/β heterodimer protein (cat #: 9358-CD)	rhCD8α (Ser22-Asp182) Accession #P01732	SQFRVSPLDRTWNLGETVELKCQVLLSNP TSGCSWLFQPRGAAASPTFLLYLSQNKPK AAEGLDTQRFSGKRLGDTFVLTLSDFRRE NEGYYFCSALSNSIMYFSHFVPVFLPAKP TTTPAPRPPTPAPTIASQPLSLRPEACRP AAGGAVHTRGLDFACD-[proprietary R&D System acidic tails]-HHHHHH	2177 2322
	rhCD8β (Asn19-Pro170) Accession #P10966	NSVLQQTPAYIKVQTNKMVMLSCEAKISL SNMRIYWLRQRQAPSSDSHHEFLALWDSA KGTIHGEEVEQEKIAVFRDASRFILNLTS VKPEDSGIYFCMIVGSPELTFGKGTQLSV VDFLPTTAQPTKKSTLKKRVCRLPRPETQ KGPLCSP-[proprietary R&D System basic tails]-DYKDDDDK	2178 2323

[00696] ***Immunization in wild-type mouse and screening of anti-CD8α antibodies, anti-CD8β antibodies, and anti-CD8αβ antibodies.*** Wild-type (WT) mice with 6 different MHC combinations was immunized using rapid immunization protocol. Eight mice were selected for cell fusion based on serum titer. Hybridoma supernatants were screening by LUMINEX using the immunogen and human pan-T cells. Hits were V-region recovered and formatted into monoclonal IgG1 antibodies.

[00697] All the monoclonal antibodies were produced as full-length antibodies as human IgG1. Nucleic acid sequences encoding variable regions were subcloned into a custom mammalian expression vectors containing constant region of IgG1 Fc expression cassettes using standard PCR restriction enzyme based cloning techniques. The mAbs were expressed by transient transfection in Chinese hamster ovary cell line. The antibodies were initially purified by MAB SELECT SURE Protein A column (GE healthcare, Piscataway, New Jersey) (Brown,

Bottomley et al. 1998). The column was equilibrated with Phosphate Buffer Saline (PBS), pH 7.2 and loaded with fermentation supernatant at a flow rate of 2 mL/min. After loading, the column was washed with PBS (4 CV) followed by elution in 30 mM sodium acetate, pH 3.5. Fractions containing protein peaks as monitored by Absorbance at 280 nm in AKTA Explorer (GE healthcare) were pooled together and were neutralized to pH 5.0 by adding 1% of 3 M sodium acetate, pH 9.0. As a polishing step, the antibodies were purified on a preparative size exclusion chromatography (SEC) using a SUPERDEX 200 column (GE healthcare). The integrity of the sample was assessed by endotoxin measurement and SDS polyacrylamide gel electrophoresis under reducing and non-reducing conditions. The intact mass was confirmed by mass spectrometry.

[00698] The VH and VL sequences of certain CD8 antibodies are provided in **Table 16**. The CDRs sequences of certain CD8 antibodies are provided in **Table 17** (Kabat), **Table 18** (Chothia), **Table 19** (AbM), **Table 20** (Contact), and **Table 21** (IMGT).

Table 16. VH and VL Amino Acid Sequences

#	Protein Name	HC Isotype	LC Isotype	VH AA sequence	VL AA sequence	Heavy Chain AA sequence	Light Chain AA sequence
1	CD8B191	IgG1	Kappa	QIQLVQSGPE LVKPGTSMKM SCKASGYTFT DYYMNWVKQS HGKSLEWIGR VIPSNGGTIY NLKFKGKATL TVDKSLSTAY MQLNSLTSED SAVYFCARED YNNQGFFLDA MDYWGQGTSV TVSS	DIVLTQSP ATLSVTPG DRVSLSCR ASQSISDF LHWYQQKS HESPRLLI KYASQSIS GIPSRFSG SGSGSDFT LTINSVEP EDVGVYYC QNGHSFPY TFGSGTKL EIK	QIQLVQSGPELVKPGTSMKMSCKASGYTFTDYYMNW VKQSHGKSLEWIGRVIPSNGGTIYNLKFKGKATLTV DKSLSTAYMQLNSLTSEDSAVYFCAREDYNNQGFFL DAMDYWGQGTSVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK	DIVLTQSPATLSVTPG DRVSLSCRASQSISDF LHWYQQKSHESPRLLI KYASQSISGIPSRFSG SGSGSDFTLTINSVEP EDVGVYYCQNGHSFPY TFGSGTKLEIKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
				31	32	33	34
2	CD8B226	IgG1	Kappa	EFQLQQSGPE LVKPGASVKM SCKASGYTFT DYYMNWVKQS HGKSLQWIGR IIPSNGATIY NQKFKGKATL TVDKSLSTAY MHLNSLTSED SAVYYCARED YSNQGFFLDA MDYWGQGTTV TVSS	DIVMTQSP ATLSVTPG DRVSLSCR ASQSISHY LHWYQQKL HESPRLLI KYASQSIS GIPSRFSG SGSGSDFT LSINSVEP EDVGVYYC QNGHSFPY TFGGGTKL EIK	EFQLQQSGPELVKPGASVKMSCKASGYTFTDYYMNW VKQSHGKSLQWIGRIIPSNGATIYNQKFKGKATLTV DKSLSTAYMHLNSLTSEDSAVYYCAREDYSNQGFFL DAMDYWGQGTTVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK	DIVMTQSPATLSVTPG DRVSLSCRASQSISHY LHWYQQKLHESPRLLI KYASQSISGIPSRFSG SGSGSDFTLSINSVEP EDVGVYYCQNGHSFPY TFGGGTKLEIKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
				65	66	67	68

3	CD8B259	IgG1	Kappa	EVQLQQSGPE LVKPGASVKM SCKASGYTFT DYYMNWVKQS HGKSLEWIGR VIPSNGGTIY NQKFRGKATL YGNQGFFLDA MDYWGQGTTV TVSS	DIVMTQSP ATLSVTPG DRVSLSCR ASQSISHF LHWYQQKS HESPRLLI KYASQSIS GSPSKFSG SGSGSDFT LTINSVEP EDVGVYYC QSGHSFPY TFGSGTKL EIK	EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMNW VKQSHGKSLEWIGRVIPSNGGTIYNQKFRGKATLTV DKSLSTAYMQLNSLTSEDSAVYYCAREDYGNQGFFL DAMDYWGQGTTVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK	DIVMTQSPATLSVTPG DRVSLSCRASQSISHF LHWYQQKSHESPRLLI KYASQSISGSPSKFSG SGSGSDFTLTINSVEP EDVGVYYCQSGHSFPY TFGSGTKLEIKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
				99	100	101	102
4	CD8B298	IgG1	Kappa	QVQLQQSGPE LVKPGASVKM SCKASGYTFT DYYMNWVKQS HGKSLEWIGR VIPNNGGTRY NQKFKGKATL TVDKSLSTAY MQLNSLTSED SAVYYCARED FSNQGFFLDA MDYWGQGTSV TVSS	DIVMTQSP ATLSVTPG DRVSLSCR ASQTISDY LHWYQQKS HESPRLLI KYASQSIS GIPSRFSG SGSGSDFT LSINSVEP EDVGVYYC QNGHSFPY TFGAGTKL ELK	QVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMNW VKQSHGKSLEWIGRVIPNNGGTRYNQKFKGKATLTV DKSLSTAYMQLNSLTSEDSAVYYCAREDFSNQGFFL DAMDYWGQGTSVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK	DIVMTQSPATLSVTPG DRVSLSCRASQTISDY LHWYQQKSHESPRLLI KYASQSISGIPSRFSG SGSGSDFTLSINSVEP EDVGVYYCQNGHSFPY TFGAGTKLELKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
				133	134	135	136
5	CD8B342	IgG1	Kappa	EFQLQQSGPE LVKPGASVKV SCKASGYTFT DYYVNWVQQS HGKSLEWIGR	DIVMTQTP ATLSVTPG DRVSLSCR ASQTISNY LHWYQQKS	EFQLQQSGPELVKPGASVKVSCKASGYTFTDYYVNW VQQSHGKSLEWIGRVIPNNGNVIYNQNFKGKATLTV DKSLSSAYLQLNSLTSEDSAVYYCTREDYSNQGFFL DAMDYWGQGTSVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV	DIVMTQTPATLSVTPG DRVSLSCRASQTISNY LHWYQQKSHESPRLLI KYASQSISGIPSRFSG SGSGSDFTLSINSVEP

			VIPNNGNVIY	HESPRLLI	LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT	EDVGVYYCQNGHSFPY
			NQNFKGKATL	KYASQSIS	KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPP	TFGGGTKLEIKRTVAA
			TVDKSLSSAY	GIPSRFSG	KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG	PSVFIFPPSDEQLKSG
			LQLNSLTSED	SGSGSDFT	VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK	TASVVCLLNNFYPREA
			SAVYYCTRED	LSINSVEP	EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP	KVQWKVDNALQSGNSQ
			YSNQGFFLDA	EDVGVYYC	SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN	ESVTEQDSKDSTYSLS
			MDYWGQGTSV	QNGHSFPY	NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC	STLTLSKADYEKHKVY
			TVSS	TFGGGTKL	SVMHEALHNHYTQKSLSLSPGK	ACEVTHQGLSSPVTKS
				EIK		FNRGEC
		167		168	169	170
6	CD8B364	IgG1	QVQLQQPGAE	DIVLTQSP	QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHW	DIVLTQSPASLSVATG
		Kappa	LVKPGASVKL	ASLSVATG	VNRRPGQGLEWIGEINPSNGDSYYNEKFKRKATLTV	EKVTIRCITSTDIDDD
			SCKASGYTFT	EKVTIRCI	DISSSTAYMQLSSLTSEDSAVYYCTRSMYYDGRAGA	MNWYQQKPGEPPKLLI
			SYWMHWVNRR	TSTDIDDD	YWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAA	SEGNTLRPGVPSRFSS
			PGQGLEWIGE	MNWYQQKP	LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS	SGYGTDFVFTIENTLS
			INPSNGDSYY	GEPPKLLI	GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK	EDVADYYCLQSDNMPL
			NEKFKRKATL	SEGNTLRP	KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKD	TFGAGTKLELKRTVAA
			TVDISSSTAY	GVPSRFSS	TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH	PSVFIFPPSDEQLKSG
			MQLSSLTSED	SGYGTDFV	NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC	TASVVCLLNNFYPREA
			SAVYYCTRSM	FTIENTLS	KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE	KVQWKVDNALQSGNSQ
			YYDGRAGAYW	EDVADYYC	MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT	ESVTEQDSKDSTYSLS
			GQGTTVTVSS	LQSDNMPL	TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH	STLTLSKADYEKHKVY
				TFGAGTKL	EALHNHYTQKSLSLSPGK	ACEVTHQGLSSPVTKS
				ELK		FNRGEC
		201		202	203	204
7	CD8B200	IgG1	EVQLQQSGAE	DIQMTQTT	EVQLQQSGAELVKPGASVKLSCKASGYTFTNYWIHW	DIQMTQTTSSLSASLG
		Kappa	LVKPGASVKL	SSLSASLG	VKQRPGQGLEWIGNIDPSDSETHYNQKFKDKATLTV	DRVTITCRASQDISPY
			SCKASGYTFT	DRVTITCR	DKSSSTAYMQLISLTSEDSAVYYCASGLTGTGYYWG	LNWYQQKPEGTIKLLI
			NYWIHWVKQR	ASQDISPY	QGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGC	YYTSKLHSGVPSRFSG
			PGQGLEWIGN	LNWYQQKP	LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY	SGSGTDYSLTISNLEQ
			IDPSDSETHY	EGTIKLLI	SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE	EDIATYFCQQDNTLPY
			NQKFKDKATL	YYTSKLHS	PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM	TFGSGTKLELKRTVAA
			TVDKSSSTAY	GVPSRFSG	ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK	PSVFIFPPSDEQLKSG
			MQLISLTSED	SGSGTDYS	TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS	TASVVCLLNNFYPREA
			SAVYYCASGL	LTISNLEQ	NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK	KVQWKVDNALQSGNSQ

				TGTGYYWGQG TTLTVSS	EDIATYFC QQDNTLPY TFGSGTKL ELK	NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK	ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
				235	236	237	238
8	CD8B247	IgG1	Kappa	EVQLQQSGPE LVKPGASVKM SCKASGYTFT DYYMNWVKQS HGKSLEWIGR VIPNNGGTIY NQKFKDKATL TVDKSLSTAY MQLNSLTSED SAVYYCARED YSNQGFFLDA MDYWGQGTSV TVSS	DIVMTQSP ATLSVTPG ERVSLSCR ASQTISHF LHWYQQKS HESPRLLI KYASQSIS GIPSRFSG GGSGSDFI LTINSVEP EDVGMYYC QSGHSFPY TFGSGTKL EIK	EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMNW VKQSHGKSLEWIGRVIPNNGGTIYNQKFKDKATLTV DKSLSTAYMQLNSLTSEDSAVYYCAREDYSNQGFFL DAMDYWGQGTSVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK	DIVMTQSPATLSVTPG ERVSLSCRASQTISHF LHWYQQKSHESPRLLI KYASQSISGIPSRFSG GGSGSDFILTINSVEP EDVGMYYCQSGHSFPY TFGSGTKLEIKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
				269	270	271	272
9	CD8B265	IgG1	Kappa	QVQLQQSGPE LVKPGASVKM SCKASGYSFT DYYMNWVKQS HGQSLEWIGR VIPRNGATTY NQNFRGKATL TVDISLRTAY MHLNSLTSDD SAVYYCARED FSNQGFFLDA MDYWGQGTSV TVSS	DIVMTQSP ATLSVTPG DRVSLSCR ASQSISHY LHWYQQKS HESPRLLI KYASQSIS GIPSRFSG SGSGSDFT LSINSVEP EDVGVYYC QNGHSFPY TFGSGTKL EMK	QVQLQQSGPELVKPGASVKMSCKASGYSFTDYYMNW VKQSHGQSLEWIGRVIPRNGATTYNQNFRGKATLTV DISLRTAYMHLNSLTSDDSAVYYCAREDFSNQGFFL DAMDYWGQGTSVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK	DIVMTQSPATLSVTPG DRVSLSCRASQSISHY LHWYQQKSHESPRLLI KYASQSISGIPSRFSG SGSGSDFTLSINSVEP EDVGVYYCQNGHSFPY TFGSGTKLEMKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
				303	304	305	306

10	CD8B270	IgG1	Kappa	QVQLQQPGAELVKPGASVMLSCKASGYTFTNYWMHW VKQRPGQGLEWIGNIDPSDSETHYNQKFKDKATLTV DKSSSTAYMQLSSLTSEDSAVYYCASGLTGTGYYWG QGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK	DIQMTQTTSSLSASLG DRVTITCRASQDIRPY LNWYQQKPEGTIKLLI YFTSKLHSGVPSRFSG SGSGTDYSLTISNLEQ EDIATYFCQQDNTLPY TFGSGTKLELKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
				337	338	339	340
11	CD8B213	IgG1	Kappa	EVQLQQSGPELVKPGDSMKMSCKASGYIFTDYYMDW VKQSHGKSLEWIGYIYPNNGITSYNQKFKGRATLTI DKSSSTAYMELHSLTSEDSAVYYCARSIYYDHGGGF PYWGQGTSVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVD KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPGK	DIVLTQSQKFMSTSVG DRVSVTCKASQNVDKY VAWYQQKPGQSPKALI YSASYRYSGVPDRFTG SGSGTDFTLTISNVQS EDLAEYFCQQYNTYPS FGSGTKLEMKRTVAAP SVFIFPPSDEQLKSGT ASVVCLLNNFYPREAK VQWKVDNALQSGNSQE SVTEQDSKDSTYSLSS TLTLSKADYEKHKVYA CEVTHQGLSSPVTKSF NRGEC
				371	372	373	374
12	CD8B240	IgG1	Kappa	QVQLQQSGPELVKPGTSVKMSCKASGYTFTDYYMNW VKQSHGKSLEWIGRVIPSNGGTIYNLKFKGKATLTV DKSLSTAYMQLNSLTSEDSAVYFCAREDYNNQGFFL DAMDYWGQGTLVTVSAASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV	DIVMTQSPATLSVTPG DRVSLSCRASQSISDF LHWYQQKSHESPRLLI KYASQSISGIPSRFSG SGSGSDFTLTINSVEP

			VIPSNGGTIY NLKFKGKATL TVDKSLSTAY MQLNSLTSED SAVYFCARED YNNQGFFLDA MDYWGQGTLV TVSA	HESPRLLI KYASQSIS GIPSRFSG SGSGSDFT LTINSVEP EDVGVYYC QNGHSFPY TFGSGTKL EIK	LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK	EDVGVYYCQNGHSFPY TFGSGTKLEIKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
			405	406	407	408
13	CD8B361	IgG1	EVQLQQSGPE LVKPGNSVKM SCKASGYTFT DYYMDWVKQS HGTSLEWIGY IYPNNGDTRY NQKFKDKATL TVDKSSSTAY MELHSLTSED SAVFYCARSI YYDHGGGFPY WGQGTLVTVS A	DIVMTQSQ KFMSTSVG DRVSVTCK ASQNVGTY VAWYQQKP GQSPKALI YSASYRYS GVPDRFTG SGSGTDFT LTINNVQS EDLAEYLC QQYNSYPT FGGGTRLE IK	EVQLQQSGPELVKPGNSVKMSCKASGYTFTDYYMDW VKQSHGTSLEWIGYIYPNNGDTRYNQKFKDKATLTV DKSSSTAYMELHSLTSEDSAVFYCARSIYYDHGGGF PYWGQGTLVTVSAASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVD KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPGK	DIVMTQSQKFMSTSVG DRVSVTCKASQNVGTY VAWYQQKPGQSPKALI YSASYRYSGVPDRFTG SGSGTDFTLTINNVQS EDLAEYLCQQYNSYPT FGGGTRLEIKRTVAAP SVFIFPPSDEQLKSGT ASVVCLLNNFYPREAK VQWKVDNALQSGNSQE SVTEQDSKDSTYSLSS TLTLSKADYEKHKVYA CEVTHQGLSSPVTKSF NRGEC
			439	440	441	442
14	CD8B246	IgG1	QVQLKESGPG ILKPSQTLSL TCSFSGFSLS TSGMNVGWIR QPSGKGLEWL AHIWWDDDKY YNPSLKSQLT ISKDTSRNQV FLKITSVDTA DTATYYCARR	DIQMTQTT SSLSASLG DRVTISCR ASQDIRNY LNWYQQKP DGTVKLLI YHTSRLHS GVPSRFSG SGSGTDYS LTISNLEQ	QVQLKESGPGILKPSQTLSLTCSFSGFSLSTSGMNV GWIRQPSGKGLEWLAHIWWDDDKYYNPSLKSQLTIS KDTSRNQVFLKITSVDTADTATYYCARRGNYGNYEF AYWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVD KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE	DIQMTQTTSSLSASLG DRVTISCRASQDIRNY LNWYQQKPDGTVKLLI YHTSRLHSGVPSRFSG SGSGTDYSLTISNLEQ EDIATYFCQQGNTLPW TFGAGTKLELKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ

			GNYGNYEFAY WGQGTTLTVS S	EDIATYFC QQGNTLPW TFGAGTKL ELK	EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPGK		ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
			473	474	475		476
15	CD8B268	IgG1	QVQLQQSGAE LVKPGASVKL SCKASGYTFT VYTIHWVKQR SGQGLEWIGW FYPGSGNIKY NEKFKDKATL TADKSSHTVY MELSRLTSED SAVYFCARHE DNHYYDGNSW FAYWGQGTLV TVSA	DIQMTQSP ASLSASVG QTVTITCR ASGNIHNY LAWFQQKQ GKSPQLLV YNAKTLAD GVPSRFSG SGSGTQYS LKINSLQT EDFGNYYC QHFWNTPY TFGGGTKL EIK	QVQLQQSGAELVKPGASVKLSCKASGYTFTVYTIHW VKQRSGQGLEWIGWFYPGSGNIKYNEKFKDKATLTA DKSSHTVYMELSRLTSEDSAVYFCARHEDNHYYDGN SWFAYWGQGTLVTVSAASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK		DIQMTQSPASLSASVG QTVTITCRASGNIHNY LAWFQQKQGKSPQLLV YNAKTLADGVPSRFSG SGSGTQYSLKINSLQT EDFGNYYCQHFWNTPY TFGGGTKLEIKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
			507	508	509		510
16	CD8B271	IgG1	DVQLQESGPG LVAPSQSLSI TCTVSGFSLS IYSIHWVRQP PGKGLEWLGM IWGGGDTDYN SALKSRLSIS KDNSESQVFL KMNSLQTDDT AMYYCARNPH YYGGTYEYFD VWGTGTTVTV SS	DIQMTQTT SSLSASLG DRVTISCS ASQGISNY LNWYQQKP DGTVKLLI YDTSILYS GVPSRFSG SGSGTQYS LTISNLEP EDVATYYC QQYSNLPY TFGSGTKL EIK	DVQLQESGPGLVAPSQSLSITCTVSGFSLSIYSIHW VRQPPGKGLEWLGMIWGGGDTDYNSALKSRLSISKD NSESQVFLKMNSLQTDDTAMYYCARNPHYYGGTYEY FDVWGTGTTVTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK		DIQMTQTTSSLSASLG DRVTISCSASQGISNY LNWYQQKPDGTVKLLI YDTSILYSGVPSRFSG SGSGTDYSLTISNLEP EDVATYYCQQYSNLPY TFGSGTKLEIKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
			541	542	543		544

17	CD8B273	IgG1	Kappa	QVQLQQSGAE LVKPGASVKL SCKASGYTFT EYTIHWVKQR SGQGLEWIGW FYPGTGSIKY NEKFKDKATL TADKSSHTVY MELSKLTSED SAVYFCARHE DNHYYDGNSW FAYWGQGTLV TVSA	DIQMTQSP ASLSASVG ETVTITCR ASGNIHNY LAWFQQKQ GKSPQLLV YNAKTLAD GVPSRFSG SGSGTQYS LKINSLQA EDFGSYYC QHFWSTPY TFGSGTKL EIK	QVQLQQSGAELVKPGASVKLSCKASGYTFTEYTIHW VKQRSGQGLEWIGWFYPGTGSIKYNEKFKDKATLTA DKSSHTVYMELSKLTSEDSAVYFCARHEDNHYYDGN SWFAYWGQGTLVTVSAASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK	DIQMTQSPASLSASVG ETVTITCRASGNIHNY LAWFQQKQGKSPQLLV YNAKTLADGVPSRFSG SGSGTQYSLKINSLQA EDFGSYYCQHFWSTPY TFGSGTKLEIKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
				575	576	577	578
18	CD8B288	IgG1	Kappa	QVQLQQSGAE LVKPGASVKL SCKASGYTFT EYTIHWVKQK SGQGLEWIGW FYPGNGNMRY NEKFKDKATL TADRSSHTVY MELSRLTSED SAVYFCARYE DNHYYDGASW FAYWGQGTSV TVSS	DIQMTQSP ASLSASVG DTVTITCR ASGNIHNY LAWFQQKQ GKSPQLLV YNAKTLAD GVPSRFSG SGSGTQFS LKINSLQP EDFGTYYC QHFWSTPF TFGSGTKL EMK	QVQLQQSGAELVKPGASVKLSCKASGYTFTEYTIHW VKQKSGQGLEWIGWFYPGNGNMRYNEKFKDKATLTA DRSSHTVYMELSRLTSEDSAVYFCARYEDNHYYDGA SWFAYWGQGTSVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK	DIQMTQSPASLSASVG DTVTITCRASGNIHNY LAWFQQKQGKSPQLLV YNAKTLADGVPSRFSG SGSGTQFSLKINSLQP EDFGTYYCQHFWSTPF TFGSGTKLEMKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
				609	610	611	612
19	CD8B292	IgG1	Kappa	QVQLQQPGAE LVKPGASVKL SCTGSGFNFK DDYIYWVKQR PEQGLEWIGW	QIVLTQSP AIMSASLG ERVTLTCT ASSSVSSS YLHWYQQK	QVQLQQPGAELVKPGASVKLSCTGSGFNFKDDYIYW VKQRPEQGLEWIGWIDPENGATEYASKFQGKATITA DTSSNIAYLQLSSLTSEDTAVYYCSLHDYGYAMDYW GQGTSVTVSSASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL	QIVLTQSPAIMSASLG ERVTLTCTASSSVSSS YLHWYQQKPGSSPKLW IYSTSNLASGVPARFS GSGSGTSYSLTISNME

			IDPENGATEY ASKFQGKATI TADTSSNIAY LQLSSLTSED TAVYYCSLHD YGYAMDYWGQ GTSVTVSS	PGSSPKLW IYSTSNLA SGVPARFS GSGSGTSY SLTISNME AEDAATYY CHQYHRSP LTFGGGTK LEIK	YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK	AEDAATYYCHQYHRSP LTFGGGTKLEIKRTVA APSVFIFPPSDEQLKS GTASVVCLLNNFYPRE AKVQWKVDNALQSGNS QESVTEQDSKDSTYSL SSTLTLSKADYEKHKV YACEVTHQGLSSPVTK SFNRGEC
			643	644	645	646
20	CD8B303	IgG1	QVQLKESGPG LVAPSQSLSI TCTVSGFSLS IYSIHWVRQP PGKGLEWLGM IWGGGSTDYN STLNSRLSII KDNSKSQVFL KMNSLQTDDT AMYYCARNPH HYGGSTGAMD YWGQGTTVTV SS	DVQMIQSP SSLSASLG GTVTITCK ASQDIKKY MAWYQHKP GKGPRLLI HYTSSLQP GIPSRFSG SGSGRDYY FSISNLEP EDIATYFC LQYDNLFT FGSGTKLE LK	QVQLKESGPGLVAPSQSLSITCTVSGFSLSIYSIHW VRQPPGKGLEWLGMIWGGGSTDYNSTLNSRLSIIKD NSKSQVFLKMNSLQTDDTAMYYCARNPHHYGGSTGA MDYWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	DVQMIQSPSSLSASLG GTVTITCKASQDIKKY MAWYQHKPGKGPRLLI HYTSSLQPGIPSRFSG SGSGRDYYFSISNLEP EDIATYFCLQYDNLFT FGSGTKLELKRTVAAP SVFIFPPSDEQLKSGT ASVVCLLNNFYPREAK VQWKVDNALQSGNSQE SVTEQDSKDSTYSLSS TLTLSKADYEKHKVYA CEVTHQGLSSPVTKSF NRGEC
			677	678	679	680
21	CD8B304	IgG1	QVTLKESGPG ILKPSQTLSL TCSFSGFSLS TSGMNVGWIR QPSGKGLEWL AHIWWDDDKY YNPSLKSQLT ISKDTSRNQV FLKITSVDTA DTATYYCARR	DIQMTQTT SSLSASLG DRVTISCR ASQDIRNY LNWYQQKP DGTVKLLI YHTSRLHS GVPSRFSG SGSGTDYS LTISNLDQ	QVTLKESGPGILKPSQTLSLTCSFSGFSLSTSGMNV GWIRQPSGKGLEWLAHIWWDDDKYYNPSLKSQLTIS KDTSRNQVFLKITSVDTADTATYYCARRGNYGNYEF AYWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVD KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE	DIQMTQTTSSLSASLG DRVTISCRASQDIRNY LNWYQQKPDGTVKLLI YHTSRLHSGVPSRFSG SGSGTDYSLTISNLDQ EDIATYFCQQGNTLPW TFGAGTKLELKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ

			GNYGNYEFAY WGQGTTVTVS S	EDIATYFC QQGNTLPW TFGAGTKL ELK	EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPGK		ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
			711	712	713		714
22	CD8B312	IgG1	QVQLQQPGAD LVKPGASVKL SCKASGYTFT SFWMHWVKQR PGQGLEWIGN VDPSDSQTHY NQKFKDKATL TVDKSSNTAY MQLSSLTSED SAVYYCARST YYRYDGPFTY WGQGTTVTVS S	Kappa	DIVLTQSP ATLSVTPG DSVSLSCR ASQSINNN LHWYQQKS HESPRLLI KYTSQSIS GIPSRFSG SGSGPDFT LSINSVET EDFGMYFC QQSNSWPL TFGGGTKL EIK	QVQLQQPGADLVKPGASVKLSCKASGYTFTSFWMHW VKQRPGQGLEWIGNVDPSDSQTHYNQKFKDKATLTV DKSSNTAYMQLSSLTSEDSAVYYCARSTYYRYDGPF TYWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVD KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPGK		DIVLTQSPATLSVTPG DSVSLSCRASQSINNN LHWYQQKSHESPRLLI KYTSQSISGIPSRFSG SGSGPDFTLSINSVET EDFGMYFCQQSNSWPL TFGGGTKLEIKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
			745	746	747		748
23	CD8B347	IgG1	QVQLQQPGAE LAKPGTSVKM SCKASGYTFT SYWMNWIKQR PGQGLEWIGA VNPSNSYTEY AQKFKDKAIL TADKSSSTAY MSLSGLTSEA SAVYYCARSG LYNTNHLAWF AYWGQGTLVT VSA	Kappa	DIQMTQSP ASLSASVG ETVTITCR ASGNIHNY LAWYQQKQ GKSPQLLV FNAETLAD GVPSRFSG SGSGTQFS LKINSLQP EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK	DIQMTQSPASLSASVG ETVTITCRASGNIHNY LAWYQQKQGKSPQLLV FNAETLADGVPSRFSG SGSGTQFSLKINSLQP EDFGTYYCQHFWNNPL TLGAGTKLELKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
			779	780	781		782

24	CD8B350	IgG1	Kappa	EVQLQQSGAELAKPGTSVKMSCKASGYTFAAYWINW LKQRPGQGLEWIGSINPSNGYTEYSQKFKDKAILTA DKSSSTAYMQLSSLTSEDSAVYYCSRSGLYYTNHLA WCPYWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK	DIVMTQSPASLSASVG ETVTITCRASGNIHNY LAWYQQKQGKSPQVLV YNAETLADSVPSRFSG SGSGTQFSLKINSLQP EDFGNYYCQHFWNSPL TFGGGTKLEIKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
				813	814	815	816
25	CD8B356	IgG1	Kappa	DVQLQESGPG LVKPSQSLSL TCSVTGYSIT SGYYWNWIRQ FPGNKLEWMG YISYDGSNNY NPSLKNRISI TRDTSKNQFF LKLNSVTTED TATYYCVRNH GDAMDYWGQG TSVTVSS	DIVLTQSQ KFMSTTVG DRVSITCK ASQNVGTA VAWYQQKP GQSPKLLI YSASYRYT GVPDRFTG SGSGTHFT LTISNMQS EDLADYFC QQYSSYLT FGSGTKLE IK	DVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYYWN WIRQFPGNKLEWMGYISYDGSNNYNPSLKNRISITR DTSKNQFFLKLNSVTTEDTATYYCVRNHGDAMDYWG QGTSVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK	DIVLTQSQKFMSTTVG DRVSITCKASQNVGTA VAWYQQKPGQSPKLLI YSASYRYTGVPDRFTG SGSGTHFTLTISNMQS EDLADYFCQQYSSYLT FGSGTKLEIKRTVAAP SVFIFPPSDEQLKSGT ASVVCLLNNFYPREAK VQWKVDNALQSGNSQE SVTEQDSKDSTYSLSS TLTLSKADYEKHKVYA CEVTHQGLSSPVTKSF NRGEC
				847	848	849	850
26	CD8B369	IgG1	Kappa	QVQLQQSGAE LVKPGASVKL SCKTSGFTFT NTYISWLKQK PRQSLEWIAW	DIVMTQSP ASLSASVG ETVTITCR ASENIYSY LAWYQQKQ	QVQLQQSGAELVKPGASVKLSCKTSGFTFTNTYISW LKQKPRQSLEWIAWIYTGTGGTWYNQKFTDKAQLTV DTSSSTAYMQVSSLTSEDSAIYYCARTNWDWYFDVW GAGTSVTVSSASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL	DIVMTQSPASLSASVG ETVTITCRASENIYSY LAWYQQKQGKSPQLLV YYAKTLTDGVPSRFSG SGSGTQFSLKINSLQP

			IYTGTGGTWY	GKSPQLLV	YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV	EDFGSYYCQHHYGRPY
			NQKFTDKAQL	YYAKTLTD	EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL	TFGSGTKLEIKRTVAA
			TVDTSSSTAY	GVPSRFSG	MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA	PSVFIFPPSDEQLKSG
			MQVSSLTSED	SGSGTQFS	KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV	TASVVCLLNNFYPREA
			SAIYYCARTN	LKINSLQP	SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMT	KVQWKVDNALQSGNSQ
			WDWYFDVWGA	EDFGSYYC	KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP	ESVTEQDSKDSTYSLS
			GTSVTVSS	QHHYGRPY	PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA	STLTLSKADYEKHKVY
				TFGSGTKL	LHNHYTQKSLSLSPGK	ACEVTHQGLSSPVTKS
				EIK		FNRGEC
			881	882	883	884
27	CD8B371	IgG1	EVKLVESGGG	NTQMNQTP	EVKLVESGGGLVQPGSSMKLSCTASGFTFSDYYMAW	NTQMNQTPSSLSASLG
		Kappa	LVQPGSSMKL	SSLSASLG	VRQVPEKGLEWVAHINYDGSITYYLDSLKSRFIISR	DTITITCHASQNINVW
			SCTASGFTFS	DTITITCH	DNAKNILYLQMSSLKSEDTATYYCAREDYSNYGFAY	LSWYQQKPGNIPKLLI
			DYYMAWVRQV	ASQNINVW	WGQGTLVTVSAASTKGPSVFPLAPSSKSTSGGTAAL	YKASNLHTGVPSRFSG
			PEKGLEWVAH	LSWYQQKP	GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG	SGSGTGFTLTISSLQP
			INYDGSITYY	GNIPKLLI	LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK	EDIATYYCQQGQSYPL
			LDSLKSRFII	YKASNLHT	VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT	TFGSGTKLEMKRTVAA
			SRDNAKNILY	GVPSRFSG	LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN	PSVFIFPPSDEQLKSG
			LQMSSLKSED	SGSGTGFT	AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK	TASVVCLLNNFYPREA
			TATYYCARED	LTISSLQP	VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM	KVQWKVDNALQSGNSQ
			YSNYGFAYWG	EDIATYYC	TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT	ESVTEQDSKDSTYSLS
			QGTLVTVSA	QQGQSYPL	PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE	STLTLSKADYEKHKVY
				TFGSGTKL	ALHNHYTQKSLSLSPGK	ACEVTHQGLSSPVTKS
				EMK		FNRGEC
			915	916	917	918
28	CD8B182	IgG1	EVQLQQSGAA	DIKMTQSP	EVQLQQSGAALAKPGTSVKMSCKASGYTFTSYWMNW	DIKMTQSPASLSASVG
		Kappa	LAKPGTSVKM	ASLSASVG	VRQRPGQGLEWIGAVNPTNYYTEYIQKFKDKAILTA	ETVTITCRASENIHNY
			SCKASGYTFT	ETVTITCR	DKSSTAYMHLSGLTSEDSAVYYCARSGLYNTNHLA	LAWYQQIQGKSPQLLV
			SYWMNWVRQR	ASENIHNY	WFAYWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGG	YNAKTLANGVPSRFSG
			PGQGLEWIGA	LAWYQQIQ	TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL	SASGTQFSLTINSLQP
			VNPTNYYTEY	GKSPQLLV	QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK	EDFGSYYCQHFWTTPL
			IQKFKDKAIL	YNAKTLAN	VDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPK	TFGAGTKLELKRTVAA
			TADKSSSTAY	GVPSRFSG	PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV	PSVFIFPPSDEQLKSG
			MHLSGLTSED	SASGTQFS	EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE	TASVVCLLNNFYPREA
			SAVYYCARSG	LTINSLQP	YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS	KVQWKVDNALQSGNSQ

			LYNTNHLAWF AYWGQGTTVT VSS	EDFGSYYC QHFWTTPL TFGAGTKL ELK	REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK		ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
			949	950	951		952
29	CD8B205	IgG1	QVQLQQPGAE LVKPGASVKL SCKASGYSFN SYWMHWVKQR PGQGLEWIGN IDPSDSETHY NQKFKDKATL TVDKSSSTAY MQLSSLTSED SAVYYCARVY YSYYSYDATY FDYWGQGTTL TVSS	DIQMTQSP ASLSASVG ETVTITCR ASENIYSY LAWYQQKQ GKSPQLLV YNAKTLAE GVPSRFSG SGSGTQFS LKINSLQP EDFGSYYC QHHYTTPL TFGGGTKL EIK	QVQLQQPGAELVKPGASVKLSCKASGYSFNSYWMHW VKQRPGQGLEWIGNIDPSDSETHYNQKFKDKATLTV DKSSTAYMQLSSLTSEDSAVYYCARVYYSYYSYDA TYFDYWGQGTTLTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK		DIQMTQSPASLSASVG ETVTITCRASENIYSY LAWYQQKQGKSPQLLV YNAKTLAEGVPSRFSG SGSGTQFSLKINSLQP EDFGSYYCQHHYTTPL TFGGGTKLEIKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
			983	984	985		986
30	CD8B223	IgG1	DVQLQESGPI LVAPSQSLSI TCTVSGFSLT SYSVHWVRQP PGKGLEWLGV IWAGGSTNYN SAFMSRLTIS KDNSESQVFL KMISLQTDDT AMYYCAKHSY YSFDAFDYWG QGTTLTVSS	DIVMTQSQ KFMSTSVG DRVRVTCK ASQNVNTD VAWYQQKP GQSPKALI YSASYRYS GVPDRFTG SGSGTDFT LTISNVQS EDLAEYFC QQCNSYPL TFGAGTKL ELK	DVQLQESGPILVAPSQSLSITCTVSGFSLTSYSVHW VRQPPGKGLEWLGVIWAGGSTNYNSAFMSRLTISKD NSESQVFLKMISLQTDDTAMYYCAKHSYYSFDAFDY WGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK		DIVMTQSQKFMSTSVG DRVRVTCKASQNVNTD VAWYQQKPGQSPKALI YSASYRYSGVPDRFTG SGSGTDFTLTISNVQS EDLAEYFCQQCNSYPL TFGAGTKLELKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
			1017	1018	1019		1020

31	CD8B234	IgG1	Kappa	QVQLKESGPG LVKPSQSLSL TCSVTGYSIT SGYYWNWIRQ FPGNKLEWMG YINYDGRNNY NPSLKNRISI TRDTSKNHFF LKLNSVTTED TATYYCSRDQ GYSKFYFDYW GQGTTLTVSS	DIQMTQSS SSFSVSLG DRVTITCK ASEDIYNR LAWYQQRP GNAPRLLI SGATSLET GVPSRFSG GGSGKDYT LSITSLQT EDVANYYC QQYWSFPR TFGGGTKL EIK	QVQLKESGPGLVKPSQSLSLTCSVTGYSITSGYYWN WIRQFPGNKLEWMGYINYDGRNNYNPSLKNRISITR DTSKNHFFLKLNSVTTEDTATYYCSRDQGYSKFYFD YWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK	DIQMTQSSSSFSVSLG DRVTITCKASEDIYNR LAWYQQRPGNAPRLLI SGATSLETGVPSRFSG GGSGKDYTLSITSLQT EDVANYYCQQYWSFPR TFGGGTKLEIKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
				1051	1052	1053	1054
32	CD8B251	IgG1	Kappa	QVQLKGSGPG LVQPSQSLSI TCTVSGFSLT TYAVHWVRQS PGKGLEWLGV IWSGGSTDYN AAFISRLSIS KDNSKSQVFF KMNSLQADDT AIYYCARHSY YHYNAMDNWG QGTSVTVSS	DIKMTQSQ KFMSTTVG DRVSITCK ASQNVGTA VAWYQQKP GQSPKLLI YSASNRYT GVPDRFTG SGSGTDFT LTISNMQS EDLADYFC QQYSSYPF TFGSGTKL EIK	QVQLKGSGPGLVQPSQSLSITCTVSGFSLTTYAVHW VRQSPGKGLEWLGVIWSGGSTDYNAAFISRLSISKD NSKSQVFFKMNSLQADDTAIYYCARHSYYHYNAMDN WGQGTSVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK	DIKMTQSQKFMSTTVG DRVSITCKASQNVGTA VAWYQQKPGQSPKLLI YSASNRYTGVPDRFTG SGSGTDFTLTISNMQS EDLADYFCQQYSSYPF TFGSGTKLEIKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
				1085	1086	1087	1088
33	CD8B269	IgG1	Kappa	DVQLQESGPG LVKPSQSLSL TCSVTGYSIT SGYYWNWIRQ FPGNKLEWMG	DIVMTQSQ KFMSTSVG DRVRVTCK ASQNVGTD VAWYQQKP	DVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYYWN WIRQFPGNKLEWMGYISYDGSNNYNPSLKNRISITR DTSKNQFFLKLNSVTTEDTATYYCVRNHGDAMDHWG QGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY	DIVMTQSQKFMSTSVG DRVRVTCKASQNVGTD VAWYQQKPGQSPKALI YSASYRYSGVPDRFTG SGSGTDFTLTISDVQS

			YISYDGSNNY	GQSPKALI	SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE	EDLAEYFCQQYKSYPL
			NPSLKNRISI	YSASYRYS	PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM	TFGAGTKLELKRTVAA
			TRDTSKNQFF	GVPDRFTG	ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK	PSVFIFPPSDEQLKSG
			LKLNSVTTED	SGSGTDFT	TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS	TASVVCLLNNFYPREA
			TATYYCVRNH	LTISDVQS	NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK	KVQWKVDNALQSGNSQ
			GDAMDHWGQG	EDLAEYFC	NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP	ESVTEQDSKDSTYSLS
			TTLTVSS	QQYKSYPL	VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL	STLTLSKADYEKHKVY
				TFGAGTKL	HNHYTQKSLSLSPGK	ACEVTHQGLSSPVTKS
				ELK		FNRGEC
		1119		1120	1121	1122
34	CD8B290	IgG1	QVQLKESGPG	DIVMTQSH	QVQLKESGPGLVAPSQSLSITCTVSGFSLSRYSVHW	DIVMTQSHKFMSTSVG
		Kappa	LVAPSQSLSI	KFMSTSVG	VRQPPGKGLVWLGMIWGGGSTDYNSALKSRLSISKD	DRVSITCKASQDVGTV
			TCTVSGFSLS	DRVSITCK	NSKSQVFLKMNSLQTDDTAMYYCARIYFDNYVGFAY	VAWYQQKPGQSPKLLI
			RYSVHWVRQP	ASQDVGTV	WGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAAL	FWTSTRHTGVPDRFTG
			PGKGLVWLGM	VAWYQQKP	GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG	SGSGTDFTLTISNVQS
			IWGGGSTDYN	GQSPKLLI	LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK	EDLADYFCQQYSSYPY
			SALKSRLSIS	FWTSTRHT	VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT	TFGSGTKLELKRTVAA
			KDNSKSQVFL	GVPDRFTG	LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN	PSVFIFPPSDEQLKSG
			KMNSLQTDDT	SGSGTDFT	AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK	TASVVCLLNNFYPREA
			AMYYCARIYF	LTISNVQS	VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM	KVQWKVDNALQSGNSQ
			DNYVGFAYWG	EDLADYFC	TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT	ESVTEQDSKDSTYSLS
			QGTTLTVSS	QQYSSYPY	PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE	STLTLSKADYEKHKVY
				TFGSGTKL	ALHNHYTQKSLSLSPGK	ACEVTHQGLSSPVTKS
				ELK		FNRGEC
		1153		1154	1155	1156
35	CD8B310	IgG1	QVQLKESGPG	DVLMTQTP	QVQLKESGPGLVAPSQSLSITCTVSGFSLTNYAVHW	DVLMTQTPLSLPVSLG
		Kappa	LVAPSQSLSI	LSLPVSLG	VRQSPGKGLEWLGVIWTDGSTDYNAGFISRLSISKD	DQASISCRSSQTIVHS
			TCTVSGFSLT	DQASISCR	NSKSQVFFKMNSLQADDTAIYYCARNNGYFPAFFAY	NGNTYLEWYLQKPGQS
			NYAVHWVRQS	SSQTIVHS	WGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAAL	PKLLMYKVSNRFSGVP
			PGKGLEWLGV	NGNTYLEW	GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG	DRFGGSGSGTDFTLKI
			IWTDGSTDYN	YLQKPGQS	LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK	SRVEAEDLGVYYCFQG
			AGFISRLSIS	PKLLMYKV	VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT	SHAPFTFGSGTKLEIK
			KDNSKSQVFF	SNRFSGVP	LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN	RTVAAPSVFIFPPSDE
			KMNSLQADDT	DRFGGSGS	AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK	QLKSGTASVVCLLNNF
			AIYYCARNNG	GTDFTLKI	VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM	YPREAKVQWKVDNALQ

			YFPAFFAYWG QGTTVTVSS	SRVEAEDL GVYYCFQG SHAPFTFG SGTKLEIK	TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK		SGNSQESVTEQDSKDS TYSLSSTLTLSKADYE KHKVYACEVTHQGLSS PVTKSFNRGEC
			1187	1188	1189		1190
36	CD8B352	IgG1	QVQLKESGPG LVKPSQSLSL TCSVTGYSIT SGYYWNWIRQ FPGNKLEWMG YINYDGRNNY NPSLRNRISI TRDTSKNHFF LKLNSVTTED TATYYCARDQ GYSKFYFDYW GQGTTLTVSS	Kappa	QVQLKESGPGLVKPSQSLSLTCSVTGYSITSGYYWN WIRQFPGNKLEWMGYINYDGRNNYNPSLRNRISITR DTSKNHFFLKLNSVTTEDTATYYCARDQGYSKFYFD YWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK		DIQMTQSSSSFSVSLG DRVTITCKASEDIYNR LAWYQQRPGNAPRLLI SGATSLETGVPSRFSG SGSGKDYTLSITSLQT EDVANYYCQQYWSFPR TFGGGTKLEIKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
			1221	1222	1223		1224
37	CD8B319	IgG1	QVQLKESGPE LKKPGETVKI SCKASGYSFT AYYMHWVKQS PEKSLEWIGE INPSAGGTTY NQKFKAKATL TVDKSSSTAF IQLKSLTSED SAVYYCARWT NPFDYWGQGT TLTVSS	Kappa	QVQLKESGPELKKPGETVKISCKASGYSFTAYYMHW VKQSPEKSLEWIGEINPSAGGTTYNQKFKAKATLTV DKSSSTAFIQLKSLTSEDSAVYYCARWTNPFDYWGQ GTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSLSPGK		DIVMTQSQKFMSTTVG DRVSITCKASQNVGTA VAWYQQKPGQSPKLLI YSASYRYTGVPDRFTG SGSGTHFTLTISNIQS EDLADYFCQQYNNYLT FGSGTKLEIKRTVAAP SVFIFPPSDEQLKSGT ASVVCLLNNFYPREAK VQWKVDNALQSGNSQE SVTEQDSKDSTYSLSS TLTLSKADYEKHKVYA CEVTHQGLSSPVTKSF NRGEC
			1255	1256	1257		1258

38	CD8B194	IgG1	Kappa	QVQLQQPGAE LVKPGASVKL SCKASGYTFT SYWINWVKQR PGQGLEWIGN IYPGSSSTNY NEKFKSKATL TVDTSSSAAY MQLSSLTSGD SAVYYCAREL GPYYRYSAMV YWGQGTTVTV SS	DIVMTQSQ KFMSTTVG DRVSITCK ASQNVGTA VAWYQQKP GQSPKLLI YSASNRYT GVPDRFTG SGSGTDFT LTISNMQS EDLADYFC QQYSSYPF TFGSGTKL EIK	QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWINW VKQRPGQGLEWIGNIYPGSSSTNYNEKFKSKATLTV DTSSSAAYMQLSSLTSGDSAVYYCARELGPYYRYSA MVYWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	DIVMTQSQKFMSTTVG DRVSITCKASQNVGTA VAWYQQKPGQSPKLLI YSASNRYTGVPDRFTG SGSGTDFTLTISNMQS EDLADYFCQQYSSYPF TFGSGTKLEIKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
				1289	1290	1291	1292
39	CD8B231	IgG1	Kappa	EVKLVESGAE LVKPGASVKL SCKASGYTFT NYWMHWVKQR PGQGLEWIGN IDPSDSETHY NQKFKDKATL TVDKSSSTAY MQLSSLTSED SAVYYCASGL TGTGHYWGQG TTLTVSS	DIQMTQTT SSLSASLG DRVTITCR ASQDINIY LNWYQQKP EGSIKCLI YHTSRLHS GVPSRFSG SGSGTDYS LTISNLEQ EDIATYFC QQDNTLPY TFGSGTKL EIK	EVKLVESGAELVKPGASVKLSCKASGYTFTNYWMHW VKQRPGQGLEWIGNIDPSDSETHYNQKFKDKATLTV DKSSTAYMQLSSLTSEDSAVYYCASGLTGTGHYWG QGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK	DIQMTQTTSSLSASLG DRVTITCRASQDINIY LNWYQQKPEGSIKCLI YHTSRLHSGVPSRFSG SGSGTDYSLTISNLEQ EDIATYFCQQDNTLPY TFGSGTKLEIKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
				1323	1324	1325	1326
40	CD8B238	IgG1	Kappa	EFQLQQSGPE LVKPGASLKI SCKASGYTFT DYSMDWVKQS HGKTLEWIGY	DIKMTQSP SSMCPSLG ERVTITCK ASQDIKSY LSWFQQKP	EFQLQQSGPELVKPGASLKISCKASGYTFTDYSMDW VKQSHGKTLEWIGYIYTYSGGAGYNRKFKSKATLTV DKSSSTAYLELHSLTSDDSAVYYCARDSSDYEFAYW GQGTLVTVSAASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL	DIKMTQSPSSMCPSLG ERVTITCKASQDIKSY LSWFQQKPGKSPKTLI YRANRLVDGVPSRFSG SGSGQDYSLTISSLEY

			IYTYSGGAGY NRKFKSKATL TVDKSSSTAY LELHSLTSDD SAVYYCARDS SDYEFAYWGQ GTLVTVSA	GKSPKTLI YRANRLVD GVPSRFSG SGSGQDYS LTISSLEY EDMGIYYC LQYDEFRT FGGGTKLE IK	YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK	EDMGIYYCLQYDEFRT FGGGTKLEIKRTVAAP SVFIFPPSDEQLKSGT ASVVCLLNNFYPREAK VQWKVDNALQSGNSQE SVTEQDSKDSTYSLSS TLTLSKADYEKHKVYA CEVTHQGLSSPVTKSF NRGEC
			1357	1358	1359	1360
41	CD8B255	IgG1	QVTLKESGPG ILQPSQTLSL TCSFSGFSLN TSGMGVSWIR KPSGKGLEWL AHIFWDDDKR YNPSLKSRLT ISKDTSSNQV FLMITSVDTA DTATYYCARR DGYGDYAYFD VWGAGTLVTV SA	QVTLKESGPGILQPSQTLSLTCSFSGFSLNTSGMGV SWIRKPSGKGLEWLAHIFWDDDKRYNPSLKSRLTIS KDTSSNQVFLMITSVDTADTATYYCARRDGYGDYAY FDVWGAGTLVTVSAASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	DIQMTQSPASLSVSVG ETVTITCRASENIYSD LAWYQQKQGKSPQLLV YAATILTDGVPSRFSG SGSGTQYSLKINSLQS EDFGNYYCQHFWGTPW TFGDGTRLEIKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
			1391	1392	1393	1394
42	CD8B324	IgG1	QVQLQQPGAD LVKPGASVKL SCKASGYTST SHWIHWVKQR PGQGLEWIGN IYPGSSSTNY NEKFKRMATL TVDTSSSTVY MVLSSLTSDD SAVYYCARHS	QVQLQQPGADLVKPGASVKLSCKASGYTSTSHWIHW VKQRPGQGLEWIGNIYPGSSSTNYNEKFKRMATLTV DTSSSTVYMVLSSLTSDDSAVYYCARHSPGHRDYAM DYWGLGTSVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVD KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE	DIVMTQSQKFMPTTVG DRVSITCKASQNVGTA VAWYQQKPGQSPKLLI ASASNRYTGVPDRFTG SGSGTDFTLTISTMQS EDLADYFCQQYSTYPL TFGAGTKLEMKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ

			PGHRDYAMDY WGLGTSVTVS S	EDLADYFC QQYSTYPL TFGAGTKL EMK	EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPGK		ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
			1425	1426	1427		1428
43	CD8B337	IgG1	QVTLKESGPG KVQPSQTLSL TCSFSGFSLS TSGMGVSWIR KPSGKGLEWL AHIFWDDDRR YKSSLKSRLT ISKDTSSNQV FLMITSVDTA DSATYYCARR VGYGDYAYFD VWGAGTTVTV SS	DIQMTQYP ASLSVSVG ETVTITCR ASENIYSD LAWYQQKQ GKSPQLLV YAATNLAD GVPSRFSG SGSGTQYS LKINSLQS EDFGNYYC QHFWGTPW TFGGGTKL EIK	QVTLKESGPGKVQPSQTLSLTCSFSGFSLSTSGMGV SWIRKPSGKGLEWLAHIFWDDDRRYKSSLKSRLTIS KDTSSNQVFLMITSVDTADSATYYCARRVGYGDYAY FDVWGAGTTVTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK		DIQMTQYPASLSVSVG ETVTITCRASENIYSD LAWYQQKQGKSPQLLV YAATNLADGVPSRFSG SGSGTQYSLKINSLQS EDFGNYYCQHFWGTPW TFGGGTKLEIKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
			1459	1460	1461		1462
44	CD8B344	IgG1	QVQLQQSGAE LVKPGASVKL SCKASGYSFT NYWINWMKQR PGQGLEWIGN IYPGSDSSNY NEKFKTKATL TVDTSSSTAY MQLSSLTSDD SAVYYCAREE ADYRYTWFVY WGQGTLVTVS A	DIKMTQSQ KFMSTTVG DRVSITCK ASQNVGTA VAWYQQKP GQSPKLLI YSASNRYT GVPDRFTG SGSGTDFT FSNMQS LTFSNMQS EDFGNYYC QQYSSYPL TFGAGTKL EMK	QVQLQQSGAELVKPGASVKLSCKASGYSFTNYWINW MKQRPGQGLEWIGNIYPGSDSSNYNEKFKTKATLTV DTSSSTAYMQLSSLTSDDSAVYYCAREEADYRYTWF VYWGQGTLVTVSAASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVD KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPGK		DIKMTQSQKFMSTTVG DRVSITCKASQNVGTA VAWYQQKPGQSPKLLI YSASNRYTGVPDRFTG SGSGTDFTLTFSNMQS EDLADYFCQQYSSYPL TFGAGTKLEMKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
			1493	1494	1495		1496

45	CD8B264	IgG1	Kappa	EVQLQQSGTE LVKPGASVKL SCKASGYSFT SYWINWVKQR PGQGPEWIGN IYPGSSSTNY NEKFKNKATL TVDTSSSTAY MQLSSLTSDD SAVFYCAREE YSYFPSWFAY WGQGTLVTVS A	DIVMTQSQ KFMSTTVG DRVSITCK ASQNVGTA VAWYQQKP GQSPKLLI YSASNRYN YVPDRFTG SGSGTDFT LTISNMQS EDLADYFC QQYSTYPY TFGSGTKL EIK	EVQLQQSGAELVKPGASVKLSCKASGYTFTSYWISW VKQRPGQGLEWIGNIYPGSSSNYNENFKSKATLTV DTSSSTAHMQLSSLTSDDSAVFYCAREEYSYFPSWF AYWGQGTSVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVD KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPGK	1529	DIVMTQSQKFMSTTIG DRVSITCKASQNVGTA VAWFQQKPGQSPKLLI YSASNRYTGVPDRFTG SGSGTDFTLTISNMQS EDLANYFCQQYSTYPF TFGGGTKLEIKRTVAA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC	1530
				1527	1528				
46	CD8B318	IgG1	Kappa	EVQLQQSGAE LVKPGASVKL SCKASGYTFT SYWISWVKQR PGQGLEWIGN IYPGSSSSNY NENFKSKATL TVDTSSSTAH MQLSSLTSDD SAVFYCAREE YSYFPSWFAY WGQGTSVTVS S	DIVMTQSQ KFMSTTIG DRVSITCK ASQNVGTA VAWFQQKP GQSPKLLI YSASNRYT GVPDRFTG SGSGTDFT LTISNMQS EDLANYFC QQYSTYPF TFGGGTKL EIK	EVQLQQSGAELVKPGASVKLSCKASGYTFTSYWISW VKQRPGQGLEWIGNIYPGSSSNYNENFKSKATLTV DTSSSTAHMQLSSLTSDDSAVFYCAREEYSYFPSWF AYWGQGTSVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVD KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPGK	1563	DIVMTQSQKFMSTTVG DRVSITCKASQNVGTA VAWYQQKPGQSPKLLI YSASNRYNGVPDRFTG SGSGTDFTLTISNMQS EDLADYFCQQYSTYPY TFGSGTKLEIKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC	1564
				1561	1562				
47	CD8B333	IgG1	Kappa	QVQLQQPGTE LVKPGASVKL SCKASGYSFA SFWINWVKQR PGQGPEWIGN	DIVMTQSQ KFMSTTVG DRVSITCK ASQNVGTA VAWYQQKP	QVQLQQPGTELVKPGASVKLSCKASGYSFASFWINW VKQRPGQGPEWIGNIYPGSSSTNYSEKFKNKATLTV DKSSSTAYMQLSSLTSDDSAVYYCAREEYSYKSSWF AYWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS	DIVMTQSQKFMSTTVG DRVSITCKASQNVGTA VAWYQQKPGQSPKLLI YSASNRYNGVPDRFTG SGSGTDFTLTISNMQS EDLADYFCQQYSTYPY TFGSGTKLEIKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC	1530

			IYPGSSSTNY	GQSPKLLI	SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVD	EDLADYFCQQYSTYPY
			SEKFKNKATL	YSASNRYN	KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK	TFGSGTKLELKRTVAA
			TVDKSSSTAY	GVPDRFTG	DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV	PSVFIFPPSDEQLKSG
			MQLSSLTSDD	SGSGTDFT	HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK	TASVVCLLNNFYPREA
			SAVYYCAREE	LTISNMQS	CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE	KVQWKVDNALQSGNSQ
			YSYKSSWFAY	EDLADYFC	EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK	ESVTEQDSKDSTYSLS
			WGQGTTVTVS	QQYSTYPY	TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM	STLTLSKADYEKHKVY
			S	TFGSGTKL	HEALHNHYTQKSLSLSPGK	ACEVTHQGLSSPVTKS
				ELK		FNRGEC
		1595		1596	1597	1598
48	CD8B366	IgG1	Kappa			
			EVQLQQSGPE	DIKMTQSP	EVQLQQSGPELVRPGASVKLSCTASGFNIKDDYIHW	DIKMTQSPSYLAASPG
			LVRPGASVKL	SYLAASPG	VKQRPEQGLEWIGRIDPANGNPRYAPKFQDKATLTA	ETITINCRASKSISKY
			SCTASGFNIK	ETITINCR	DTSSNTAYLQLSSLTSEDTAVYYCARDDEGYYYFDV	LAWYQEKPGKTNKVLI
			DDYIHWVKQR	ASKSISKY	WGAGTSVTVSSASTKGPSVFPLAPSSKSTSGGTAAL	YSGSTLQSGIPSRFSG
			PEQGLEWIGR	LAWYQEKP	GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG	SGSGTDFTLTISSLEP
			IDPANGNPRY	GKTNKVLI	LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK	EDFAIYYCQQHNEYPL
			APKFQDKATL	YSGSTLQS	VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT	TFGDGTRLEIKRTVAA
			TADTSSNTAY	GIPSRFSG	LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN	PSVFIFPPSDEQLKSG
			LQLSSLTSED	SGSGTDFT	AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK	TASVVCLLNNFYPREA
			TAVYYCARDD	LTISSLEP	VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM	KVQWKVDNALQSGNSQ
			EGYYYFDVWG	EDFAIYYC	TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT	ESVTEQDSKDSTYSLS
			AGTSVTVSS	QQHNEYPL	PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE	STLTLSKADYEKHKVY
				TFGDGTRL	ALHNHYTQKSLSLSPGK	ACEVTHQGLSSPVTKS
				EIK		FNRGEC
		1629		1630	1631	1632
49	CD8B368	IgG1	Kappa			
			QVQLQQPGTE	DIVMTQSQ	QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWINW	DIVMTQSQKFMSTTVG
			LVKPGASVKL	KFMSTTVG	MKQRPGQGLEWIGNIYPFSSSTNYNEKFKKKATLTV	DRVSITCKASQNVGIA
			SCKASGYTFT	DRVSITCK	DASSSTASMQLSSLTSDDSAVYFCAREEFSHYPSWF	VAWFQQKPGQSPKLLI
			SYWINWMKQR	ASQNVGIA	AYWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTA	YSASNRYTGVPDRFTG
			PGQGLEWIGN	VAWFQQKP	ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS	SGSGTDFTLTIGNMQS
			IYPFSSSTNY	GQSPKLLI	SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVD	EDLADYFCQQYSTDPY
			NEKFKKKATL	YSASNRYT	KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK	TFGSGTKLEIKRTVAA
			TVDASSSTAS	GVPDRFTG	DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV	PSVFIFPPSDEQLKSG
			MQLSSLTSDD	SGSGTDFT	HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK	TASVVCLLNNFYPREA
			SAVYFCAREE	LTIGNMQS	CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE	KVQWKVDNALQSGNSQ

				FSHYPSWFAY WGQGTTLTVS S	EDLADYFC QQYSTDPY TFGSGTKL EIK	EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPGK	ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
				1663	1664	1665	1666
50	CD8B370	IgG1	Kappa	EVQLQQSGAE LVKPGASVKL SCKASGYTFT SYWINWVKQR PGQGLEWIGN IYPGSSSTNY NEKFKNKATL TVDTSSSTVY MQLSSLTSDD SAVYYCTREL GAYYHYSAMD YWGQGTSVTV SS	DIVLTQSQ KIMSTTVG DRVSITCK ASQNVGTA VAWYQQKP GQSPKLLI YSASNRYT GVPDRFTG SGSGTDFT LTISNMQS EDLADYFC QQYSIYPF TFGSGTKL EIK	EVQLQQSGAELVKPGASVKLSCKASGYTFTSYWINW VKQRPGQGLEWIGNIYPGSSSTNYNEKFKNKATLTV DTSSSTVYMQLSSLTSDDSAVYYCTRELGAYYHYSA MDYWGQGTSVTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	DIVLTQSQKIMSTTVG DRVSITCKASQNVGTA VAWYQQKPGQSPKLLI YSASNRYTGVPDRFTG SGSGTDFTLTISNMQS EDLADYFCQQYSIYPF TFGSGTKLEIKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
				1697	1698	1699	1700
51	CD8B186	IgG1	Kappa	QVQLQQSGAE LAKPGASVKM SCKASGYIFT SYWMHWVKQR PGQGLEWIGN INPSSGYAVY NQKFKDKATL TADQSSSTAY IQLNSLTSED SAVYYCARRV FYGDSWFAYW GQGTSVTVSS	DVQMIQSP ASLSASVG ETVTITCR ASGNIHNY LAWYQQKQ GKSPQLLV YNAKTLAD GVPSRFSG SGSGTQYS LKINSLQP EDFGSYYC QHFWSTTW TFGGGTKL EIK	QVQLQQSGAELAKPGASVKMSCKASGYIFTSYWMHW VKQRPGQGLEWIGNINPSSGYAVYNQKFKDKATLTA DQSSSTAYIQLNSLTSEDSAVYYCARRVFYGDSWFA YWGQGTSVTVSSASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK	DVQMIQSPASLSASVG ETVTITCRASGNIHNY LAWYQQKQGKSPQLLV YNAKTLADGVPSRFSG SGSGTQYSLKINSLQP EDFGSYYCQHFWSTTW TFGGGTKLEIKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
				1731	1732	1733	1734

52	CD8B190	IgG1	Kappa	EFQLQQSGPE LMKPGASVKI SCKASGYSFT SYYMHWMKQS HGKSLEWIGY IDPFNGNTNY KQKFKGKATL TVDKSSSTAY MHLSSLTSED SAVYYCASPN SNYVGTWFAY WGQGTTVTVS S	NTQMNQTP SSLSASLG DTVTITCH ASQNINVW LSWYQQKP GNIPKLLI YKASNLHT GVPSRFSG SGSGTGFT LTISSLQP DDIATYYC QQGQSFPF TFGSGTKL EIK	EFQLQQSGPELMKPGASVKISCKASGYSFTSYYMHW MKQSHGKSLEWIGYIDPFNGNTNYKQKFKGKATLTV DKSSSTAYMHLSSLTSEDSAVYYCASPNSNYVGTWF AYWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVD KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPGK	NTQMNQTPSSLSASLG DTVTITCHASQNINVW LSWYQQKPGNIPKLLI YKASNLHTGVPSRFSG SGSGTGFTLTISSLQP DDIATYYCQQGQSFPF TFGSGTKLEIKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
				1765	1766	1767	1768
53	CD8B192	IgG1	Kappa	QVQLQQSGPV LVKPGASVKM SCKASGYTFT DYYMNWVMQS HGKSLEWIGV INPYNGGTTY NQRFTGKATL TVDKSSSTAY MELNSLTSED SAVYYCARNY GAMDSWGQGT SVTVSS	DIQMTQSP ASLSASVG ETVTITCR ASGNIHNY LAWYQQKQ GKSPQLLV SNAKTLAD GVPSRFGG SGSGTQYS LKINSLQP EDFGSYYC QHFWITPP TFGAGTRL EIK	QVQLQQSGPVLVKPGASVKMSCKASGYTFTDYYMNW VMQSHGKSLEWIGVINPYNGGTTYNQRFTGKATLTV DKSSSTAYMELNSLTSEDSAVYYCARNYGAMDSWGQ GTSVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSLSPGK	DIQMTQSPASLSASVG ETVTITCRASGNIHNY LAWYQQKQGKSPQLLV SNAKTLADGVPSRFGG SGSGTQYSLKINSLQP EDFGSYYCQHFWITPP TFGAGTRLEIKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
				1799	1800	1801	1802
54	CD8B193	IgG1	Kappa	DVQLQESGPE LVKPGASVKI ACKTSGYKFT DYYMNWVKQS LGKSLDWIGD	DIVMTQSQ KFMSTTVG DRVSITCK ASQNVGTA VAWYQQKP	DVQLQESGPELVKPGASVKIACKTSGYKFTDYYMNW VKQSLGKSLDWIGDINPNGGGTSDNPKFKGKATLTV DKSSSTAYMELRSLTSEDSGVYYCARTSGTDWYFDV WGTGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG	DIVMTQSQKFMSTTVG DRVSITCKASQNVGTA VAWYQQKPGQSPKLLI YSASNRYTGVPDRFTG SGSGTDFTLTISNMQS

			INPNGGGTSD	GQSPKLLI	LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK	EDLADYFCQQYSSYPF
			NPKFKGKATL	YSASNRYT	VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT	TFGSGTKLEMKRTVAA
			TVDKSSSTAY	GVPDRFTG	LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN	PSVFIFPPSDEQLKSG
			MELRSLTSED	SGSGTDFT	AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK	TASVVCLLNNFYPREA
			SGVYYCARTS	LTISNMQS	VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM	KVQWKVDNALQSGNSQ
			GTDWYFDVWG	EDLADYFC	TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT	ESVTEQDSKDSTYSLS
			TGTTVTVSS	QQYSSYPF	PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE	STLTLSKADYEKHKVY
				TFGSGTKL	ALHNHYTQKSLSLSPGK	ACEVTHQGLSSPVTKS
				EMK		FNRGEC
		1833		1834	1835	1836
55	CD8B214	IgG1	Kappa	DIQMTQTT	QVQLQQSGPELKKPGETVKISCKASGYTFTTAGIQW	DIQMTQTTSSLSASLG
				SSLSASLG	VQKMPGKGFKWIGWINTHAGESKYADDFKGRFAVSL	DRVTITCRASQDIRFY
				DRVTITCR	ETSASTAYLQISNLKNEDTATYFCARSGDYDGSHPF	LNWYQQKPEGTIKLLI
				ASQDIRFY	AYWGQGTSVTVSSASTKGPSVFPLAPSSKSTSGGTA	YYTSRLHSGVPSRFSG
				LNWYQQKP	ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS	SGSGTDYSLTISNLEQ
				EGTIKLLI	SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVD	EDIATYFCQQDNTLPY
				YYTSRLHS	KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK	TFGSGTKLEIKRTVAA
				GVPSRFSG	DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV	PSVFIFPPSDEQLKSG
				SGSGTDYS	HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK	TASVVCLLNNFYPREA
				LTISNLEQ	CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE	KVQWKVDNALQSGNSQ
				EDIATYFC	EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK	ESVTEQDSKDSTYSLS
				QQDNTLPY	TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM	STLTLSKADYEKHKVY
				TFGSGTKL	HEALHNHYTQKSLSLSPGK	ACEVTHQGLSSPVTKS
				EIK		FNRGEC
		1867		1868	1869	1870
56	CD8B230	IgG1	Kappa	QIQLVQSGPE	DIVMTQSQ	QIQLVQSGPELVKPGASVKISCKASGYTFTDYYMNW	DIVMTQSQKFMSTTVG
				LVKPGASVKI	KFMSTTVG	VKQSHGKSLDWIGDINPNGGGTSDNPKFKGKATLTV	DRVSITCKASQNVGTA
				SCKASGYTFT	DRVSITCK	DKSSNTAYMELRSLTSEDSAVYYCARTSGTDWYFDV	VAWYQQKPGQSPKLLI
				DYYMNWVKQS	ASQNVGTA	WGTGTLVTVSAASTKGPSVFPLAPSSKSTSGGTAAL	YSTSNRYTGVPDRFTG
				HGKSLDWIGD	VAWYQQKP	GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG	SGSGTDFTLTISNMQS
				INPNGGGTSD	GQSPKLLI	LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK	EDLADYFCQQYSIYPF
				NPKFKGKATL	YSTSNRYT	VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT	TFGSGTKLEMKRTVAA
				TVDKSSNTAY	GVPDRFTG	LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN	PSVFIFPPSDEQLKSG
				MELRSLTSED	SGSGTDFT	AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK	TASVVCLLNNFYPREA
				SAVYYCARTS	LTISNMQS	VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM	KVQWKVDNALQSGNSQ

				GTDWYFDVWG TGTLVTVSA	EDLADYFC QQYSIYPF TFGSGTKL EMK	TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK	ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
				1901	1902	1903	1904
57	CD8B245	IgG1	Kappa	EFQLQQSGGG LVQPGGSLSL SCAAPGFTFT DYYMSWVRQS PGKALEWLAL SRNKGNGYTT EYSASVKGRF TISRDNSQSI LYLQMNVLRA EDSATYYCAR TVTGTLFYYA LDYWGQGTTV TVSS	DIQMTQSP ASLSASVG ETVTITCR ASENIYSY LAWYQQKQ GKSPQFLV YNAKTLAA GVPSRFSG SGSGTQFS LKINRLQP EDFGTYYC QHHYGTPL TFGDGTRL EIK	EFQLQQSGGGLVQPGGSLSLSCAAPGFTFTDYYMSW VRQSPGKALEWLALSRNKGNGYTTEYSASVKGRFTI SRDNSQSILYLQMNVLRAEDSATYYCARTVTGTLFY YALDYWGQGTTVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK	DIQMTQSPASLSASVG ETVTITCRASENIYSY LAWYQQKQGKSPQFLV YNAKTLAAGVPSRFSG SGSGTQFSLKINRLQP EDFGTYYCQHHYGTPL TFGDGTRLEIKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
				1935	1936	1937	1938
58	CD8B248	IgG1	Kappa	EVQLQQSGAE LARPGASVKM SCKASGYTFT TYTMHWVKQR PGQGLEWIGY INPSSGYTKY NQKFTDKATL SAVYYCARLW AYWGQGTLVT VSA	DVVMTQTP LSLPVSLG DQASISCR SSQSLVHS SGNTYLHW YLQKPGQS PKLLIYKG SNRFSGVS DRFSGSGS GTDFTLKI SRVEAEDL GVYFCSQS THVPFTFG SGTKLEMK	EVQLQQSGAELARPGASVKMSCKASGYTFTTYTMHW VKQRPGQGLEWIGYINPSSGYTKYNQKFTDKATLTA DKSSSTAYMQLSSLTSEDSAVYYCARLWAYWGQGTL VTVSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	DVVMTQTPLSLPVSLG DQASISCRSSQSLVHS SGNTYLHWYLQKPGQS PKLLIYKGSNRFSGVS DRFSGSGSGTDFTLKI SRVEAEDLGVYFCSQS THVPFTFGSGTKLEMK RTVAAPSVFIFPPSDE QLKSGTASVVCLLNNF YPREAKVQWKVDNALQ SGNSQESVTEQDSKDS TYSLSSTLTLSKADYE KHKVYACEVTHQGLSS PVTKSFNRGEC
				1969	1970	1971	1972

59	CD8B250	IgG1	Kappa	QVQLKESGPG	DIVMTQSQ	QVQLKESGPGLVAPSQSLSITCTVSGFSLSNYVVHW
				LVAPSQSLSI	KFMSTSVG	VRQSPGKGLEWLGVIWTDGSTDYNAAFISRLSISKD
				TCTVSGFSLS	DRVSVTCK	NSKSQVFFKMNSLQADDTAIYYCARNNGYFPAFFAY
				NYVVHWVRQS	ASQNVDTD	WGQGTLVTVSAASTKGPSVFPLAPSSKSTSGGTAAL
				PGKGLEWLGV	ITWYQQKP	GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
				IWTDGSTDYN	GQSPKALI	LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK
				AAFISRLSIS	YSASYRYS	VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT
				KDNSKSQVFF	GVPDRFTG	LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
				KMNSLQADDT	SGSGTDFT	AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK
				AIYYCARNNG	LTITNVQS	VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM
				YFPAFFAYWG	EDLAEYFC	TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
				QGTLVTVSA	QQYNSYPL	PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE
					TFGSGTKL	ALHNHYTQKSLSLSPGK
					EMK	
				2003	2004	2005
60	CD8B254	IgG1	Kappa	EVQLQQSGAE	DVVMTQTP	EVQLQQSGAELVKPGASVKMSCKTSGYTFSSYWITW
				LVKPGASVKM	LSLPVSLG	VKQRPGQGLEWVGDIYPGSGSTNYNEKFKSKAALTV
				SCKTSGYTFS	DQASISCR	DTSSSTAFMQLNSLTSEDSAVYYCARESITTRITPF
				SYWITWVKQR	SSQSLVHS	DHWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTA
				PGQGLEWVGD	SGNTYLHW	ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS
				IYPGSGSTNY	YLQKPGQS	SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVD
				NEKFKSKAAL	PKLLIYKG	KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK
				TVDTSSSTAF	SNRFSGVS	DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV
				MQLNSLTSED	DRFSGSGS	HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK
				SAVYYCARES	GTDFTLKI	CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE
				ITTRITPFDH	SRVEAEDL	EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK
				WGQGTTLTVS	GVYFCSQS	TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
				S	THVPFTFG	HEALHNHYTQKSLSLSPGK
					SGTKLEIK	
				2037	2038	2039
61	CD8B261	IgG1	Kappa	QVQLQQPGAE	DIVLTQSP	QVQLQQPGAELVKPGASVKLSCKASGYTFNSYWINW
				LVKPGASVKL	SSMYASLG	MKQRPGQGLEWIGNIYPGSSSTNYNEKFKSKATLTV
				SCKASGYTFN	ERVTITCK	DTSSSTAYMQLSSLTSDDSAVYYCARELGGYYRYNA
				SYWINWMKQR	ASQDINRY	MDYWGQGTSVTVSSASTKGPSVFPLAPSSKSTSGGT
				PGQGLEWIGN	LSWFQQKP	AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ

59	CD8B250	IgG1	Kappa	DIVMTQSQKFMSTSVG		
				DRVSVTCKASQNVDTD		
				ITWYQQKPGQSPKALI		
				YSASYRYSGVPDRFTG		
				SGSGTDFTLTITNVQS		
				EDLAEYFCQQYNSYPL		
				TFGSGTKLEMKRTVAA		
				PSVFIFPPSDEQLKSG		
				TASVVCLLNNFYPREA		
				KVQWKVDNALQSGNSQ		
				ESVTEQDSKDSTYSLS		
				STLTLSKADYEKHKVY		
				ACEVTHQGLSSPVTKS		
				FNRGEC		
				2006		
60	CD8B254	IgG1	Kappa	DVVMTQTPLSLPVSLG		
				DQASISCRSSQSLVHS		
				SGNTYLHWYLQKPGQS		
				PKLLIYKGSNRFSGVS		
				DRFSGSGSGTDFTLKI		
				SRVEAEDLGVYFCSQS		
				THVPFTFGSGTKLEIK		
				RTVAAPSVFIFPPSDE		
				QLKSGTASVVCLLNNF		
				YPREAKVQWKVDNALQ		
				SGNSQESVTEQDSKDS		
				TYSLSSTLTLSKADYE		
				KHKVYACEVTHQGLSS		
				PVTKSFNRGEC		
				2040		
61	CD8B261	IgG1	Kappa	DIVLTQSPSSMYASLG		
				ERVTITCKASQDINRY		
				LSWFQQKPGKSPKTLI		
				YRANTLVDGVPSRFSG		
				SGSGQDYSLTISSLEY		

			IYPGSSSTNY	GKSPKTLI	SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV		EDMGIYYCLQYDEFPY
			NEKFKSKATL	YRANTLVD	DKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKP		TFGSGTKLEMKRTVAA
			TVDTSSSTAY	GVPSRFSG	KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE		PSVFIFPPSDEQLKSG
			MQLSSLTSDD	SGSGQDYS	VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY		TASVVCLLNNFYPREA
			SAVYYCAREL	LTISSLEY	KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR		KVQWKVDNALQSGNSQ
			GGYYRYNAMD	EDMGIYYC	EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY		ESVTEQDSKDSTYSLS
			YWGQGTSVTV	LQYDEFPY	KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV		STLTLSKADYEKHKVY
			SS	TFGSGTKL	MHEALHNHYTQKSLSLSPGK		ACEVTHQGLSSPVTKS
				EMK			FNRGEC
			2071	2072	2073		2074
62	CD8B311	IgG1	QVQLKESGPE	DIQMTQTT	QVQLKESGPELVKPGASVKLSCKASGYTFTSYWMHW		DIQMTQTTSSLSASLG
		Kappa	LVKPGASVKL	SSLSASLG	VKQRPGQGLEWIGMIHPNSGSTNYNEKFKSKATLTV		DRVTISCSASQGISNC
			SCKASGYTFT	DRVTISCS	DKSSSTAYMQLSSLTSEDSAVYYCARCGYDGAWFAY		LNWYQQKPDGTVKLLI
			SYWMHWVKQR	ASQGISNC	WGQGTSVTVSSASTKGPSVFPLAPSSKSTSGGTAAL		HYTSSLHSGVPSRFSG
			PGQGLEWIGM	LNWYQQKP	GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG		GGSGTHYSLTISNLEP
			IHPNSGSTNY	DGTVKLLI	LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK		EDIATYYCQQYSKVPY
			NEKFKSKATL	HYTSSLHS	VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT		TFGSGTKLEIKRTVAA
			TVDKSSSTAY	GVPSRFSG	LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN		PSVFIFPPSDEQLKSG
			MQLSSLTSED	GGSGTHYS	AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK		TASVVCLLNNFYPREA
			SAVYYCARCG	LTISNLEP	VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM		KVQWKVDNALQSGNSQ
			YDGAWFAYWG	EDIATYYC	TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT		ESVTEQDSKDSTYSLS
			QGTSVTVSS	QQYSKVPY	PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE		STLTLSKADYEKHKVY
				TFGSGTKL	ALHNHYTQKSLSLSPGK		ACEVTHQGLSSPVTKS
				EIK			FNRGEC
			2105	2106	2107		2108
63	CD8B340	IgG1	QVQLQQPGAE	DIVMTQTP	QVQLQQPGAELVKPGASVRLSCKASGYTFTNYWMQW		DIVMTQTPLTLSVTIG
		Kappa	LVKPGASVRL	LTLSVTIG	VQQRPGQGLEWIGEIDPSDTFTNYNQNFKDKATLTV		QPASISCKSSQSLLYS
			SCKASGYTFT	QPASISCK	DTSSSTAYLQLSSLTSEDSAVYYCARGDWDRDWYFD		DGKTYLNWLLQRPGES
			NYWMQWVQQR	SSQSLLYS	VWGTGTLVTVSAASTKGPSVFPLAPSSKSTSGGTAA		PKLLIYLVSKLDSGVP
			PGQGLEWIGE	DGKTYLNW	LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS		DRFTGSGSGTDFTLKI
			IDPSDTFTNY	LLQRPGES	GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK		SRVETEDLGIYYCLQA
			NQNFKDKATL	PKLLIYLV	KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKD		THFPHTFGAGTKLELK
			TVDTSSSTAY	SKLDSGVP	TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH		RTVAAPSVFIFPPSDE
			LQLSSLTSED	DRFTGSGS	NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC		QLKSGTASVVCLLNNF
			SAVYYCARGD	GTDFTLKI	KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE		YPREAKVQWKVDNALQ

			WDRDWYFDVW GTGTLVTVSA	SRVETEDL GIYYCLQA THFPHTFG AGTKLELK	MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK	SGNSQESVTEQDSKDS TYSLSSTLTLSKADYE KHKVYACEVTHQGLSS PVTKSFNRGEC
			2139	2140	2141	2142
64	CD8B362	IgG1	EVKLVESGAE LVKPGASVKL SCTASGFNIK DTYMHWVKQR PEQGLEWIGR IDPANGHTKF DPKFQGKATI TADTSSNTAY LQLSSLTSED TAVYYCAIRF AYWGQGTLVT VSA	DIQMTQSP SSLSASLG DRVSLTCR ASHEISGY LSWLQQKP DGTFKRLI YAASTLDS GVPKRFSG SRSGSDYS LSISSLES EDFADYYC LQYSSYPY TFGSGTKL EMK	EVKLVESGAELVKPGASVKLSCTASGFNIKDTYMHW VKQRPEQGLEWIGRIDPANGHTKFDPKFQGKATITA DTSSNTAYLQLSSLTSEDTAVYYCAIRFAYWGQGTL VTVSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	DIQMTQSPSSLSASLG DRVSLTCRASHEISGY LSWLQQKPDGTFKRLI YAASTLDSGVPKRFSG SRSGSDYSLSISSLES EDFADYYCLQYSSYPY TFGSGTKLEMKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLS STLTLSKADYEKHKVY ACEVTHQGLSSPVTKS FNRGEC
			2173	2174	2175	2176

Table 17. Kabat CDR Amino Acid Sequences

#	Protein Name	HC Kabat CDR1	HC Kabat CDR2	HC Kabat CDR3	LC Kabat CDR1	LC Kabat CDR2	LC Kabat CDR3
1	CD8B191	DYYMN	RVIPSNGGTIYNLKFKG	EDYNNQGFFLDAMDY	RASQSISDFLH	YASQSIS	QNGHSFPYT
		1	2	3	4	5	6
2	CD8B226	DYYMN	RIIPSNGATIYNQKFKG	EDYSNQGFFLDAMDY	RASQSISHYLH	YASQSIS	QNGHSFPYT
		35	36	37	38	39	40
3	CD8B259	DYYMN	RVIPSNGGTIYNQKFRG	EDYGNQGFFLDAMDY	RASQSISHFLH	YASQSIS	QSGHSFPYT
		69	70	71	72	73	74
4	CD8B298	DYYMN	RVIPNNGGTRYNQKFKG	EDFSNQGFFLDAMDY	RASQTISDYLH	YASQSIS	QNGHSFPYT
		103	104	105	106	107	108
5	CD8B342	DYYVN	RVIPNNGNVIYNQNFKG	EDYSNQGFFLDAMDY	RASQTISNYLH	YASQSIS	QNGHSFPYT
		137	138	139	140	141	142
6	CD8B364	SYWMH	EINPSNGDSYYNEKFKR	SMYYDGRAGAY	ITSTDIDDDMN	EGNTLRP	LQSDNMPLT
		171	172	173	174	175	176
7	CD8B200	NYWIH	NIDPSDSETHYNQKFKD	GLTGTGYY	RASQDISPYLN	YTSKLHS	QQDNTLPYT
		205	206	207	208	209	210
8	CD8B247	DYYMN	RVIPNNGGTIYNQKFKD	EDYSNQGFFLDAMDY	RASQTISHFLH	YASQSIS	QSGHSFPYT
		239	240	241	242	243	244
9	CD8B265	DYYMN	RVIPRNGATTYNQNFRG	EDFSNQGFFLDAMDY	RASQSISHYLH	YASQSIS	QNGHSFPYT
		273	274	275	276	277	278
10	CD8B270	NYWMH	NIDPSDSETHYNQKFKD	GLTGTGYY	RASQDIRPYLN	FTSKLHS	QQDNTLPYT
		307	308	309	310	311	312
11	CD8B213	DYYMD	YIYPNNGITSYNQKFKG	SIYYDHGGGFPY	KASQNVDKYVA	SASYRYS	QQYNTYPS
		341	342	343	344	345	346
12	CD8B240	DYYMN	RVIPSNGGTIYNLKFKG	EDYNNQGFFLDAMDY	RASQSISDFLH	YASQSIS	QNGHSFPYT
		375	376	377	378	379	380
13	CD8B361	DYYMD	YIYPNNGDTRYNQKFKD	SIYYDHGGGFPY	KASQNVGTYVA	SASYRYS	QQYNSYPT
		409	410	411	412	413	414
14	CD8B246	TSGMNVG	HIWWDDDKYYNPSLKS	RGNYGNYEFAY	RASQDIRNYLN	HTSRLHS	QQGNTLPWT
		443	444	445	446	447	448
15	CD8B268	VYTIH	WFYPGSGNIKYNEKFKD	HEDNHYYDGNSWFAY	RASGNIHNYLA	NAKTLAD	QHFWNTPYT
		477	478	479	480	481	482
16	CD8B271	IYSIH	MIWGGGDTDYNSALKS	NPHYYGGTYEYFDV	SASQGISNYLN	DTSILYS	QQYSNLPYT
		511	512	513	514	515	516
17	CD8B273	EYTIH	WFYPGTGSIKYNEKFKD	HEDNHYYDGNSWFAY	RASGNIHNYLA	NAKTLAD	QHFWSTPYT

		545	546	547	548	549	550
18	CD8B288	EYTIH	WFYPGNGNMRYNEKFKD	YEDNHYYDGASWFAY	RASGNIHNYLA	NAKTLAD	QHFWSTPFT
		579	580	581	582	583	584
19	CD8B292	DDYIY	WIDPENGATEYASKFQG	HDYGYAMDY	TASSSVSSSYLH	STSNLAS	HQYHRSPLT
		613	614	615	616	617	618
20	CD8B303	IYSIH	MIWGGGSTDYNSTLNS	NPHHYGGSTGAMDY	KASQDIKKYMA	YTSSLQP	LQYDNLFT
		647	648	649	650	651	652
21	CD8B304	TSGMNVG	HIWWDDDKYYNPSLKS	RGNYGNYEFAY	RASQDIRNYLN	HTSRLHS	QQGNTLPWT
		681	682	683	684	685	686
22	CD8B312	SFWMH	NVDPSDSQTHYNQKFKD	STYYRYDGPFTY	RASQSINNNLH	YTSQSIS	QQSNSWPLT
		715	716	717	718	719	720
23	CD8B347	SYWMN	AVNPSNSYTEYAQKFKD	SGLYNTNHLAWFAY	RASGNIHNYLA	NAETLAD	QHFWNNPLT
		749	750	751	752	753	754
24	CD8B350	AYWIN	SINPSNGYTEYSQKFKD	SGLYYTNHLAWCPY	RASGNIHNYLA	NAETLAD	QHFWNSPLT
		783	784	785	786	787	788
25	CD8B356	SGYYWN	YISYDGSNNYNPSLKN	NHGDAMDY	KASQNVGTAVA	SASYRYT	QQYSSYLT
		817	818	819	820	821	822
26	CD8B369	NTYIS	WIYTGTGGTWYNQKFTD	TNWDWYFDV	RASENIYSYLA	YAKTLTD	QHHYGRPYT
		851	852	853	854	855	856
27	CD8B371	DYYMA	HINYDGSITYYLDSLKS	EDYSNYGFAY	HASQNINVWLS	KASNLHT	QQGQSYPLT
		885	886	887	888	889	890
28	CD8B182	SYWMN	AVNPTNYYTEYIQKFKD	SGLYNTNHLAWFAY	RASENIHNYLA	NAKTLAN	QHFWTTPLT
		919	920	921	922	923	924
29	CD8B205	SYWMH	NIDPSDSETHYNQKFKD	VYYSYYSYDATYFDY	RASENIYSYLA	NAKTLAE	QHHYTTPLT
		953	954	955	956	957	958
30	CD8B223	SYSVH	VIWAGGSTNYNSAFMS	HSYYSFDAFDY	KASQNVNTDVA	SASYRYS	QQCNSYPLT
		987	988	989	990	991	992
31	CD8B234	SGYYWN	YINYDGRNNYNPSLKN	DQGYSKFYFDY	KASEDIYNRLA	GATSLET	QQYWSFPRT
		1021	1022	1023	1024	1025	1026
32	CD8B251	TYAVH	VIWSGGSTDYNAAFIS	HSYYHYNAMDN	KASQNVGTAVA	SASNRYT	QQYSSYPFT
		1055	1056	1057	1058	1059	1060
33	CD8B269	SGYYWN	YISYDGSNNYNPSLKN	NHGDAMDH	KASQNVGTDVA	SASYRYS	QQYKSYPLT
		1089	1090	1091	1092	1093	1094
34	CD8B290	RYSVH	MIWGGGSTDYNSALKS	IYFDNYVGFAY	KASQDVGTVVA	WTSTRHT	QQYSSYPYT
		1123	1124	1125	1126	1127	1128
35	CD8B310	NYAVH	VIWTDGSTDYNAGFIS	NNGYFPAFFAY	RSSQTIVHSNGNTYLE	KVSNRFS	FQGSHAPFT
		1157	1158	1159	1160	1161	1162
36	CD8B352	SGYYWN	YINYDGRNNYNPSLRN	DQGYSKFYFDY	KASEDIYNRLA	GATSLET	QQYWSFPRT

		1191	1192	1193	1194	1195	1196
37	CD8B319	AYYMH	EINPSAGGTTYNQKFKA	WTNPFDY	KASQNVGTAVA	SASYRYT	QQYNNYLT
		1225	1226	1227	1228	1229	1230
38	CD8B194	SYWIN	NIYPGSSSTNYNEKFKS	ELGPYYRYSAMVY	KASQNVGTAVA	SASNRYT	QQYSSYPFT
		1259	1260	1261	1262	1263	1264
39	CD8B231	NYWMH	NIDPSDSETHYNQKFKD	GLTGTGHY	RASQDINIYLN	HTSRLHS	QQDNTLPYT
		1293	1294	1295	1296	1297	1298
40	CD8B238	DYSMD	YIYTYSGGAGYNRKFKS	DSSDYEFAY	KASQDIKSYLS	RANRLVD	LQYDEFRT
		1327	1328	1329	1330	1331	1332
41	CD8B255	TSGMGVS	HIFWDDDKRYNPSLKS	RDGYGDYAYFDV	RASENIYSDLA	AATTLTD	QHFWGTPWT
		1361	1362	1363	1364	1365	1366
42	CD8B324	SHWIH	NIYPGSSSTNYNEKFKR	HSPGHRDYAMDY	KASQNVGTAVA	SASNRYT	QQYSTYPLT
		1395	1396	1397	1398	1399	1400
43	CD8B337	TSGMGVS	HIFWDDDRRYKSSLKS	RVGYGDYAYFDV	RASENIYSDLA	AATNLAD	QHFWGTPWT
		1429	1430	1431	1432	1433	1434
44	CD8B344	NYWIN	NIYPGSDSSNYNEKFKT	EEADYRYTWFVY	KASQNVGTAVA	SASNRYT	QQYSSYPLT
		1463	1464	1465	1466	1467	1468
45	CD8B264	SYWIN	NIYPGSSSTNYNEKFKN	EEYSYKSSWFAY	KASQNVGTAVA	SASNRYN	QQYSTYPYT
		1497	1498	1499	1500	1501	1502
46	CD8B318	SYWIS	NIYPGSSSSNYNENFKS	EEYSYFPSWFAY	KASQNVGTAVA	SASNRYT	QQYSTYPFT
		1531	1532	1533	1534	1535	1536
47	CD8B333	SFWIN	NIYPGSSSTNYSEKFKN	EEYSYKSSWFAY	KASQNVGTAVA	SASNRYN	QQYSTYPYT
		1565	1566	1567	1568	1569	1570
48	CD8B366	DDYIH	RIDPANGNPRYAPKFQD	DDEGYYYFDV	RASKSISKYLA	SGSTLQS	QQHNEYPLT
		1599	1600	1601	1602	1603	1604
49	CD8B368	SYWIN	NIYPFSSSTNYNEKFKK	EEFSHYPSWFAY	KASQNVGIAVA	SASNRYT	QQYSTDPYT
		1633	1634	1635	1636	1637	1638
50	CD8B370	SYWIN	NIYPGSSSTNYNEKFKN	ELGAYYHYSAMDY	KASQNVGTAVA	SASNRYT	QQYSIYPFT
		1667	1668	1669	1670	1671	1672
51	CD8B186	SYWMH	NINPSSGYAVYNQKFKD	RVFYGDSWFAY	RASGNIHNYLA	NAKTLAD	QHFWSTTWT
		1701	1702	1703	1704	1705	1706
52	CD8B190	SYYMH	YIDPFNGNTNYKQKFKG	PNSNYVGTWFAY	HASQNINVWLS	KASNLHT	QQGQSFPFT
		1735	1736	1737	1738	1739	1740
53	CD8B192	DYYMN	VINPYNGGTTYNQRFTG	NYGAMDS	RASGNIHNYLA	NAKTLAD	QHFWITPPT
		1769	1770	1771	1772	1773	1774
54	CD8B193	DYYMN	DINPNGGGTSDNPKFKG	TSGTDWYFDV	KASQNVGTAVA	SASNRYT	QQYSSYPFT
		1803	1804	1805	1806	1807	1808
55	CD8B214	TAGIQ	WINTHAGESKYADDFKG	SGDYDGSHPFAY	RASQDIRPYLN	YTSRLHS	QQDNTLPYT

		1837	1838	1839	1840	1841	1842
56	CD8B230	DYYMN	DINPNGGGTSDNPKFKG	TSGTDWYFDV	KASQNVGTAVA	STSNRYT	QQYSIYPFT
		1871	1872	1873	1874	1875	1876
57	CD8B245	DYYMS	LSRNKGNGYTTEYSASVKG	TVTGTLFYYALDY	RASENIYSYLA	NAKTLAA	QHHYGTPLT
		1905	1906	1907	1908	1909	1910
58	CD8B248	TYTMH	YINPSSGYTKYNQKFTD	LWAY	RSSQSLVHSSGNTYLH	KGSNRFS	SQSTHVPFT
		1939	1940	1941	1942	1943	1944
59	CD8B250	NYVVH	VIWTDGSTDYNAAFIS	NNGYFPAFFAY	KASQNVDTDIT	SASYRYS	QQYNSYPLT
		1973	1974	1975	1976	1977	1978
60	CD8B254	SYWIT	DIYPGSGSTNYNEKFKS	ESITTRITPFDH	RSSQSLVHSSGNTYLH	KGSNRFS	SQSTHVPFT
		2007	2008	2009	2010	2011	2012
61	CD8B261	SYWIN	NIYPGSSSTNYNEKFKS	ELGGYYRYNAMDY	KASQDINRYLS	RANTLVD	LQYDEFPYT
		2041	2042	2043	2044	2045	2046
62	CD8B311	SYWMH	MIHPNSGSTNYNEKFKS	CGYDGAWFAY	SASQGISNCLN	YTSSLHS	QQYSKVPYT
		2075	2076	2077	2078	2079	2080
63	CD8B340	NYWMQ	EIDPSDTFTNYNQNFKD	GDWDRDWYFDV	KSSQSLLYSDGKTYLN	LVSKLDS	LQATHFPHT
		2109	2110	2111	2112	2113	2114
64	CD8B362	DTYMH	RIDPANGHTKFDPKFQG	RFAY	RASHEISGYLS	AASTLDS	LQYSSYPYT
		2143	2144	2145	2146	2147	2148

Table 18. Chothia CDR Amino Acid Sequences

#	Protein Name	HC Chothia CDR1	HC Chothia CDR2	HC Chothia CDR3	LC Chothia CDR1	LC Chothia CDR2	LC Chothia CDR3
1	CD8B191	GYTFTDY	IPSNGG	EDYNNQGFFLDAMD	SQSISDF	YAS	GHSFPY
		7	8	9	10	11	12
2	CD8B226	GYTFTDY	IPSNGA	EDYSNQGFFLDAMD	SQSISHY	YAS	GHSFPY
		41	42	43	44	45	46
3	CD8B259	GYTFTDY	IPSNGG	EDYGNQGFFLDAMD	SQSISHF	YAS	GHSFPY
		75	76	77	78	79	80
4	CD8B298	GYTFTDY	IPNNGG	EDFSNQGFFLDAMD	SQTISDY	YAS	GHSFPY
		109	110	111	112	113	114
5	CD8B342	GYTFTDY	IPNNGN	EDYSNQGFFLDAMD	SQTISNY	YAS	GHSFPY
		143	144	145	146	147	148
6	CD8B364	GYTFTSY	NPSNGD	SMYYDGRAGA	STDIDDD	EGN	SDNMPL
		177	178	179	180	181	182

7	CD8B200	GYTFTNY	DPSDSE	GLTGTGY	SQDISPY	YTS	DNTLPY
		211	212	213	214	215	216
8	CD8B247	GYTFTDY	IPNNGG	EDYSNQGFFLDAMD	SQTISHF	YAS	GHSFPY
		245	246	247	248	249	250
9	CD8B265	GYSFTDY	IPRNGA	EDFSNQGFFLDAMD	SQSISHY	YAS	GHSFPY
		279	280	281	282	283	284
10	CD8B270	GYTFTNY	DPSDSE	GLTGTGY	SQDIRPY	FTS	DNTLPY
		313	314	315	316	317	318
11	CD8B213	GYIFTDY	YPNNGI	SIYYDHGGGFP	SQNVDKY	SAS	YNTYP
		347	348	349	350	351	352
12	CD8B240	GYTFTDY	IPSNGG	EDYNNQGFFLDAMD	SQSISDF	YAS	GHSFPY
		381	382	383	384	385	386
13	CD8B361	GYTFTDY	YPNNGD	SIYYDHGGGFP	SQNVGTY	SAS	YNSYP
		415	416	417	418	419	420
14	CD8B246	GFSLSTSGM	WWDDD	RGNYGNYEFA	SQDIRNY	HTS	GNTLPW
		449	450	451	452	453	454
15	CD8B268	GYTFTVY	YPGSGN	HEDNHYYDGNSWFA	SGNIHNY	NAK	FWNTPY
		483	484	485	486	487	488
16	CD8B271	GFSLSIY	WGGGD	NPHYYGGTYEYFD	SQGISNY	DTS	YSNLPY
		517	518	519	520	521	522
17	CD8B273	GYTFTEY	YPGTGS	HEDNHYYDGNSWFA	SGNIHNY	NAK	FWSTPY
		551	552	553	554	555	556
18	CD8B288	GYTFTEY	YPGNGN	YEDNHYYDGASWFA	SGNIHNY	NAK	FWSTPF
		585	586	587	588	589	590
19	CD8B292	GFNFKDD	DPENGA	HDYGYAMD	SSSVSSSY	STS	YHRSPL
		619	620	621	622	623	624
20	CD8B303	GFSLSIY	WGGGS	NPHHYGGSTGAMD	SQDIKKY	YTS	YDNLF
		653	654	655	656	657	658
21	CD8B304	GFSLSTSGM	WWDDD	RGNYGNYEFA	SQDIRNY	HTS	GNTLPW
		687	688	689	690	691	692
22	CD8B312	GYTFTSF	DPSDSQ	STYYRYDGPFT	SQSINNN	YTS	SNSWPL
		721	722	723	724	725	726
23	CD8B347	GYTFTSY	NPSNSY	SGLYNTNHLAWFA	SGNIHNY	NAE	FWNNPL
		755	756	757	758	759	760
24	CD8B350	GYTFAAY	NPSNGY	SGLYYTNHLAWCP	SGNIHNY	NAE	FWNSPL
		789	790	791	792	793	794
25	CD8B356	GYSITSGY	SYDGS	NHGDAMD	SQNVGTA	SAS	YSSYL
		823	824	825	826	827	828

26	CD8B369	GFTFTNT	YTGTGG	TNWDWYFD	SENIYSY	YAK	HYGRPY
		857	858	859	860	861	862
27	CD8B371	GFTFSDY	NYDGSI	EDYSNYGFA	SQNINVW	KAS	GQSYPL
		891	892	893	894	895	896
28	CD8B182	GYTFTSY	NPTNYY	SGLYNTNHLAWFA	SENIHNY	NAK	FWTTPL
		925	926	927	928	929	930
29	CD8B205	GYSFNSY	DPSDSE	VYYSYYSYDATYFD	SENIYSY	NAK	HYTTPL
		959	960	961	962	963	964
30	CD8B223	GFSLTSY	WAGGS	HSYYSFDAFD	SQNVNTD	SAS	CNSYPL
		993	994	995	996	997	998
31	CD8B234	GYSITSGY	NYDGR	DQGYSKFYFD	SEDIYNR	GAT	YWSFPR
		1027	1028	1029	1030	1031	1032
32	CD8B251	GFSLTTY	WSGGS	HSYYHYNAMD	SQNVGTA	SAS	YSSYPF
		1061	1062	1063	1064	1065	1066
33	CD8B269	GYSITSGY	SYDGS	NHGDAMD	SQNVGTD	SAS	YKSYPL
		1095	1096	1097	1098	1099	1100
34	CD8B290	GFSLSRY	WGGGS	IYFDNYVGFA	SQDVGTV	WTS	YSSYPY
		1129	1130	1131	1132	1133	1134
35	CD8B310	GFSLTNY	WTDGS	NNGYFPAFFA	SQTIVHSNGNTY	KVS	GSHAPF
		1163	1164	1165	1166	1167	1168
36	CD8B352	GYSITSGY	NYDGR	DQGYSKFYFD	SEDIYNR	GAT	YWSFPR
		1197	1198	1199	1200	1201	1202
37	CD8B319	GYSFTAY	NPSAGG	WTNPFD	SQNVGTA	SAS	YNNYL
		1231	1232	1233	1234	1235	1236
38	CD8B194	GYTFTSY	YPGSSS	ELGPYYRYSAMV	SQNVGTA	SAS	YSSYPF
		1265	1266	1267	1268	1269	1270
39	CD8B231	GYTFTNY	DPSDSE	GLTGTGH	SQDINIY	HTS	DNTLPY
		1299	1300	1301	1302	1303	1304
40	CD8B238	GYTFTDY	YTYSGG	DSSDYEFA	SQDIKSY	RAN	YDEFR
		1333	1334	1335	1336	1337	1338
41	CD8B255	GFSLNTSGM	FWDDD	RDGYGDYAYFD	SENIYSD	AAT	FWGTPW
		1367	1368	1369	1370	1371	1372
42	CD8B324	GYTSTSH	YPGSSS	HSPGHRDYAMD	SQNVGTA	SAS	YSTYPL
		1401	1402	1403	1404	1405	1406
43	CD8B337	GFSLSTSGM	FWDDD	RVGYGDYAYFD	SENIYSD	AAT	FWGTPW
		1435	1436	1437	1438	1439	1440
44	CD8B344	GYSFTNY	YPGSDS	EEADYRYTWFV	SQNVGTA	SAS	YSSYPL
		1469	1470	1471	1472	1473	1474

45	CD8B264	GYSFTSY	YPGSSS	EEYSYKSSWFA	SQNVGTA	SAS	YSTYPY
		1503	1504	1505	1506	1507	1508
46	CD8B318	GYTFTSY	YPGSSS	EEYSYFPSWFA	SQNVGTA	SAS	YSTYPF
		1537	1538	1539	1540	1541	1542
47	CD8B333	GYSFASF	YPGSSS	EEYSYKSSWFA	SQNVGTA	SAS	YSTYPY
		1571	1572	1573	1574	1575	1576
48	CD8B366	GFNIKDD	DPANGN	DDEGYYYFD	SKSISKY	SGS	HNEYPL
		1605	1606	1607	1608	1609	1610
49	CD8B368	GYTFTSY	YPFSSS	EEFSHYPSWFA	SQNVGIA	SAS	YSTDPY
		1639	1640	1641	1642	1643	1644
50	CD8B370	GYTFTSY	YPGSSS	ELGAYYHYSAMD	SQNVGTA	SAS	YSIYPF
		1673	1674	1675	1676	1677	1678
51	CD8B186	GYIFTSY	NPSSGY	RVFYGDSWFA	SGNIHNY	NAK	FWSTTW
		1707	1708	1709	1710	1711	1712
52	CD8B190	GYSFTSY	DPFNGN	PNSNYVGTWFA	SQNINVW	KAS	GQSFPF
		1741	1742	1743	1744	1745	1746
53	CD8B192	GYTFTDY	NPYNGG	NYGAMD	SGNIHNY	NAK	FWITPP
		1775	1776	1777	1778	1779	1780
54	CD8B193	GYKFTDY	NPNGGG	TSGTDWYFD	SQNVGTA	SAS	YSSYPF
		1809	1810	1811	1812	1813	1814
55	CD8B214	GYTFTTA	NTHAGE	SGDYDGSHPFA	SQDIRPY	YTS	DNTLPY
		1843	1844	1845	1846	1847	1848
56	CD8B230	GYTFTDY	NPNGGG	TSGTDWYFD	SQNVGTA	STS	YSIYPF
		1877	1878	1879	1880	1881	1882
57	CD8B245	GFTFTDY	RNKGNGYT	TVTGTLFYYALD	SENIYSY	NAK	HYGTPL
		1911	1912	1913	1914	1915	1916
58	CD8B248	GYTFTTY	NPSSGY	LWA	SQSLVHSSGNTY	KGS	STHVPF
		1945	1946	1947	1948	1949	1950
59	CD8B250	GFSLSNY	WTDGS	NNGYFPAFFA	SQNVDTD	SAS	YNSYPL
		1979	1980	1981	1982	1983	1984
60	CD8B254	GYTFSSY	YPGSGS	ESITTRITPFD	SQSLVHSSGNTY	KGS	STHVPF
		2013	2014	2015	2016	2017	2018
61	CD8B261	GYTFNSY	YPGSSS	ELGGYYRYNAMD	SQDINRY	RAN	YDEFPY
		2047	2048	2049	2050	2051	2052
62	CD8B311	GYTFTSY	HPNSGS	CGYDGAWFA	SQGISNC	YTS	YSKVPY
		2081	2082	2083	2084	2085	2086
63	CD8B340	GYTFTNY	DPSDTF	GDWDRDWYFD	SQSLLYSDGKTY	LVS	ATHFPH
		2115	2116	2117	2118	2119	2120

64	CD8B362	GFNIKDT	DPANGH	RFA	SHEISGY	AAS	YSSYPY
		2149	2150	2151	2152	2153	2154

Table 19. AbM CDR Amino Acid Sequences

#	Protein Name	HC AbM CDR1	HC AbM CDR2	HC AbM CDR3	LC AbM CDR1	LC AbM CDR2	LC AbM CDR3
1	CD8B191	GYTFTDYYMN	RVIPSNGGTI	EDYNNQGFFLDAMDY	RASQSISDFLH	YASQSIS	QNGHSFPYT
		13	14	15	16	17	18
2	CD8B226	GYTFTDYYMN	RIIPSNGATI	EDYSNQGFFLDAMDY	RASQSISHYLH	YASQSIS	QNGHSFPYT
		47	48	49	50	51	52
3	CD8B259	GYTFTDYYMN	RVIPSNGGTI	EDYGNQGFFLDAMDY	RASQSISHFLH	YASQSIS	QSGHSFPYT
		81	82	83	84	85	86
4	CD8B298	GYTFTDYYMN	RVIPNNGGTR	EDFSNQGFFLDAMDY	RASQTISDYLH	YASQSIS	QNGHSFPYT
		115	116	117	118	119	120
5	CD8B342	GYTFTDYYVN	RVIPNNGNVI	EDYSNQGFFLDAMDY	RASQTISNYLH	YASQSIS	QNGHSFPYT
		149	150	151	152	153	154
6	CD8B364	GYTFTSYWMH	EINPSNGDSY	SMYYDGRAGAY	ITSTDIDDDMN	EGNTLRP	LQSDNMPLT
		183	184	185	186	187	188
7	CD8B200	GYTFTNYWIH	NIDPSDSETH	GLTGTGYY	RASQDISPYLN	YTSKLHS	QQDNTLPYT
		217	218	219	220	221	222
8	CD8B247	GYTFTDYYMN	RVIPNNGGTI	EDYSNQGFFLDAMDY	RASQTISHFLH	YASQSIS	QSGHSFPYT
		251	252	253	254	255	256
9	CD8B265	GYSFTDYYMN	RVIPRNGATT	EDFSNQGFFLDAMDY	RASQSISHYLH	YASQSIS	QNGHSFPYT
		285	286	287	288	289	290
10	CD8B270	GYTFTNYWMH	NIDPSDSETH	GLTGTGYY	RASQDIRPYLN	FTSKLHS	QQDNTLPYT
		319	320	321	322	323	324
11	CD8B213	GYIFTDYYMD	YIYPNNGITS	SIYYDHGGGFPY	KASQNVDKYVA	SASYRYS	QQYNTYPS
		353	354	355	356	357	358
12	CD8B240	GYTFTDYYMN	RVIPSNGGTI	EDYNNQGFFLDAMDY	RASQSISDFLH	YASQSIS	QNGHSFPYT
		387	388	389	390	391	392
13	CD8B361	GYTFTDYYMD	YIYPNNGDTR	SIYYDHGGGFPY	KASQNVGTYVA	SASYRYS	QQYNSYPT
		421	422	423	424	425	426
14	CD8B246	GFSLSTSGMNVG	HIWWDDDKY	RGNYGNYEFAY	RASQDIRNYLN	HTSRLHS	QQGNTLPWT
		455	456	457	458	459	460
15	CD8B268	GYTFTVYTIH	WFYPGSGNIK	HEDNHYYDGNSWFAY	RASGNIHNYLA	NAKTLAD	QHFWNTPYT
		489	490	491	492	493	494
16	CD8B271	GFSLSIYSIH	MIWGGGDTD	NPHYYGGTYEYFDV	SASQGISNYLN	DTSILYS	QQYSNLPYT
		523	524	525	526	527	528
17	CD8B273	GYTFTEYTIH	WFYPGTGSIK	HEDNHYYDGNSWFAY	RASGNIHNYLA	NAKTLAD	QHFWSTPYT
		557	558	559	560	561	562

18	CD8B288	GYTFTEYTIH	WFYPGNGNMR	YEDNHYYDGASWFAY	RASGNIHNYLA	NAKTLAD	QHFWSTPFT
		591	592	593	594	595	596
19	CD8B292	GFNFKDDYIY	WIDPENGATE	HDYGYAMDY	TASSSVSSSYLH	STSNLAS	HQYHRSPLT
		625	626	627	628	629	630
20	CD8B303	GFSLSIYSIH	MIWGGGSTD	NPHHYGGSTGAMDY	KASQDIKKYMA	YTSSLQP	LQYDNLFT
		659	660	661	662	663	664
21	CD8B304	GFSLSTSGMNVG	HIWWDDDKY	RGNYGNYEFAY	RASQDIRNYLN	HTSRLHS	QQGNTLPWT
		693	694	695	696	697	698
22	CD8B312	GYTFTSFWMH	NVDPSDSQTH	STYYRYDGPFTY	RASQSINNNLH	YTSQSIS	QQSNSWPLT
		727	728	729	730	731	732
23	CD8B347	GYTFTSYWMN	AVNPSNSYTE	SGLYNTNHLAWFAY	RASGNIHNYLA	NAETLAD	QHFWNNPLT
		761	762	763	764	765	766
24	CD8B350	GYTFAAYWIN	SINPSNGYTE	SGLYYTNHLAWCPY	RASGNIHNYLA	NAETLAD	QHFWNSPLT
		795	796	797	798	799	800
25	CD8B356	GYSITSGYYWN	YISYDGSNN	NHGDAMDY	KASQNVGTAVA	SASYRYT	QQYSSYLT
		829	830	831	832	833	834
26	CD8B369	GFTFTNTYIS	WIYTGTGGTW	TNWDWYFDV	RASENIYSYLA	YAKTLTD	QHHYGRPYT
		863	864	865	866	867	868
27	CD8B371	GFTFSDYYMA	HINYDGSITY	EDYSNYGFAY	HASQNINVWLS	KASNLHT	QQGQSYPLT
		897	898	899	900	901	902
28	CD8B182	GYTFTSYWMN	AVNPTNYYTE	SGLYNTNHLAWFAY	RASENIHNYLA	NAKTLAN	QHFWTTPLT
		931	932	933	934	935	936
29	CD8B205	GYSFNSYWMH	NIDPSDSETH	VYYSYYSYDATYFDY	RASENIYSYLA	NAKTLAE	QHHYTTPLT
		965	966	967	968	969	970
30	CD8B223	GFSLTSYSVH	VIWAGGSTN	HSYYSFDAFDY	KASQNVNTDVA	SASYRYS	QQCNSYPLT
		999	1000	1001	1002	1003	1004
31	CD8B234	GYSITSGYYWN	YINYDGRNN	DQGYSKFYFDY	KASEDIYNRLA	GATSLET	QQYWSFPRT
		1033	1034	1035	1036	1037	1038
32	CD8B251	GFSLTTYAVH	VIWSGGSTD	HSYYHYNAMDN	KASQNVGTAVA	SASNRYT	QQYSSYPFT
		1067	1068	1069	1070	1071	1072
33	CD8B269	GYSITSGYYWN	YISYDGSNN	NHGDAMDH	KASQNVGTDVA	SASYRYS	QQYKSYPLT
		1101	1102	1103	1104	1105	1106
34	CD8B290	GFSLSRYSVH	MIWGGGSTD	IYFDNYVGFAY	KASQDVGTVVA	WTSTRHT	QQYSSYPYT
		1135	1136	1137	1138	1139	1140
35	CD8B310	GFSLTNYAVH	VIWTDGSTD	NNGYFPAFFAY	RSSQTIVHSNGNTYLE	KVSNRFS	FQGSHAPFT
		1169	1170	1171	1172	1173	1174
36	CD8B352	GYSITSGYYWN	YINYDGRNN	DQGYSKFYFDY	KASEDIYNRLA	GATSLET	QQYWSFPRT
		1203	1204	1205	1206	1207	1208

37	CD8B319	GYSFTAYYMH	EINPSAGGTT	WTNPFDY	KASQNVGTAVA	SASYRYT	QQYNNYLT	
		1237	1238	1239	1240	1241	1242	
38	CD8B194	GYTFTSYWIN	NIYPGSSSTN	ELGPYYRYSAMVY	KASQNVGTAVA	SASNRYT	QQYSSYPFT	
		1271	1272	1273	1274	1275	1276	
39	CD8B231	GYTFTNYWMH	NIDPSDSETH	GLTGTGHY	RASQDINIYLN	HTSRLHS	QQDNTLPYT	
		1305	1306	1307	1308	1309	1310	
40	CD8B238	GYTFTDYSMD	YIYTYSGGAG	DSSDYEFAY	KASQDIKSYLS	RANRLVD	LQYDEFRT	
		1339	1340	1341	1342	1343	1344	
41	CD8B255	GFSLNTSGMGVS	HIFWDDDKR	RDGYGDYAYFDV	RASENIYSDLA	AATILTD	QHFWGTPWT	
		1373	1374	1375	1376	1377	1378	
42	CD8B324	GYTSTSHWIH	NIYPGSSSTN	HSPGHRDYAMDY	KASQNVGTAVA	SASNRYT	QQYSTYPLT	
		1407	1408	1409	1410	1411	1412	
43	CD8B337	GFSLSTSGMGVS	HIFWDDDRR	RVGYGDYAYFDV	RASENIYSDLA	AATNLAD	QHFWGTPWT	
		1441	1442	1443	1444	1445	1446	
44	CD8B344	GYSFTNYWIN	NIYPGSDSSN	EEADYRYTWFVY	KASQNVGTAVA	SASNRYT	QQYSSYPLT	
		1475	1476	1477	1478	1479	1480	
45	CD8B264	GYSFTSYWIN	NIYPGSSSTN	EEYSYKSSWFAY	KASQNVGTAVA	SASNRYN	QQYSTYPYT	
		1509	1510	1511	1512	1513	1514	
46	CD8B318	GYTFTSYWIS	NIYPGSSSSN	EEYSYFPSWFAY	KASQNVGTAVA	SASNRYT	QQYSTYPFT	
		1543	1544	1545	1546	1547	1548	
47	CD8B333	GYSFASFWIN	NIYPGSSSTN	EEYSYKSSWFAY	KASQNVGTAVA	SASNRYN	QQYSTYPYT	
		1577	1578	1579	1580	1581	1582	
48	CD8B366	GFNIKDDYIH	RIDPANGNPR	DDEGYYYFDV	RASKSISKYLA	SGSTLQS	QQHNEYPLT	
		1611	1612	1613	1614	1615	1616	
49	CD8B368	GYTFTSYWIN	NIYPFSSSTN	EEFSHYPSWFAY	KASQNVGIAVA	SASNRYT	QQYSTDPYT	
		1645	1646	1647	1648	1649	1650	
50	CD8B370	GYTFTSYWIN	NIYPGSSSTN	ELGAYYHYSAMDY	KASQNVGTAVA	SASNRYT	QQYSIYPFT	
		1679	1680	1681	1682	1683	1684	
51	CD8B186	GYIFTSYWMH	NINPSSGYAV	RVFYGDSWFAY	RASGNIHNYLA	NAKTLAD	QHFWSTTWT	
		1713	1714	1715	1716	1717	1718	
52	CD8B190	GYSFTSYYMH	YIDPFNGNTN	PNSNYVGTWFAY	HASQNINVWLS	KASNLHT	QQGQSFPFT	
		1747	1748	1749	1750	1751	1752	
53	CD8B192	GYTFTDYYMN	VINPYNGGTT	NYGAMDS	RASGNIHNYLA	NAKTLAD	QHFWITPPT	
		1781	1782	1783	1784	1785	1786	
54	CD8B193	GYKFTDYYMN	DINPNGGGTS	TSGTDWYFDV	KASQNVGTAVA	SASNRYT	QQYSSYPFT	
		1815	1816	1817	1818	1819	1820	
55	CD8B214	GYTFTTAGIQ	WINTHAGESK	SGDYDGSHPFAY	RASQDIRPYLN	YTSRLHS	QQDNTLPYT	
		1849	1850	1851	1852	1853	1854	

56	CD8B230	GYTFTDYYMN	DINPNGGGTS	TSGTDWYFDV	KASQNVGTAVA	STSNRYT	QQYSIYPFT	
		1883	1884	1885	1886	1887	1888	
57	CD8B245	GFTFTDYYMS	LSRNKGNGYTT E	TVTGTLFYYALDY	RASENIYSYLA	NAKTLAA	QHHYGTPLT	
		1917	1918	1919	1920	1921	1922	
58	CD8B248	GYTFTTYTMH	YINPSSGYTK	LWAY	RSSQSLVHSSGNTYLH	KGSNRFS	SQSTHVPFT	
		1951	1952	1953	1954	1955	1956	
59	CD8B250	GFSLSNYVVH	VIWTDGSTD	NNGYFPAFFAY	KASQNVDTDIT	SASYRYS	QQYNSYPLT	
		1985	1986	1987	1988	1989	1990	
60	CD8B254	GYTFSSYWIT	DIYPGSGSTN	ESITTRITPFDH	RSSQSLVHSSGNTYLH	KGSNRFS	SQSTHVPFT	
		2019	2020	2021	2022	2023	2024	
61	CD8B261	GYTFNSYWIN	NIYPGSSSTN	ELGGYYRYNAMDY	KASQDINRYLS	RANTLVD	LQYDEFPYT	
		2053	2054	2055	2056	2057	2058	
62	CD8B311	GYTFTSYWMH	MIHPNSGSTN	CGYDGAWFAY	SASQGISNCLN	YTSSLHS	QQYSKVPYT	
		2087	2088	2089	2090	2091	2092	
63	CD8B340	GYTFTNYWMQ	EIDPSDTFTN	GDWDRDWYFDV	KSSQSLLYSDGKTYLN	LVSKLDS	LQATHFPHT	
		2121	2122	2123	2124	2125	2126	
64	CD8B362	GFNIKDTYMH	RIDPANGHTK	RFAY	RASHEISGYLS	AASTLDS	LQYSSYPYT	
		2155	2156	2157	2158	2159	2160	

Table 20. Contact CDR Amino Acid Sequences

#	Protein Name	HC Contact CDR1	HC Contact CDR2	HC Contact CDR3	LC Contact CDR1	LC Contact CDR2	LC Contact CDR3
1	CD8B191	TDYYMN	WIGRVIPSNGGTI	AREDYNNQGFFLDAMD	SDFLHWY	LLIKYASQSI	QNGHSFPY
		19	20	21	22	23	24
2	CD8B226	TDYYMN	WIGRIIPSNGATI	AREDYSNQGFFLDAMD	SHYLHWY	LLIKYASQSI	QNGHSFPY
		53	54	55	56	57	58
3	CD8B259	TDYYMN	WIGRVIPSNGGTI	AREDYGNQGFFLDAMD	SHFLHWY	LLIKYASQSI	QSGHSFPY
		87	88	89	90	91	92
4	CD8B298	TDYYMN	WIGRVIPNNGGTR	AREDFSNQGFFLDAMD	SDYLHWY	LLIKYASQSI	QNGHSFPY
		121	122	123	124	125	126
5	CD8B342	TDYYVN	WIGRVIPNNGNVI	TREDYSNQGFFLDAMD	SNYLHWY	LLIKYASQSI	QNGHSFPY
		155	156	157	158	159	160
6	CD8B364	TSYWMH	WIGEINPSNGDSY	TRSMYYDGRAGA	DDDMNWY	LLISEGNTLR	LQSDNMPL
		189	190	191	192	193	194
7	CD8B200	TNYWIH	WIGNIDPSDSETH	ASGLTGTGY	SPYLNWY	LLIYYTSKLH	QQDNTLPY
		223	224	225	226	227	228
8	CD8B247	TDYYMN	WIGRVIPNNGGTI	AREDYSNQGFFLDAMD	SHFLHWY	LLIKYASQSI	QSGHSFPY
		257	258	259	260	261	262
9	CD8B265	TDYYMN	WIGRVIPRNGATT	AREDFSNQGFFLDAMD	SHYLHWY	LLIKYASQSI	QNGHSFPY
		291	292	293	294	295	296
10	CD8B270	TNYWMH	WIGNIDPSDSETH	ASGLTGTGY	RPYLNWY	LLIYFTSKLH	QQDNTLPY
		325	326	327	328	329	330
11	CD8B213	TDYYMD	WIGYIYPNNGITS	ARSIYYDHGGGFP	DKYVAWY	ALIYSASYRY	QQYNTYP
		359	360	361	362	363	364
12	CD8B240	TDYYMN	WIGRVIPSNGGTI	AREDYNNQGFFLDAMD	SDFLHWY	LLIKYASQSI	QNGHSFPY
		393	394	395	396	397	398
13	CD8B361	TDYYMD	WIGYIYPNNGDTR	ARSIYYDHGGGFP	GTYVAWY	ALIYSASYRY	QQYNSYP
		427	428	429	430	431	432
14	CD8B246	STSGMNVG	WLAHIWWDDDKY	ARRGNYGNYEFA	RNYLNWY	LLIYHTSRLH	QQGNTLPW
		461	462	463	464	465	466
15	CD8B268	TVYTIH	WIGWFYPGSGNIK	ARHEDNHYYDGNSWFA	HNYLAWF	LLVYNAKTLA	QHFWNTPY
		495	496	497	498	499	500
16	CD8B271	SIYSIH	WLGMIWGGGDTD	ARNPHYYGGTYEYFD	SNYLNWY	LLIYDTSILY	QQYSNLPY
		529	530	531	532	533	534
17	CD8B273	TEYTIH	WIGWFYPGTGSIK	ARHEDNHYYDGNSWFA	HNYLAWF	LLVYNAKTLA	QHFWSTPY
		563	564	565	566	567	568

18	CD8B288	TEYTIH	WIGWFYPGNGNMR	ARYEDNHYYDGASWFA	HNYLAWF	LLVYNAKTLA	QHFWSTPF
		597	598	599	600	601	602
19	CD8B292	KDDYIY	WIGWIDPENGATE	SLHDYGYAMD	SSSYLHWY	LWIYSTSNLA	HQYHRSPL
		631	632	633	634	635	636
20	CD8B303	SIYSIH	WLGMIWGGGSTD	ARNPHHYGGSTGAMD	KKYMAWY	LLIHYTSSLQ	LQYDNLF
		665	666	667	668	669	670
21	CD8B304	STSGMNVG	WLAHIWWDDDKY	ARRGNYGNYEFA	RNYLNWY	LLIYHTSRLH	QQGNTLPW
		699	700	701	702	703	704
22	CD8B312	TSFWMH	WIGNVDPSDSQTH	ARSTYYRYDGPFT	NNNLHWY	LLIKYTSQSI	QQSNSWPL
		733	734	735	736	737	738
23	CD8B347	TSYWMN	WIGAVNPSNSYTE	ARSGLYNTNHLAWFA	HNYLAWY	LLVFNAETLA	QHFWNNPL
		767	768	769	770	771	772
24	CD8B350	AAYWIN	WIGSINPSNGYTE	SRSGLYYTNHLAWCP	HNYLAWY	VLVYNAETLA	QHFWNSPL
		801	802	803	804	805	806
25	CD8B356	TSGYYWN	WMGYISYDGSNN	VRNHGDAMD	GTAVAWY	LLIYSASYRY	QQYSSYL
		835	836	837	838	839	840
26	CD8B369	TNTYIS	WIAWIYTGTGGTW	ARTNWDWYFD	YSYLAWY	LLVYYAKTLT	QHHYGRPY
		869	870	871	872	873	874
27	CD8B371	SDYYMA	WVAHINYDGSITY	AREDYSNYGFA	NVWLSWY	LLIYKASNLH	QQGQSYPL
		903	904	905	906	907	908
28	CD8B182	TSYWMN	WIGAVNPTNYYTE	ARSGLYNTNHLAWFA	HNYLAWY	LLVYNAKTLA	QHFWTTPL
		937	938	939	940	941	942
29	CD8B205	NSYWMH	WIGNIDPSDSETH	ARVYYSYYSYDATYFD	YSYLAWY	LLVYNAKTLA	QHHYTTPL
		971	972	973	974	975	976
30	CD8B223	TSYSVH	WLGVIWAGGSTN	AKHSYYSFDAFD	NTDVAWY	ALIYSASYRY	QQCNSYPL
		1005	1006	1007	1008	1009	1010
31	CD8B234	TSGYYWN	WMGYINYDGRNN	SRDQGYSKFYFD	YNRLAWY	LLISGATSLE	QQYWSFPR
		1039	1040	1041	1042	1043	1044
32	CD8B251	TTYAVH	WLGVIWSGGSTD	ARHSYYHYNAMD	GTAVAWY	LLIYSASNRY	QQYSSYPF
		1073	1074	1075	1076	1077	1078
33	CD8B269	TSGYYWN	WMGYISYDGSNN	VRNHGDAMD	GTDVAWY	ALIYSASYRY	QQYKSYPL
		1107	1108	1109	1110	1111	1112
34	CD8B290	SRYSVH	WLGMIWGGGSTD	ARIYFDNYVGFA	GTVVAWY	LLIFWTSTRH	QQYSSYPY
		1141	1142	1143	1144	1145	1146
35	CD8B310	TNYAVH	WLGVIWTDGSTD	ARNNGYFPAFFA	VHSNGNTYLE WY	LLMYKVSNRF	FQGSHAPF
		1175	1176	1177	1178	1179	1180
36	CD8B352	TSGYYWN	WMGYINYDGRNN	ARDQGYSKFYFD	YNRLAWY	LLISGATSLE	QQYWSFPR

		1209	1210	1211	1212	1213	1214
37	CD8B319	TAYYMH	WIGEINPSAGGTT	ARWTNPFD	GTAVAWY	LLIYSASYRY	QQYNNYL
		1243	1244	1245	1246	1247	1248
38	CD8B194	TSYWIN	WIGNIYPGSSSTN	ARELGPYYRYSAMV	GTAVAWY	LLIYSASNRY	QQYSSYPF
		1277	1278	1279	1280	1281	1282
39	CD8B231	TNYWMH	WIGNIDPSDSETH	ASGLTGTGH	NIYLNWY	CLIYHTSRLH	QQDNTLPY
		1311	1312	1313	1314	1315	1316
40	CD8B238	TDYSMD	WIGYIYTYSGGAG	ARDSSDYEFA	KSYLSWF	TLIYRANRLV	LQYDEFR
		1345	1346	1347	1348	1349	1350
41	CD8B255	NTSGMGVS	WLAHIFWDDDKR	ARRDGYGDYAYFD	YSDLAWY	LLVYAATILT	QHFWGTPW
		1379	1380	1381	1382	1383	1384
42	CD8B324	TSHWIH	WIGNIYPGSSSTN	ARHSPGHRDYAMD	GTAVAWY	LLIASASNRY	QQYSTYPL
		1413	1414	1415	1416	1417	1418
43	CD8B337	STSGMGVS	WLAHIFWDDDRR	ARRVGYGDYAYFD	YSDLAWY	LLVYAATNLA	QHFWGTPW
		1447	1448	1449	1450	1451	1452
44	CD8B344	TNYWIN	WIGNIYPGSDSSN	AREEADYRYTWFV	GTAVAWY	LLIYSASNRY	QQYSSYPL
		1481	1482	1483	1484	1485	1486
45	CD8B264	TSYWIN	WIGNIYPGSSSTN	AREEYSYKSSWFA	GTAVAWY	LLIYSASNRY	QQYSTYPY
		1515	1516	1517	1518	1519	1520
46	CD8B318	TSYWIS	WIGNIYPGSSSSN	AREEYSYFPSWFA	GTAVAWF	LLIYSASNRY	QQYSTYPF
		1549	1550	1551	1552	1553	1554
47	CD8B333	ASFWIN	WIGNIYPGSSSTN	AREEYSYKSSWFA	GTAVAWY	LLIYSASNRY	QQYSTYPY
		1583	1584	1585	1586	1587	1588
48	CD8B366	KDDYIH	WIGRIDPANGNPR	ARDDEGYYYFD	SKYLAWY	VLIYSGSTLQ	QQHNEYPL
		1617	1618	1619	1620	1621	1622
49	CD8B368	TSYWIN	WIGNIYPFSSSTN	AREEFSHYPSWFA	GIAVAWF	LLIYSASNRY	QQYSTDPY
		1651	1652	1653	1654	1655	1656
50	CD8B370	TSYWIN	WIGNIYPGSSSTN	TRELGAYYHYSAMD	GTAVAWY	LLIYSASNRY	QQYSIYPF
		1685	1686	1687	1688	1689	1690
51	CD8B186	TSYWMH	WIGNINPSSGYAV	ARRVFYGDSWFA	HNYLAWY	LLVYNAKTLA	QHFWSTTW
		1719	1720	1721	1722	1723	1724
52	CD8B190	TSYYMH	WIGYIDPFNGNTN	ASPNSNYVGTWFA	NVWLSWY	LLIYKASNLH	QQGQSFPF
		1753	1754	1755	1756	1757	1758
53	CD8B192	TDYYMN	WIGVINPYNGGTT	ARNYGAMD	HNYLAWY	LLVSNAKTLA	QHFWITPP
		1787	1788	1789	1790	1791	1792
54	CD8B193	TDYYMN	WIGDINPNGGGTS	ARTSGTDWYFD	GTAVAWY	LLIYSASNRY	QQYSSYPF
		1821	1822	1823	1824	1825	1826
55	CD8B214	TTAGIQ	WIGWINTHAGESK	ARSGDYDGSHPFA	RPYLNWY	LLIYYTSRLH	QQDNTLPY

		1855	1856	1857	1858	1859	1860
56	CD8B230	TDYYMN	WIGDINPNGGGTS	ARTSGTDWYFD	GTAVAWY	LLIYSTSNRY	QQYSIYPF
		1889	1890	1891	1892	1893	1894
57	CD8B245	TDYYMS	WLALSRNKGNGYTT E	ARTVTGTLFYYALD	YSYLAWY	FLVYNAKTLA	QHHYGTPL
		1923	1924	1925	1926	1927	1928
58	CD8B248	TTYTMH	WIGYINPSSGYTK	ARLWA	VHSSGNTYLH WY	LLIYKGSNRF	SQSTHVPF
		1957	1958	1959	1960	1961	1962
59	CD8B250	SNYVVH	WLGVIWTDGSTD	ARNNGYFPAFFA	DTDITWY	ALIYSASYRY	QQYNSYPL
		1991	1992	1993	1994	1995	1996
60	CD8B254	SSYWIT	WVGDIYPGSGSTN	ARESITTRITPFD	VHSSGNTYLH WY	LLIYKGSNRF	SQSTHVPF
		2025	2026	2027	2028	2029	2030
61	CD8B261	NSYWIN	WIGNIYPGSSSTN	ARELGGYYRYNAMD	NRYLSWF	TLIYRANTLV	LQYDEFPY
		2059	2060	2061	2062	2063	2064
62	CD8B311	TSYWMH	WIGMIHPNSGSTN	ARCGYDGAWFA	SNCLNWY	LLIHYTSSLH	QQYSKVPY
		2093	2094	2095	2096	2097	2098
63	CD8B340	TNYWMQ	WIGEIDPSDTFTN	ARGDWDRDWYFD	LYSDGKTYLN WL	LLIYLVSKLD	LQATHFPH
		2127	2128	2129	2130	2131	2132
64	CD8B362	KDTYMH	WIGRIDPANGHTK	AIRFA	SGYLSWL	RLIYAASTLD	LQYSSYPY
		2161	2162	2163	2164	2165	2166

Table 21. IMGT CDR Amino Acid Sequences

#	Protein Name	HC IMGT CDR1	HC IMGT CDR2	HC IMGT CDR3	LC IMGT CDR1	LC IMGT CDR2	LC IMGT CDR3
1	CD8B191	GYTFTDYY	VIPSNGGT	AREDYNNQGFFLDAMDY	QSISDF	YAS	QNGHSFPYT
		25	26	27	28	29	30
2	CD8B226	GYTFTDYY	IIPSNGAT	AREDYSNQGFFLDAMDY	QSISHY	YAS	QNGHSFPYT
		59	60	61	62	63	64
3	CD8B259	GYTFTDYY	VIPSNGGT	AREDYGNQGFFLDAMDY	QSISHF	YAS	QSGHSFPYT
		93	94	95	96	97	98
4	CD8B298	GYTFTDYY	VIPNNGGT	AREDFSNQGFFLDAMDY	QTISDY	YAS	QNGHSFPYT
		127	128	129	130	131	132
5	CD8B342	GYTFTDYY	VIPNNGNV	TREDYSNQGFFLDAMDY	QTISNY	YAS	QNGHSFPYT
		161	162	163	164	165	166
6	CD8B364	GYTFTSYW	INPSNGDS	TRSMYYDGRAGAY	TDIDDD	EGN	LQSDNMPLT
		195	196	197	198	199	200
7	CD8B200	GYTFTNYW	IDPSDSET	ASGLTGTGYY	QDISPY	YTS	QQDNTLPYT
		229	230	231	232	233	234
8	CD8B247	GYTFTDYY	VIPNNGGT	AREDYSNQGFFLDAMDY	QTISHF	YAS	QSGHSFPYT
		263	264	265	266	267	268
9	CD8B265	GYSFTDYY	VIPRNGAT	AREDFSNQGFFLDAMDY	QSISHY	YAS	QNGHSFPYT
		297	298	299	300	301	302
10	CD8B270	GYTFTNYW	IDPSDSET	ASGLTGTGYY	QDIRPY	FTS	QQDNTLPYT
		331	332	333	334	335	336
11	CD8B213	GYIFTDYY	IYPNNGIT	ARSIYYDHGGGFPY	QNVDKY	SAS	QQYNTYPS
		365	366	367	368	369	370
12	CD8B240	GYTFTDYY	VIPSNGGT	AREDYNNQGFFLDAMDY	QSISDF	YAS	QNGHSFPYT
		399	400	401	402	403	404
13	CD8B361	GYTFTDYY	IYPNNGDT	ARSIYYDHGGGFPY	QNVGTY	SAS	QQYNSYPT
		433	434	435	436	437	438
14	CD8B246	GFSLSTSGMN	IWWDDDK	ARRGNYGNYEFAY	QDIRNY	HTS	QQGNTLPWT
		467	468	469	470	471	472
15	CD8B268	GYTFTVYT	FYPGSGNI	ARHEDNHYYDGNSWFAY	GNIHNY	NAK	QHFWNTPYT
		501	502	503	504	505	506
16	CD8B271	GFSLSIYS	IWGGGDT	ARNPHYYGGTYEYFDV	QGISNY	DTS	QQYSNLPYT
		535	536	537	538	539	540
17	CD8B273	GYTFTEYT	FYPGTGSI	ARHEDNHYYDGNSWFAY	GNIHNY	NAK	QHFWSTPYT
		569	570	571	572	573	574

18	CD8B288	GYTFTEYT	FYPGNGNM	ARYEDNHYYDGASWFAY	GNIHNY	NAK	QHFWSTPFT
		603	604	605	606	607	608
19	CD8B292	GFNFKDDY	IDPENGAT	SLHDYGYAMDY	SSVSSSY	STS	HQYHRSPLT
		637	638	639	640	641	642
20	CD8B303	GFSLSIYS	IWGGGST	ARNPHHYGGSTGAMDY	QDIKKY	YTS	LQYDNLFT
		671	672	673	674	675	676
21	CD8B304	GFSLSTSGMN	IWWDDDK	ARRGNYGNYEFAY	QDIRNY	HTS	QQGNTLPWT
		705	706	707	708	709	710
22	CD8B312	GYTFTSFW	VDPSDSQT	ARSTYYRYDGPFTY	QSINNN	YTS	QQSNSWPLT
		739	740	741	742	743	744
23	CD8B347	GYTFTSYW	VNPSNSYT	ARSGLYNTNHLAWFAY	GNIHNY	NAE	QHFWNNPLT
		773	774	775	776	777	778
24	CD8B350	GYTFAAYW	INPSNGYT	SRSGLYYTNHLAWCPY	GNIHNY	NAE	QHFWNSPLT
		807	808	809	810	811	812
25	CD8B356	GYSITSGYY	ISYDGSN	VRNHGDAMDY	QNVGTA	SAS	QQYSSYLT
		841	842	843	844	845	846
26	CD8B369	GFTFTNTY	IYTGTGGT	ARTNWDWYFDV	ENIYSY	YAK	QHHYGRPYT
		875	876	877	878	879	880
27	CD8B371	GFTFSDYY	INYDGSIT	AREDYSNYGFAY	QNINVW	KAS	QQGQSYPLT
		909	910	911	912	913	914
28	CD8B182	GYTFTSYW	VNPTNYYT	ARSGLYNTNHLAWFAY	ENIHNY	NAK	QHFWTTPLT
		943	944	945	946	947	948
29	CD8B205	GYSFNSYW	IDPSDSET	ARVYYSYYSYDATYFDY	ENIYSY	NAK	QHHYTTPLT
		977	978	979	980	981	982
30	CD8B223	GFSLTSYS	IWAGGST	AKHSYYSFDAFDY	QNVNTD	SAS	QQCNSYPLT
		1011	1012	1013	1014	1015	1016
31	CD8B234	GYSITSGYY	INYDGRN	SRDQGYSKFYFDY	EDIYNR	GAT	QQYWSFPRT
		1045	1046	1047	1048	1049	1050
32	CD8B251	GFSLTTYA	IWSGGST	ARHSYYHYNAMDN	QNVGTA	SAS	QQYSSYPFT
		1079	1080	1081	1082	1083	1084
33	CD8B269	GYSITSGYY	ISYDGSN	VRNHGDAMDH	QNVGTD	SAS	QQYKSYPLT
		1113	1114	1115	1116	1117	1118
34	CD8B290	GFSLSRYS	IWGGGST	ARIYFDNYVGFAY	QDVGTV	WTS	QQYSSYPYT
		1147	1148	1149	1150	1151	1152
35	CD8B310	GFSLTNYA	IWTDGST	ARNNGYFPAFFAY	QTIVHSNGNTY	KVS	FQGSHAPFT
		1181	1182	1183	1184	1185	1186
36	CD8B352	GYSITSGYY	INYDGRN	ARDQGYSKFYFDY	EDIYNR	GAT	QQYWSFPRT
		1215	1216	1217	1218	1219	1220

37	CD8B319	GYSFTAYY	INPSAGGT	ARWTNPFDY	QNVGTA	SAS	QQYNNYLT	
		1249	1250	1251	1252	1253	1254	
38	CD8B194	GYTFTSYW	IYPGSSST	ARELGPYYRYSAMVY	QNVGTA	SAS	QQYSSYPFT	
		1283	1284	1285	1286	1287	1288	
39	CD8B231	GYTFTNYW	IDPSDSET	ASGLTGTGHY	QDINIY	HTS	QQDNTLPYT	
		1317	1318	1319	1320	1321	1322	
40	CD8B238	GYTFTDYS	IYTYSGGA	ARDSSDYEFAY	QDIKSY	RAN	LQYDEFRT	
		1351	1352	1353	1354	1355	1356	
41	CD8B255	GFSLNTSGMG	IFWDDDK	ARRDGYGDYAYFDV	ENIYSD	AAT	QHFWGTPWT	
		1385	1386	1387	1388	1389	1390	
42	CD8B324	GYTSTSHW	IYPGSSST	ARHSPGHRDYAMDY	QNVGTA	SAS	QQYSTYPLT	
		1419	1420	1421	1422	1423	1424	
43	CD8B337	GFSLSTSGMG	IFWDDDR	ARRVGYGDYAYFDV	ENIYSD	AAT	QHFWGTPWT	
		1453	1454	1455	1456	1457	1458	
44	CD8B344	GYSFTNYW	IYPGSDSS	AREEADYRYTWFVY	QNVGTA	SAS	QQYSSYPLT	
		1487	1488	1489	1490	1491	1492	
45	CD8B264	GYSFTSYW	IYPGSSST	AREEYSYKSSWFAY	QNVGTA	SAS	QQYSTYPYT	
		1521	1522	1523	1524	1525	1526	
46	CD8B318	GYTFTSYW	IYPGSSSS	AREEYSYFPSWFAY	QNVGTA	SAS	QQYSTYPFT	
		1555	1556	1557	1558	1559	1560	
47	CD8B333	GYSFASFW	IYPGSSST	AREEYSYKSSWFAY	QNVGTA	SAS	QQYSTYPYT	
		1589	1590	1591	1592	1593	1594	
48	CD8B366	GFNIKDDY	IDPANGNP	ARDDEGYYYFDV	KSISKY	SGS	QQHNEYPLT	
		1623	1624	1625	1626	1627	1628	
49	CD8B368	GYTFTSYW	IYPFSSST	AREEFSHYPSWFAY	QNVGIA	SAS	QQYSTDPYT	
		1657	1658	1659	1660	1661	1662	
50	CD8B370	GYTFTSYW	IYPGSSST	TRELGAYYHYSAMDY	QNVGTA	SAS	QQYSIYPFT	
		1691	1692	1693	1694	1695	1696	
51	CD8B186	GYIFTSYW	INPSSGYA	ARRVFYGDSWFAY	GNIHNY	NAK	QHFWSTTWT	
		1725	1726	1727	1728	1729	1730	
52	CD8B190	GYSFTSYY	IDPFNGNT	ASPNSNYVGTWFAY	QNINVW	KAS	QQGQSFPFT	
		1759	1760	1761	1762	1763	1764	
53	CD8B192	GYTFTDYY	INPYNGGT	ARNYGAMDS	GNIHNY	NAK	QHFWITPPT	
		1793	1794	1795	1796	1797	1798	
54	CD8B193	GYKFTDYY	INPNGGGT	ARTSGTDWYFDV	QNVGTA	SAS	QQYSSYPFT	
		1827	1828	1829	1830	1831	1832	
55	CD8B214	GYTFTTAG	INTHAGES	ARSGDYDGSHPFAY	QDIRPY	YTS	QQDNTLPYT	
		1861	1862	1863	1864	1865	1866	

56	CD8B230	GYTFTDYY	INPNGGGT	ARTSGTDWYFDV	QNVGTA	STS	QQYSIYPFT	
		1895	1896	1897	1898	1899	1900	
57	CD8B245	GFTFTDYY	SRNKGNGYTT	ARTVTGTLFYYALDY	ENIYSY	NAK	QHHYGTPLT	
		1929	1930	1931	1932	1933	1934	
58	CD8B248	GYTFTTYT	INPSSGYT	ARLWAY	QSLVHSSGNTY	KGS	SQSTHVPFT	
		1963	1964	1965	1966	1967	1968	
59	CD8B250	GFSLSNYV	IWTDGST	ARNNGYFPAFFAY	QNVDTD	SAS	QQYNSYPLT	
		1997	1998	1999	2000	2001	2002	
60	CD8B254	GYTFSSYW	IYPGSGST	ARESITTRITPFDH	QSLVHSSGNTY	KGS	SQSTHVPFT	
		2031	2032	2033	2034	2035	2036	
61	CD8B261	GYTFNSYW	IYPGSSST	ARELGGYYRYNAMDY	QDINRY	RAN	LQYDEFPYT	
		2065	2066	2067	2068	2069	2070	
62	CD8B311	GYTFTSYW	IHPNSGST	ARCGYDGAWFAY	QGISNC	YTS	QQYSKVPYT	
		2099	2100	2101	2102	2103	2104	
63	CD8B340	GYTFTNYW	IDPSDTFT	ARGDWDRDWYFDV	QSLLYSDGKTY	LVS	LQATHFPHT	
		2133	2134	2135	2136	2137	2138	
64	CD8B362	GFNIKDTY	IDPANGHT	AIRFAY	HEISGY	AAS	LQYSSYPYT	
		2167	2168	2169	2170	2171	2172	

4.2: EVALUATION OF BINDING TO HUMAN CD8+ T CELLS AND BIOPHYSICAL CHARACTERIZATION OF CD8 ANTIBODIES

[00699] ***Cell binding:*** Twenty nM antibody was incubated with human pan T cell in assay media (RPMI 1640 + 10% HI FBS+ Pen/strep) for 1 hour at 37°C. Secondary antibodies were A647-conjugated goat anti human IgG Fc antibody at 2 µg/mL, and A488-conjugated mouse anti-human CD4 at 1 µg/mL in staining buffer. Live cells were also gated based on OKT8 control mAb binding. Percent CD8 positive population was calculated by percentage of CD8-positive cell count/live cell count. Results are shown in **Table 22** and are reported as Geomean ratios from CD4-negative population (% CD8-positive population).

[00700] ***Cross-interaction chromatography (CIC):*** CIC was conducted as previously described (Jacobs *et al.* (2010) *Pharm. Res.* 27(1):65-71). Results are shown in **Table 22**.

[00701] ***Thermal unfolding and aggregation (Tm/Tagg):*** Thermal unfolding and aggregation was measured 20°C-95°C in 1 C/min ramp using Nanodsf Nanotemper's PROMETHIUSNT.48 instrument. Samples of 20 µL (0.2 mg/mL) in PBS buffer were transferred to 384-well plate in duplicate. Data was analyzed using PR.THERMCONTROL software. Results are shown in **Table 22**.

[00702] **Table 22. Antibody Stability and Binding to Human Pan T Cells**

		Cell Binding to Human PanT	CIC	Protein Stability	
#	Protein Name	Signal/ Background (of CD4 negative population)	Peak Retention Time	Tm1 (°C)	Tagg (°C)
1	CD8B191	2440	4.32	70.3	76.6
2	CD8B226	1752	4.34	70.2	78.0
3	CD8B259	1934	4.41	70.5	76.8
4	CD8B298	306	4.29	70.6	76.2
5	CD8B342	1324	4.27	67.5	68.7
6	CD8B364	1562	4.24	65.3	70.7
7	CD8B200	1990	4.23	69.3	82.3
8	CD8B247	1646	4.31	70.1	77.4
9	CD8B265	2076	4.39	70.3	79.0
10	CD8B270	2497	4.32	70.1	79.7
11	CD8B213	827	4.51	67.8	69.9
12	CD8B240	1312	4.30	70.0	81.5
13	CD8B361	1051	4.65	71.1	74.4
14	CD8B246	1112	4.47	60.9	63.1

15	CD8B268	1173	4.44	69.6	72.4
16	CD8B271	911	4.34	69.1	80.4
17	CD8B273	938	4.27	73.0	76.9
18	CD8B288	934	4.32	71.0	73.5
19	CD8B292	910	4.23	68.1	69.2
20	CD8B303	1182	4.37	70.2	79.9
21	CD8B304	923	4.43	64.4	66.4
22	CD8B312	1087	4.29	71.3	78.0
23	CD8B347	1201	4.30	71.1	73.1
24	CD8B350	537	4.61		81.3
25	CD8B356	777	4.46	73.9	76.7
26	CD8B369	685	5.83	67.4	76.2
27	CD8B371	64	4.29	69.1	75.0
28	CD8B182	1490	4.58	70.7	77.8
29	CD8B205	655	4.77	68.9	72.2
30	CD8B223	489	4.46	68.3	74.3
31	CD8B234	856	5.16	67.7	69.0
32	CD8B251	37	5.30	69.4	73.0
33	CD8B269	26	4.28	69.8	81.4
34	CD8B290	1155	4.48	60.5	72.0
35	CD8B310	29	4.32	70.7	78.7
36	CD8B352	827	5.56	72.1	72.6
37	CD8B319	16	4.54	64.8	75.6
38	CD8B194	1972	4.81	69.8	87.2
39	CD8B231	1785	4.19	61.7	77.5
40	CD8B238	1	4.38	69.9	78.3
41	CD8B255	1317	4.25	69.5	78.4
42	CD8B324	1611	4.44	66.9	68.9
43	CD8B337	1983	4.42	68.8	73.2
44	CD8B344	1758	4.26	72.4	75.4
45	CD8B264	122	4.34	70.0	87.2
46	CD8B318	1613	4.78		78.0
47	CD8B333	1843	4.24	70.4	85.0
48	CD8B366	318	4.26	71.8	74.9
49	CD8B368	2007	4.46	70.5	74.7
50	CD8B370	1932	4.69	70.1	86.9
51	CD8B186	36	4.94	65.1	66.4
52	CD8B190	44	4.34	67.9	77.0
53	CD8B192	22	4.84	70.2	79.9
54	CD8B193	641	5.48	70.3	79.6
55	CD8B214	232	4.16	68.1	73.9
56	CD8B230	63	4.88	69.6	82.5
57	CD8B245	44	4.36	66.7	68.3
58	CD8B248	20	4.57	68.4	73.8
59	CD8B250	61	4.42	69.9	79.3
60	CD8B254	23	4.22	65.8	69.8
61	CD8B261	34	4.52	70.5	79.0
62	CD8B311	1	4.28	69.8	78.0

63	CD8B340	8	4.21	64.8	78.0
64	CD8B362	4	4.37	69.6	76.0

[00703] ***Protein binding kinetics by surface plasmon resonance (SPR).*** All 64 mAbs were captured at 1 μg/ml, with a final capture level ranging from 100 to 400 Rus. Binding to human CD8αβ heterodimer (R&D cat # 9358-CD) and hCD8αα homodimer (**Table 23**) at 11.1 nM, 33.3 nM and 100 nM was measured using a single cycle kinetics method with an association and dissociation of 3 and 10 minutes, respectively, using a flow rate of 50 μL/mL. Biacore 8k was utilized for these assays, and data was analyzed by modeling to a 1:1 binding equation. Results are shown in **Table 24**.

Table 23. CD8αα screening reagents

Name	Protein ID	Sequence	SEQ ID NO
Human CD8αα fused to human Fc	hCDaa	MAWVWTLLFLMAAAQSIQASQFRVSPLDR TWNLGETVELKCQVLLSNPTSGCSWLFQP RGAAASPTFLLYLSQNKPKAAEGLDTQRF SGKRLGDTFVLTLSDFRRENEGYYFCSAL SNSIMYFSHFVPVFLPAKPTTTPAPRPPT PAPTIASQPLSLRPEACRPAAGGAVHTRG LDFACDEPKSCDKTHTCPPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQY NSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPS RDELTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGK	2179

Table 24. Antibody Binding by SPR

		Protein binding by SPR to human CD8αα homodimer				Protein binding by SPR to human CD8 αβ heterodimer				Based on SPR Data
#	Protein Name	ka (1/Ms)	kd (1/s)	KD (M)	Comment	hCD8αβ ka (1/Ms)	hCD8α kd (1/s)	hCD8αβ KD (M)	hCD8αβ Comment	Predicted Epitope
1	CD8B191	1.23E+05	1.19E-04	9.68E-10		1.23E+05	1.19E-04	9.68E-10		CD8 α
2	CD8B226	1.55E+05	3.42E-04	2.21E-09		1.55E+05	3.42E-04	2.21E-09		CD8 α
3	CD8B259	2.09E+05	2.52E-04	1.20E-09		2.09E+05	2.52E-04	1.20E-09		CD8 α
4	CD8B298	1.32E+05	2.11E-04	1.60E-09		1.32E+05	2.11E-04	1.60E-09		CD8 α
5	CD8B342	1.48E+05	3.84E-04	2.59E-09		1.48E+05	3.84E-04	2.59E-09		CD8 α
6	CD8B364	1.43E+06	3.12E-02	2.19E-08		1.43E+06	3.12E-02	2.19E-08		CD8 α
7	CD8B200	3.32E+06	1.26E-04	3.80E-11		3.32E+06	1.26E-04	3.80E-11		CD8 α
8	CD8B247	2.73E+05	2.81E-04	1.03E-09		2.73E+05	2.81E-04	1.03E-09		CD8 α
9	CD8B265	1.68E+05	1.33E-04	7.91E-10		1.68E+05	1.33E-04	7.91E-10		CD8 α
10	CD8B270	2.41E+06	9.47E-05	3.93E-11		2.41E+06	9.47E-05	3.93E-11		CD8 α
11	CD8B213	-	-	-	Poor Fit, ~5 nM	-	-	-	Poor Fit, ~5 nM	CD8 α
12	CD8B240	-	-	-	Poor Fit, ~1 nM	-	-	-	Poor Fit, ~1 nM	CD8 α
13	CD8B361	-	-	-	Poor Fit, ~1 nM	-	-	-	Poor Fit, ~1 nM	CD8 α
14	CD8B246	-	-	-	Low/No Binding	-	-	-	Low/No Binding	CD8 β
15	CD8B268	-	-	-	Low/No Binding	-	-	-	Low/No Binding	CD8 β
16	CD8B271	-	-	-	Low/No Binding	-	-	-	Low/No Binding	CD8 β
17	CD8B273	-	-	-	Low/No Binding	-	-	-	Low/No Binding	CD8 β

18	CD8B288	-	-	-	Low/No Binding	-	-	Low/No Binding	CD8 β
19	CD8B292	-	-	-	Low/No Binding	-	-	Low/No Binding	CD8 β
20	CD8B303	-	-	-	Low/No Binding	-	-	Low/No Binding	CD8 β
21	CD8B304	-	-	-	Low/No Binding	-	-	Low/No Binding	CD8 β
22	CD8B312	-	-	-	Low/No Binding	-	-	Low/No Binding	CD8 β
23	CD8B347	-	-	-	Low/No Binding	-	-	Low/No Binding	CD8 β
24	CD8B350	-	-	-	Low/No Binding	-	-	Low/No Binding	CD8 β
25	CD8B356	-	-	-	Low/No Binding	-	-	Low/No Binding	CD8 β
26	CD8B369	-	-	-	Low/No Binding	-	-	Low/No Binding	CD8 β
27	CD8B371	-	-	-	Low/No Binding	-	-	Low/No Binding	CD8 β
28	CD8B182	-	-	-	Low/No Binding	-	-	Low/No Binding	CD8 β
29	CD8B205	-	-	-	Low/No Binding	-	-	Low/No Binding	CD8 β
30	CD8B223	-	-	-	Low/No Binding	-	-	Low/No Binding	CD8 β
31	CD8B234	-	-	-	Low/No Binding	-	-	Low/No Binding	CD8 β
32	CD8B251	-	-	-	Low/No Binding	-	-	Low/No Binding	CD8 β

33	CD8B269	-	-	-	Low/No Binding	-	-	Low/No Binding	CD8 β
34	CD8B290	-	-	-	Low/No Binding	-	-	Low/No Binding	CD8 β
35	CD8B310	-	-	-	Low/No Binding	-	-	Low/No Binding	CD8 β
36	CD8B352	-	-	-	Low/No Binding	-	-	Low/No Binding	CD8 β
37	CD8B319	-	-	-	Low/No Binding	-	-	Low/No Binding	CD8 β
38	CD8B194	-	-	-	Poor Fit, ~1 nM	-	-	Poor Fit, ~1 nM	CD8 α/β interface
39	CD8B231	-	-	-	Poor Fit, ~0.5 nM	-	-	Poor Fit, ~0.5 nM	CD8 α/β interface
40	CD8B238	-	-	-	Poor Fit, ~200 pM	-	-	Poor Fit, ~200 pM	CD8 α/β interface
41	CD8B255	-	-	-	Poor Fit, ~1 nM	-	-	Poor Fit, ~1 nM	CD8 α/β interface
42	CD8B324	-	-	-	Poor Fit, ~1 nM	-	-	Poor Fit, ~1 nM	CD8 α/β interface
43	CD8B337	-	-	-	Poor Fit, ~1 nM	-	-	Poor Fit, ~1 nM	CD8 α/β interface
44	CD8B344	-	-	-	Poor Fit, ~5 nM	-	-	Poor Fit, ~5 nM	CD8 α/β interface
45	CD8B264	-	-	-	Poor Fit, ~0.5 nM	-	-	Poor Fit, ~0.5 nM	CD8 α/β interface
46	CD8B318	-	-	-	Poor Fit, ~1 nM	-	-	Poor Fit, ~1 nM	CD8 α/β interface
47	CD8B333	-	-	-	Poor Fit, ~1 nM	-	-	Poor Fit, ~1 nM	CD8 α/β interface

48	CD8B366	-	-	-	Poor Fit, ~20 nM	-	-	Poor Fit, ~20 nM	CD8 α/β interface
49	CD8B368	-	-	-	Poor Fit, ~0.5 nM	-	-	Poor Fit, ~0.5 nM	CD8 α/β interface
50	CD8B370	-	-	-	Poor Fit, ~5 nM	-	-	Poor Fit, ~5 nM	CD8 α/β interface
51	CD8B186	-	-	-	Low/No Binding	-	-	Low/No Binding	-
52	CD8B190	-	-	-	Low/No Binding	-	-	Low/No Binding	-
53	CD8B192	-	-	-	Low/No Binding	-	-	Low/No Binding	-
54	CD8B193	-	-	-	Low/No Binding	-	-	Low/No Binding	-
55	CD8B214	-	-	-	Low/No Binding	-	-	Low/No Binding	-
56	CD8B230	-	-	-	Low/No Binding	-	-	Low/No Binding	-
57	CD8B245	-	-	-	Low/No Binding	-	-	Low/No Binding	-
58	CD8B248	-	-	-	Low/No Binding	-	-	Low/No Binding	-
59	CD8B250	-	-	-	Low/No Binding	-	-	Low/No Binding	-
60	CD8B254	-	-	-	Low/No Binding	-	-	Low/No Binding	-
61	CD8B261	-	-	-	Low/No Binding	-	-	Low/No Binding	-
62	CD8B311	-	-	-	Low/No Binding	-	-	Low/No Binding	-

63	CD8B340	-	-	-	Low/No Binding	-	-	Low/No Binding	-
64	CD8B362	-	-	-	Low/No Binding	-	-	Low/No Binding	-

* * * * *

[00704] It will be appreciated by those skilled in the art that changes could be made to the embodiments described above without departing from the broad inventive concept thereof. It is understood, therefore, that this invention is not limited to the particular embodiments disclosed, but it is intended to cover modifications within the spirit and scope of the present invention as defined by the present description.

We claim:

1. An isolated molecule, comprising: a first antigen binding domain and a second antigen binding domain, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds a T cell receptor (TCR) complex.
2. The isolated molecule of claim 1, further comprising a third antigen binding domain that specifically binds a third antigen.
3. The isolated molecule of claim 2, wherein the third antigen comprises an antigen expressed by an undesired cells.
4. The isolated molecule of any one of claims 1-3, wherein the isolated molecule activates or recruits $CD8^+$ cytotoxic T lymphocytes (CTLs) upon co-engagement of the TCR complex and CD8.
5. The isolated molecule of any one of claims 1-4, wherein the isolated molecule is unable to activate or recruit $CD8^+$ CTLs in the absence of co-engagement of the TCR complex and CD8.
6. The isolated molecule of any one of claims 1-5, wherein the first antigen binding domain specifically binds CD8 and the second antigen binding domain specifically binds the TCR complex with affinities that result in activation or recruitment of $CD8^+$ CTLs only upon co-engagement of the TCR complex and CD8.
7. The isolated molecule of any one of claims 1-6, wherein the first antigen binding domain, the second antigen binding domain or the third antigen binding domain comprises a scFv, a Fab, a Fab', a $F(ab')_2$, a Fd, a Fv, a domain antibody (dAb), a VHH, a heavy chain variable domain (VH), a light chain variable domain (VL), a non-antibody scaffold, or fragments thereof.
8. The isolated molecule of claim 7, wherein the first antigen binding domain comprises the Fab.
9. The isolated molecule of claim 7 or 8, wherein the second antigen binding domain comprises the scFv.
10. The isolated molecule of any one of claims 7-9, wherein the third antigen binding domain comprises the scFv.
11. The isolated molecule of any one of claims 1-10, comprising:

a) a first polypeptide comprising, from N- to C-terminus, the second antigen binding domain comprising the scFv, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain;

b) a second polypeptide comprising, from N- to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and

c) a third polypeptide comprising, from N- to C-terminus, the third antigen binding domain comprising the scFv and a Fc or a fragment of the Fc.

12. The isolated molecule of any one of claims 1-10, comprising:

a) a first polypeptide comprising, from N- to C-terminus, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain;

b) a second polypeptide comprising, from N- to C-terminus, a VL that is capable of specifically binding CD8, a CL domain and the second antigen binding domain comprising the scFv; and

c) a third polypeptide comprising, from N- to C-terminus, the third antigen binding domain comprising the scFv and a Fc or a fragment of the Fc.

13. The isolated molecule of any one of claims 1-10, comprising:

a) a first polypeptide comprising, from N- to C-terminus, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain, a CH3 domain and the second antigen binding domain comprising the scFv;

b) a second polypeptide comprising, from N- to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and

c) a third polypeptide comprising, from N- to C-terminus, the third antigen binding domain comprising the scFv and a Fc or a fragment of the Fc.

14. The isolated molecule of any one of claims 11-13, wherein the first antigen binding domain comprising the Fab, the second antigen binding domain comprising the scFv or the third antigen binding domain comprising the scFv is conjugated to the Fc or the fragment of the Fc, to the VH that is capable of specifically biding CD8, to the CL domain or to the CH3 domain via a linker.

15. The isolated molecule of claim 14, wherein the linker comprises a polypeptide of SEQ ID NOs: 2183-2290.

16. The isolated molecule of any one of claims 11-15, wherein the fragment of the Fc comprises a CH2 domain and a CH3 domain.

17. The isolated molecule of claim 16, wherein the CH3 domain comprises one or more substitutions when compared to a wild-type CH3 domain.

18. The isolated molecule of claim 17, wherein the one or more substitutions comprise T350V, L351Y, F405A,Y407V, T366Y, T366W, F405W, T394W, T394S, Y407T, Y407A, T366S/L368A/Y407V, L351Y/F405A/Y407V, T366I/K392M/T394W, F405A/Y407V, T366L/K392M/T394W, L351Y/Y407A, T366A/K409F, L351Y/Y407A, T366V/K409F, T366A/K409F, T350V/L351Y/F405A/Y407V or T350V/T366L/K392L/T394W, wherein residue numbering is according to the EU index.

19. An isolated molecule, comprising: a first polypeptide, a second polypeptide and a third polypeptide, wherein

a) the first polypeptide comprises, from N- to C-terminus, a second antigen binding domain comprising a scFv that specifically binds a TCR complex, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain;

b) the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and

c) the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc.

20. An isolated molecule, comprising: a first polypeptide, a second polypeptide and a third polypeptide, wherein

a) the first polypeptide comprises, from N- to C-terminus, a VH that is capable of specifically binding CD8, a CH1 domain, a hinge, a CH2 domain and a CH3 domain;

b) the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8, a CL domain and a second antigen binding domain comprising a scFv that specifically binds a TCR complex; and

c) the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc.

21. An isolated molecule, comprising: a first polypeptide, a second polypeptide and a third polypeptide, wherein

a) the first polypeptide comprises, from N- to C-terminus, a VH that is capable of specifically CD8, a CH1 domain, a hinge, a CH2 domain, a CH3 domain and a second antigen binding domain comprising a scFv that specifically binds a TCR complex;

b) the second polypeptide comprises, from N-to C-terminus, a VL that is capable of specifically binding CD8 and a CL domain; and

c) the third polypeptide comprises, from N- to C-terminus, a third antigen binding domain comprising a scFv that specifically binds an antigen expressed by an undesired cell and a Fc or a fragment of the Fc.

22. The isolated molecule of any one of claims 19-21, wherein the first antigen binding domain comprising the Fab, the second antigen binding domain comprising the scFv or the third antigen binding domain comprising the scFv is conjugated to the Fc or the fragment of the Fc, to the VH that is capable of specifically biding CD8, to the CL domain or to the CH3 domain via a linker.

23. The isolated molecule of claim 22, wherein the linker comprises a polypeptide of SEQ ID NOs: 2183-2290.

24. The isolated molecule of any one of claims 11-23, wherein

a) the first polypeptide comprises a CH3 domain comprising one or more substitutions when compared to a wild-type CH3 domain which promote heterodimerization of the first polypeptide with the third polypeptide;

b) the third polypeptide comprises a CH3 domain comprising one or more substitutions when compared to the wild-type CH3 domain which promote heterodimerization of the third polypeptide with the first polypeptide; or

c) the first polypeptide comprises the CH3 domain comprising one or more substitutions when compared to the wild-type CH3 which promote heterodimerization of the first polypeptide with the third polypeptide and the third polypeptide comprises the CH3

domain comprising one or more substitutions when compared to the wild-type CH3 which promote heterodimerization of the third polypeptide with the first polypeptide.

25. The isolated molecule of claim 24, wherein the one or more substitutions comprise T350V, L351Y, F405A,Y407V, T366Y, T366W, F405W, T394W, T394S, Y407T, Y407A, T366S/L368A/Y407V, L351Y/F405A/Y407V, T366I/K392M/T394W, F405A/Y407V, T366L/K392M/T394W, L351Y/Y407A, T366A/K409F, L351Y/Y407A, T366V/K409F, T366A/K409F, T350V/L351Y/F405A/Y407V or T350V/T366L/K392L/T394W, wherein residue numbering is according to the EU index.

26. The isolated molecule of any one of claims 11-25, wherein the Fc, the CH2 domain or the CH3 domain is an IgG1, IgG2, IgG3 or IgG4 isotype.

27. The isolated molecule of any one of claims 1-26, wherein the second antigen binding domain specifically binds CD3, TCRα chain, TCRβ chain, TCRγ chain or TCRδ chain, or any combination thereof.

28. The isolated molecule of claim 27, wherein the TCRβ chain comprises TCRVB17.

29. The isolated molecule of claim 27, wherein CD3 comprises CD3ε, CD3γ, CD3δ or CD3ζ.

30. The isolated molecule of claim 29, wherein the second antigen binding domain that specifically binds CD3 comprises a heavy chain complementarity determining region 1 (HCDR1_ of SEQ ID NO: 2291, a HCDR2 of SEQ ID NO: 2292, a HCDR3 of SEQ ID NO: 2293, a LCDR1 of SEQ ID NO: 2294, a LCDR2 of SEQ ID NO: 2295 and a LCDR3 of SEQ ID NO: 2296.

31. The isolated molecule of claim 30, wherein the second antigen binding domain that specifically binds CD3 comprises the VH of SEQ ID NO: 2297 and the VL of SEQ ID NO: 2298.

32. The isolated molecule of any one of claims 1-31, wherein the first antigen binding domain comprises the HCDR1 of SEQ ID NO: 2307, the HCDR2 of SEQ ID NO: 2308, the HCDR3 of SEQ ID NO: 2309, the LCDR1 of SEQ ID NO: 2310, the LCDR2 of SEQ ID NO: 2311 and the LCDR3 of SEQ ID NO: 2312.

33. The isolated molecule of any one of claims 1-32, wherein the first antigen binding domain comprises the VH of SEQ ID NO: 2313 and the VL of SEQ ID NO: 2314.

34. The isolated molecule of any one of claims 1-33, wherein the undesired cell is a pathogenic cell.

35. The isolated molecule of any one of claims 1-34, wherein the undesired cell is a cancer cell, an infected cell, a virus infected cell, a bacterial infected cell, an immune cell, an inflamed cell, a damaged cells, a foreign cell, an apoptotic cell, a dysplastic cell, an immunogenic cell, a metaplastic cell or a mutant cell, or any combination thereof.

36. The isolated molecule of any one of claims 1-35, wherein the isolated molecule is an antibody or a non-antibody molecule.

37. The isolated molecule of claim 36, wherein the antibody comprises a first half molecule and a second half molecule, wherein the first half molecule comprises the first antigen binding domain and the second antigen binding domain and the second half molecule comprises the third antigen binding domain.

38. The isolated molecule of any one of claims 1-37, wherein the antigen expressed by the undesired cell comprises mesothelin, alpha-fetoprotein (ALP), BAGE, BCR-ABL, beta-catenin, beta-HCG, BrE3-antigen, BCA225, BCMA, BTAA, CA125, CA195, CA242, CA-50, CAM43, CAMEL, CAP-l, carbonic anhydrase IX, CA19-9, CA72-4, CAM 17.1, CASP-8, CCCL19, CCCL21, CD1, CD la, CD2, CD4, CD5, CD11A, CD14, CD15, CD16, CD18, CD19, CD20, CD21, CD22, CD23, CD25, CD29, CD30, CD32b, CD33, CD37, CD38, CD40, CD40L, CD44, CD45, CD46, CD47, CD52, CD54, CD55, CD59, CD64, CD66a-e, CD67, CD68, CD70, CD70L, CD74, CD79a, CD79b, CD80, CD83, CD95, CD123, CD126, CD132, CD133, CD138, CD147, CD154, CDC27, CDK4, CDK4m, CDKN2A, CO-029, CTLA4, CXCR4, CXCR7, CXCL12, HIF-la, colon-specific antigen-p (CSAp), CEACAM5) CEACAM6, c-Met, DAM, E2A-PRL, EGFR, EGFRvIII, EGP-l , EGP-2, ELF2-M, Ep-CAM, FGF, FGF-5, Flt-l, Flt- 3, folate receptor, G250 antigen, Ga733VEpCAM, GAGE, gplOO, GRO-b, H4-RET, HLA-DR, HM1.24, human chorionic gonadotropin (HCG) HER2, HER3, HMGB-l, HIF-l, HSP70-2M, HST-2, HTgp-l75, la, IGF-1R, IFN-g, IFN-a, IFN-b, IFN- l, IL-4R, IL-6R, IL-13R, IL-15R, IL-17R, IL-18R, IL-2, IL-6, IL-8, IL-12, IL-15, IL-17, IL-18, IL-23, IL-25, insulin-like growth factor- 1 (IGF-l), KC4-antigen, KLK2, KSA, KS-l-antigen, KS1-4, LAGE-la, Le-Y, LDR/FUT, M344, MA-50, macrophage migration inhibitory factor (MIF), MAGE, MAGE-l, MAGE-3, MAGE-4, MAGE-5, MAGE-6, MART-l, MART-2, TRAG-3, MCP-

l, MIP-1A, MIP-1B, MIF, MG7-Ag, MOV18, MUC1, MUC2, MUC3, MUC4, MUC5ac, MUC13, MUC16, MUM- 1/2, MUM-3, MYL-RAR, NB/70K, Nm23Hl, NuMA, NCA66, NCA95, NCA90, NY-ESO-l, pl5, pl6, pl85erbB2, pl80erbB3, PAM4 antigen, pancreatic cancer mucin, PD-l, PD-L1, PD-L2, PI5, placental growth factor, p53, PLAGL2, Pmell7 prostatic acid phosphatase, PSA, PRAME, PSMA, P1GF, ILGF, ILGF-1R, IL-6, IL-25, RCAS1, RS5, RAGE, RANTES, Ras, T101, SAGE, S100, SLAMF7, survivin, survivin-2B, SDDCAG16, TA-90\Mac2 binding protein, TAAL6, TAC, TAG-72, TLP, tenascin, TMEFF2, TRAIL receptors, TRP-l, TRP-2, TSP-180, VEGFR, ED-B fibronectin, WT-l, l7-lA-antigen, C3, C3a, C3b, C5a, C5, bcl-2, K-ras, tumor neoantigen, a viral antigen associated with cancer, FcγRIIB, IL-12β2R, CD28, CD56, CD11c, CD66b, CD41, CD61, CD62, CD235a, CD146, CD326, or CD203c.

39. A kit, comprising the isolated molecule of any one of claims 1-38.

40. The kit of claim 39, further comprising means for diluting or administering the isolated molecule of any one of claims 1-38.

41. A pharmaceutical composition, comprising the isolated molecule of any one of clams 1-38 and a pharmaceutically acceptable excipient.

42. A method of selectively activating or recruiting $CD8^+$ CTLs towards an undesired cell, comprising: contacting a population of lymphocytes with an isolated molecule of any one of claims 1-38.

43. The method of claim 42, wherein the selective activation or recruitment of $CD8^+$ CTLs comprises *in vitro* selective activation or recruitment of $CD8^+$ CTLs.

44. The method of claim 42, wherein the selective activation or recruitment of $CD8^+$ CTLs comprises *ex vivo* selective activation or recruitment of $CD8^+$ CTLs.

45. The method of claim 42, wherein the selective activation or recruitment of $CD8^+$ CTLs comprises *in vivo* selective activation or recruitment of $CD8^+$ CTLs.

46. A method of selectively activating or recruiting $CD8^+$ CTLs towards an undesired cell in a subject, comprising administering to the subject an isolated molecule of any one of claims 1-38.

47. A method of providing an improved T cell redirection therapy for a subject in need thereof, comprising administering to the subject an isolated molecule of any one of claims 1-38.

48. A method of targeting $CD8^+$ CTLs to an undesired cell in a subject, comprising administering to the subject an isolated molecule of any one of claims 1-38.
49. A method of treating a cancer in a subject, comprising administering to the subject an isolated molecule of any one of claims 1-38.
50. A method of enhancing a $CD8^+$ CTL response against an undesired cell in a subject, comprising: administering to the subject an isolated molecule of any one of claims 1-38.
51. The method of any one of claims 46-50, wherein the subject has a cancer, an infection, or an immune-mediated disease.
52. The method of claim 51, wherein the cancer is a hematological malignancy or a solid tumor.
53. The method of claim 52, wherein the hematological malignancy comprises acute lymphoblastic leukemia, acute myeloid leukemia, anaplastic large-cell lymphoma, Burkitt's lymphoma, chronic lymphocytic leukemia, chronic myeloid leukemia, diffuse large B-cell lymphoma, dendritic cell neoplasm, follicular lymphoma, hairy cell leukemia, Hodgkin's lymphoma, leukemia, B cell leukemia, T cell leukemia, light chain amyloidosis, lymphoma, B cell lymphoma, NK cell lymphoma, T cell lymphoma, mantle-cell lymphoma, marginal zone B-cell lymphoma, monoclonal gammopathy of undetermined significance, mucosa-associated lymphatic tissue lymphoma, multiple myeloma, myelodysplastic syndrome, non-Hodgkin's lymphoma, plasma cell leukemia, precursor B-cell lymphoblastic leukemia, smoldering multiple myeloma, Waldenstrom's macroglobulinemia, B cell malignancy, T cell malignancy, NK cell malignancy, or any combination thereof.
54. The method of claim 52, wherein the solid tumor comprises adenocarcinoma, anal cancer, basal cell carcinoma, biliary tract cancer, bladder cancer, bone cancer, breast cancer, cancer associated with infection, cancer of the adrenal gland, cancer of the endocrine system, cancer of the head or neck, cancer of the parathyroid gland, cancer of the penis, cancer of the thyroid gland, cancer of the urethra, cervical cancer, carcinoma of the breast, carcinoma of the fallopian tubes, carcinoma of the liver, carcinoma of the lung, carcinoma of the prostate, carcinoma of the renal pelvis, carcinoma of the vagina, carcinoma of the vulva, choriocarcinoma, clear cell carcinoma, colon cancer, colon carcinoma, colorectal cancer, connective tissue cancer, cutaneous or intraocular

malignant melanoma, environmentally induced cancer, gastric cancer, gastrointestinal cancer, glioma, glioblastoma, endometrial cancer, epithelial cancer, esophageal cancer, eye cancer, larynx cancer, liver cancer, hepatocellular carcinoma, hormone refractory prostate adenocarcinoma, Kaposi's sarcoma, kidney cancer, lung cancer gastro-esophageal cancer, melanoma, mesothelioma, Merkel cell cancer, neuroblastoma, non-small cell lung cancer (NSCLC), osteosarcoma, ovarian cancer, pancreatic cancer, prostate cancer, rectal cancer, renal cell carcinoma, retinoblastoma rhabdomyosarcoma, squamous cell cancer, soft tissue sarcoma, solid tumors of childhood, spinal axis tumor, stomach cancer, testicular cancer, thyroid cancer, uterine cancer, urothelial carcinoma or sarcomas, or any combination thereof.

55. The method of claim 51, wherein the infection comprises infection with adenovirus, arboviral encephalitis virus, coronavirus, coxsackie virus, cytomegalovirus (CMV), dengue virus, echovirus, Epstein Barr virus, flaviviruses, human immunodeficiency virus (HIV), hepatitis A virus, hepatitis B virus, hepatitis C virus, herpes virus, HTLV virus, influenza virus, JC virus, measles virus, molluscum virus, mumps virus, papillomavirus, parvovirus, poliovirus, rabies virus, respiratory syncytial virus, rhinovirus, rotavirus, rubella virus or vaccinia virus, bacteria, virus, fungi, protozoa, parasite or prion, or any combination thereof.

56. The method of claim 51, wherein the immune-mediated disease comprises systemic lupus erythematosus (SLE), ankylosing spondylitis, Chagas disease, chronic obstructive pulmonary disease, Crohn's Disease, dermatomyositis, diabetes mellitus type 1, endometriosis, Goodpasture's syndrome, Graves' disease, Guillain-Barre syndrome (GBS), Hashimoto's disease, hidradenitis suppurativa, Kawasaki disease, IgA nephropathy, idiopathic thrombocytopenic purpura, interstitial cystitis, mixed connective tissue disease, morphea, multiple sclerosis, myasthenia gravis, narcolepsy, neuromyotonia, pemphigus vulgaris, pernicious anaemia, psoriasis, psoriatic arthritis, polymyositis, primary biliary cirrhosis, relapsing polychondritis, rheumatoid arthritis (RA), sarcoidosis, schizophrenia, scleroderma, Sjogren's syndrome, temporal arteritis, ulcerative colitis, vasculitis, vitiligo, Wegener's granulomatosis, IgG4-related disease, anti-synthetase syndrome, and autoimmunity associated with immunodeficiency including chronic variable immunodeficiency, Wiskott-Aldrich syndrome, Good

syndrome, IgA deficiency, Hyper IgM syndrome, complement disorders, seropositive RA, SLE, postmyocardial infarction syndrome, subacute bacterial endocarditis, anti-glomerular basement membrane nephritis, autoimmune hepatitis, primary biliary cirrhosis, alopecia areata, bullous pemphigoid, cicatricial pemphigoid, dermatitis herpetiformis, gestational pemphigoid, pemphigus vulgaris, systemic scleroderma, Addison's disease, autoimmune polyendocrine syndrome type 2, autoimmune pancreatitis, diabetes mellitus type 1, autoimmune thyroiditis, Graves' disease, Sjogren's syndrome, celiac disease, antiphospholipid syndrome, autoimmune thrombocytopenic purpura, cold agglutinin disease, pernicious anemia, thrombocytopenia, adult onset Still's disease, CREST syndrome, drug-induced lupus, enthesitis-related arthritis, juvenile arthritis, mixed connective tissue disease, palindromic rheumatism, Parry Romberg syndrome, rheumatic fever, undifferentiated connective tissue disease, dermatomysitis, myasthenia gravis, neuromyotonia, paraneoplastic cerebellar degeneration, polymyositis, Bickerstaff's encephalitis, chronic inflammatory demyelinating polyneuropathy, Guillain-Barre syndrome, Hashimoto's encephalopathy, Lambert-Eaton myasthenic syndrome, multiple sclerosis, progressive inflammatory neuropathy, Stiff person syndrome, autoimmune uveitis, neuromyelitis optica, symphathetic ophthalmia, Meniere's disease, anti-neutrophil cytoplasmic antibody-associated vasculitis, Churg-Strauss syndrome, Henoch-Schonlein purpura, microscopic polyangiitis, urticarial vasculitis, and vasculitis. Examples of autoantibody-associated autoimmune conditions include gastritis and POEMS syndrome. Examples of autoantibody-associated (non-autoimmune) diseases include agammaglobulinemia, amyotrophic lateral sclerosis, Castleman's disease, cutaneous leukocytoclastic angiitis, eczema, eosinophilic gastroenteritis, erythroblastosis fetalis, fibrodysplasia ossificans progressive, hypogammaglobulinemia, idiopathic pulmonary fibrosis, IgA nephropathy, Majeed syndrome, narcolepsy, Rasmussen's encephalitis, spondyloarthropathy or Sweet's syndrome, or any combination thereof.

57. A system comprising a means for selective activation or recruitment of $CD8^+$ CTLs.

58. A composition comprising an antibody comprising a first antigen binding domain and a second antigen binding domain, and means for selective activation or recruitment of $CD8^+$ CTLs.

59. A composition for enhancing an immune response against an antigen expressed by an undesired cell, comprising means for selective activation or recruitment of $CD8^+$ CTLs.

60. A composition for treating a cancer in subject, comprising means for selective activation or recruitment of $CD8^+$ CTLs.

61. A system comprising a means for providing an improved T cell redirecting therapeutic treatment to a subject.

62. The system of claim 61, wherein the T cell redirecting therapeutic treatment comprises administration of an isolated molecule of any one of claims 1-38

63. A T cell redirecting therapeutic comprising a means for improving safety of the T cell redirecting therapeutic.

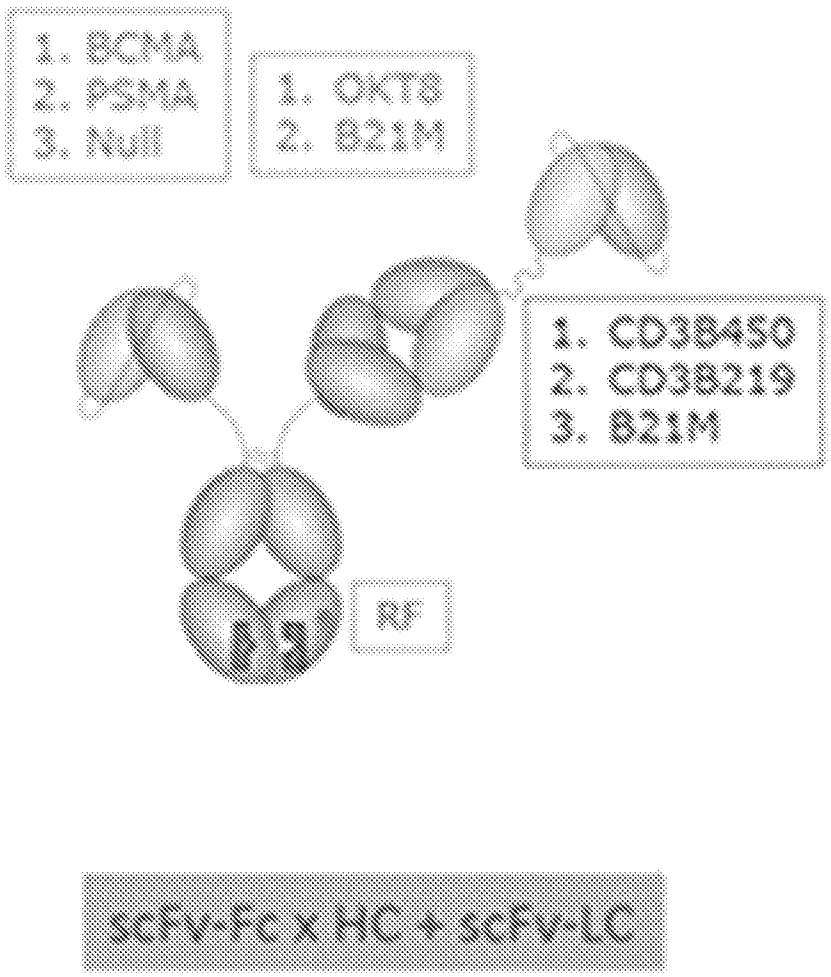
64. A process for generating an improved T cell redirecting therapeutic, comprising:
    a) a step for performing a function of designing the T cell redirecting therapeutic comprising the means of claim 61; and
    b) a step for performing a function of producing the T cell redirecting therapeutic comprising the means of claim 61.

65. A method of isolating, separating, purifying, sorting, selecting or capturing a CD8+ CTL comprising:
    a) providing a sample comprising the CD8+ CTL;
    b) contacting the sample with an isolated molecule of any one of claims 1-38; and
    c) isolating, separating, purifying, sorting, selecting or capturing the $CD8^+$ CTL bound to the isolated molecule.

66. The method of claim 65, wherein the sample is a blood sample or a tissue sample.

67. The method of claim 65 or claim 66, wherein the method is conducted in suspension or on a solid support.

68. The method of any one of claims 65-67, wherein the method is conducted using particles, microfluidics, fluorescent cell sorting, chips, columns or surfaces.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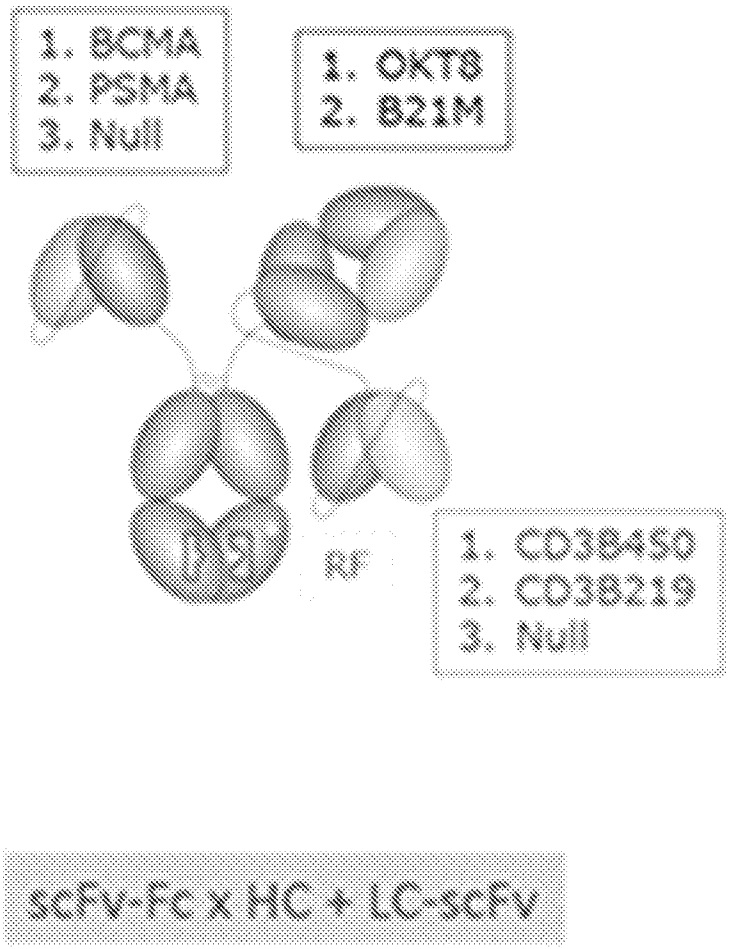
2. PSMA
3. Null
1. OKT3
2. B21M
1. CD3B450
2. CD3B219
3. B21M
RF
scFv-Fc x HC + scFv-LC

FIG. 1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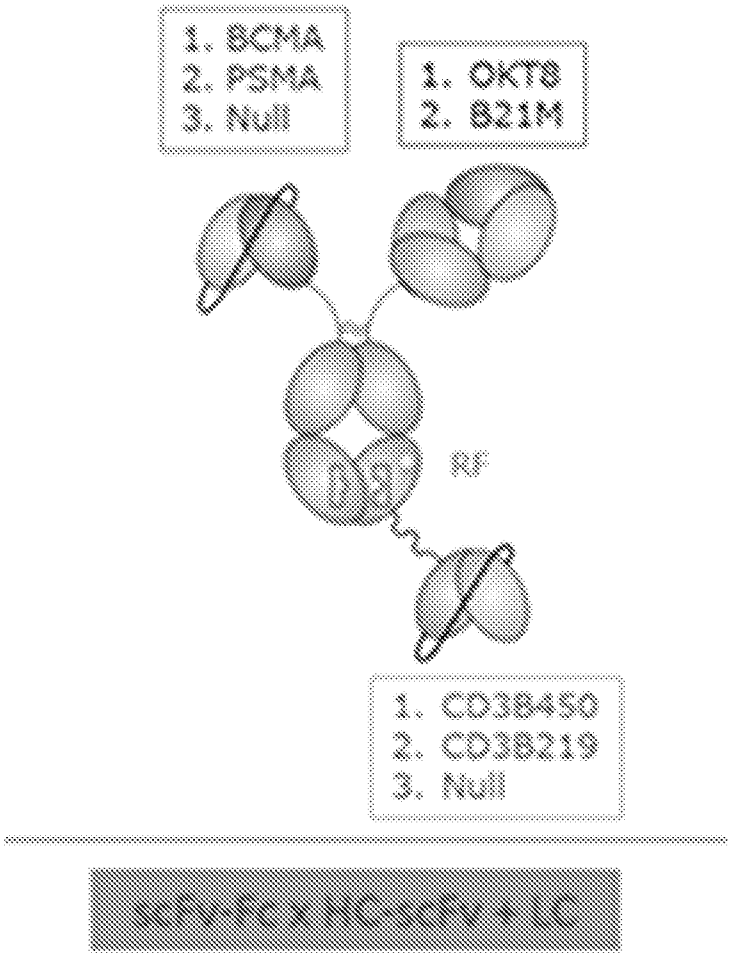
2. CD38219
3. Null
scFv-Fc x HC + LC-scFv

FIG. 2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1. OKT8
2. B21M
Fc
RF
1. CD3B450
2. CD3B219
3. Null

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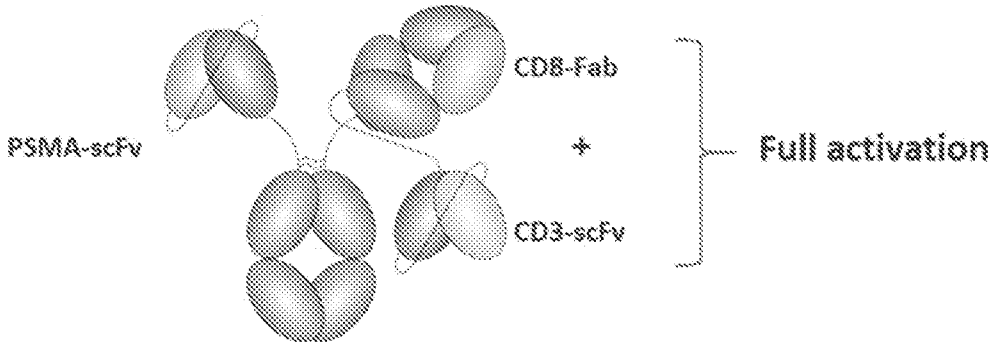
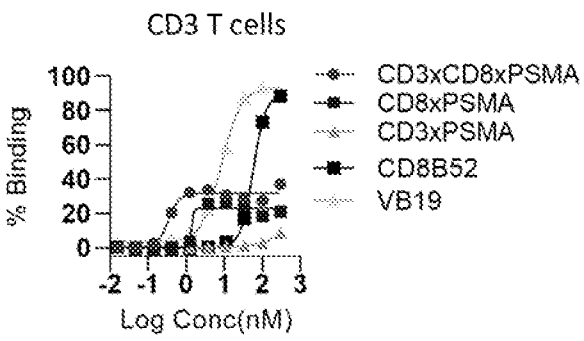
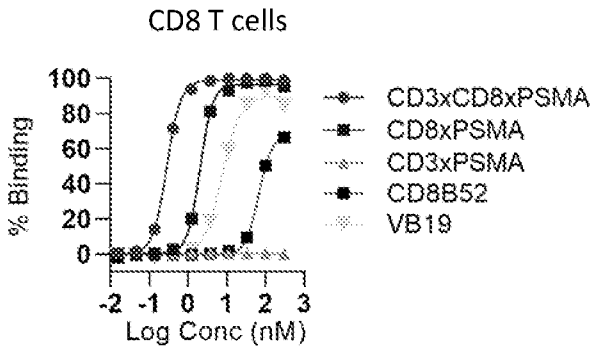
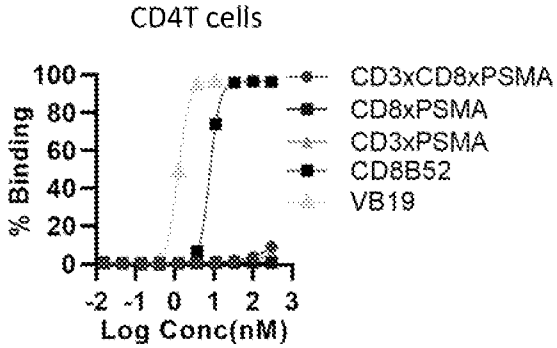


FIG. 4A

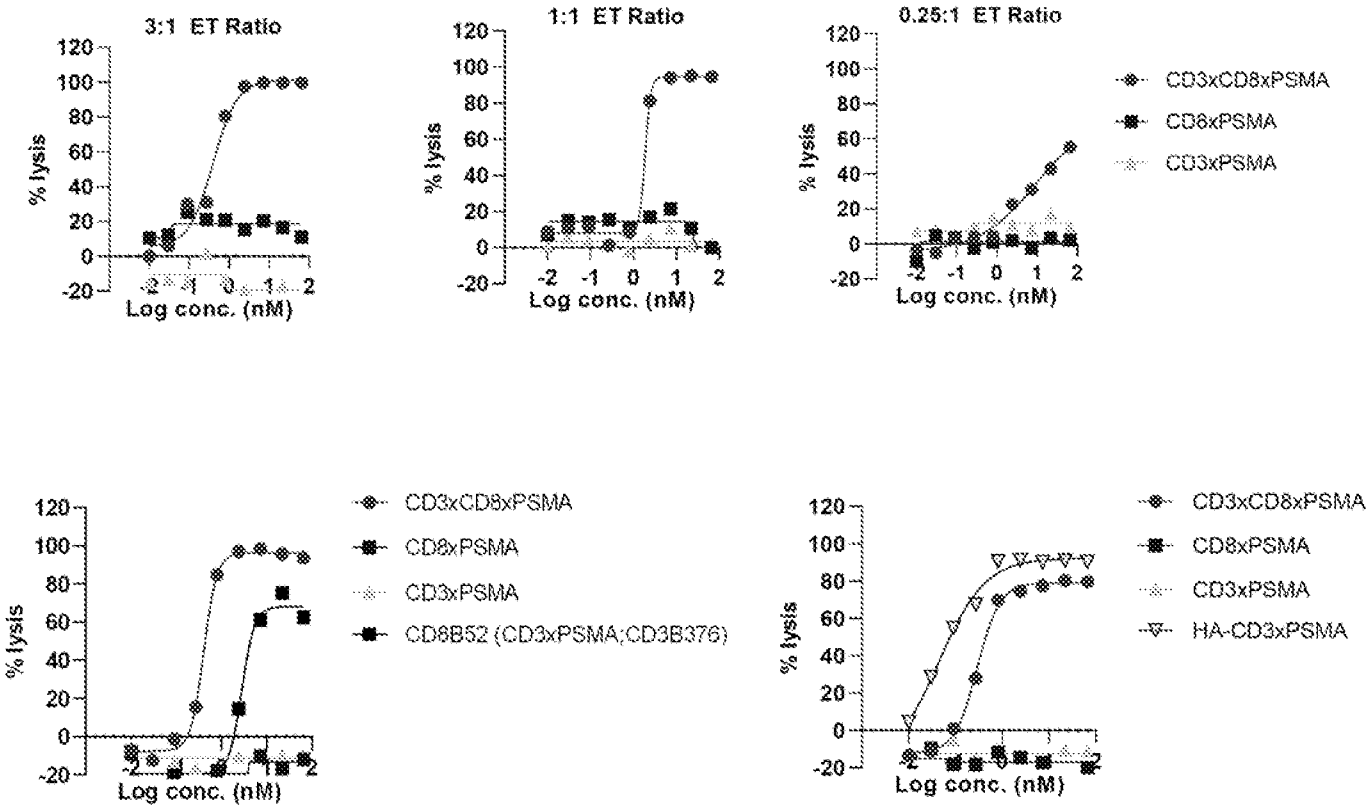






Antibody	CD3 T cells	CD8 T cells	CD4 T cells
CD8B573	0.33	0.28	No binding
CD8B574	~1.3	2	No binding
CD8B155	>300nM	Not determined	No binding
CD8B52	56.9	7.8	66.2
VB19	8.2	1.1	7.5

FIG. 4B



CD8B573.001	ET ratio (3:1)	ET ratio (1:1)	ET ratio (0.25:1)
EC_{50} (nM)	0.39	1.8	>10nM

Antibody	EC_{50} (nM)
CD3xCD8xPSMA	0.3
CD3xPSMA (CD8B52, CD3B376)	2.8
CD3xPSMA (CD3B220, HA)	<0.01

FIG. 5A

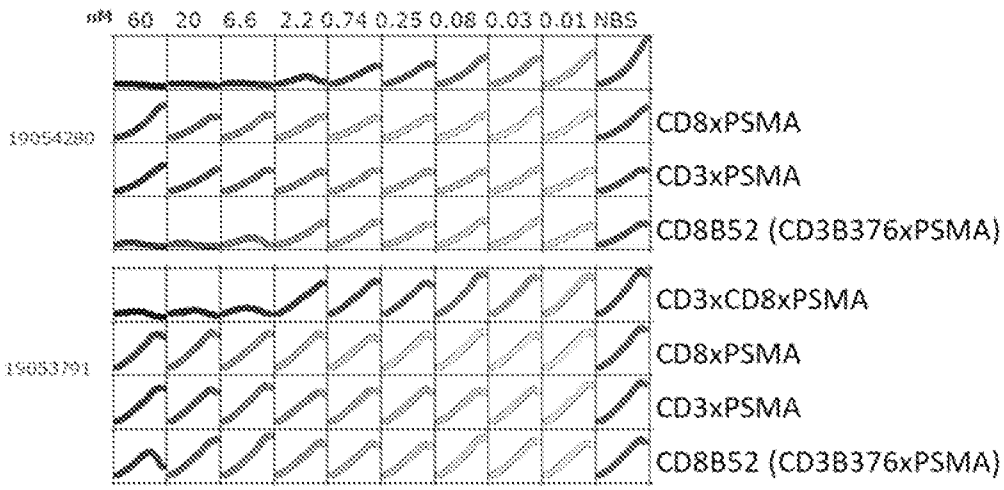

nM 60 20 6.6 2.2 0.74 0.25 0.08 0.03 0.01 NBS
19054280
CD8xPSMA
CD3xPSMA
CD8B52 (CD3B376xPSMA)
19053791
CD3xCD8xPSMA
CD8xPSMA
CD3xPSMA
CD8B52 (CD3B376xPSMA)

FIG. 5B

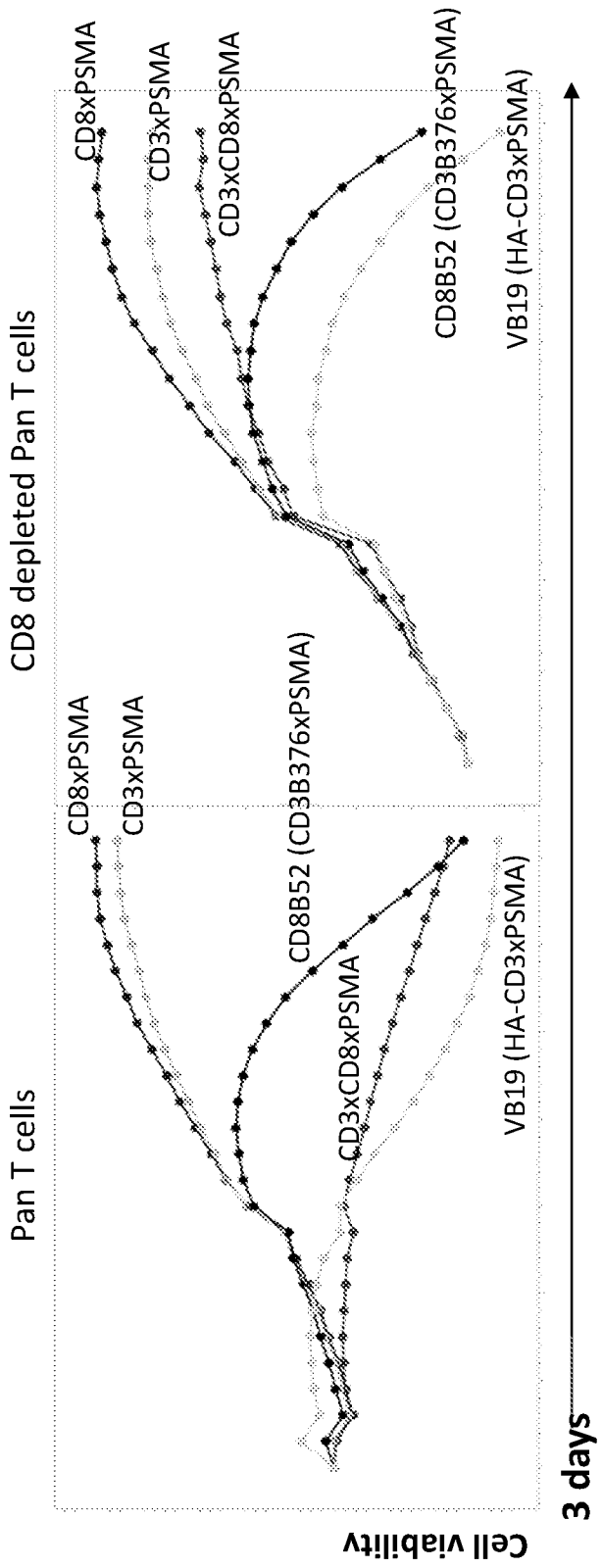

Pan T cells
CD8 depleted Pan T cells
CD8xPSMA
CD3xPSMA
CD8B52 (CD3B376xPSMA)
CD3xCD8xPSMA
VB19 (HA-CD3xPSMA)
Cell viability
3 days

FIG. 6

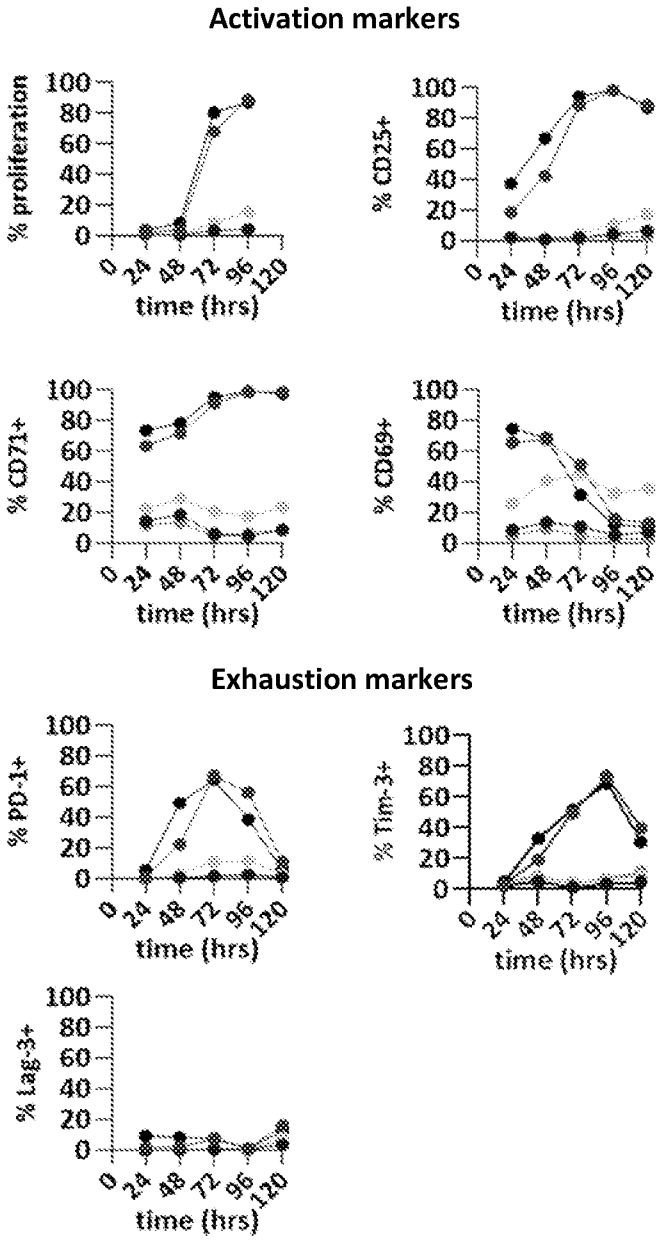

Activation markers
% proliferation
% CD25+
% CD71+
% CD69+
Exhaustion markers
% PD-1+
% Tim-3+
% Lag-3+
time (hrs)
0
24
48
72
96
120
100
80
60
40
20

FIG. 7

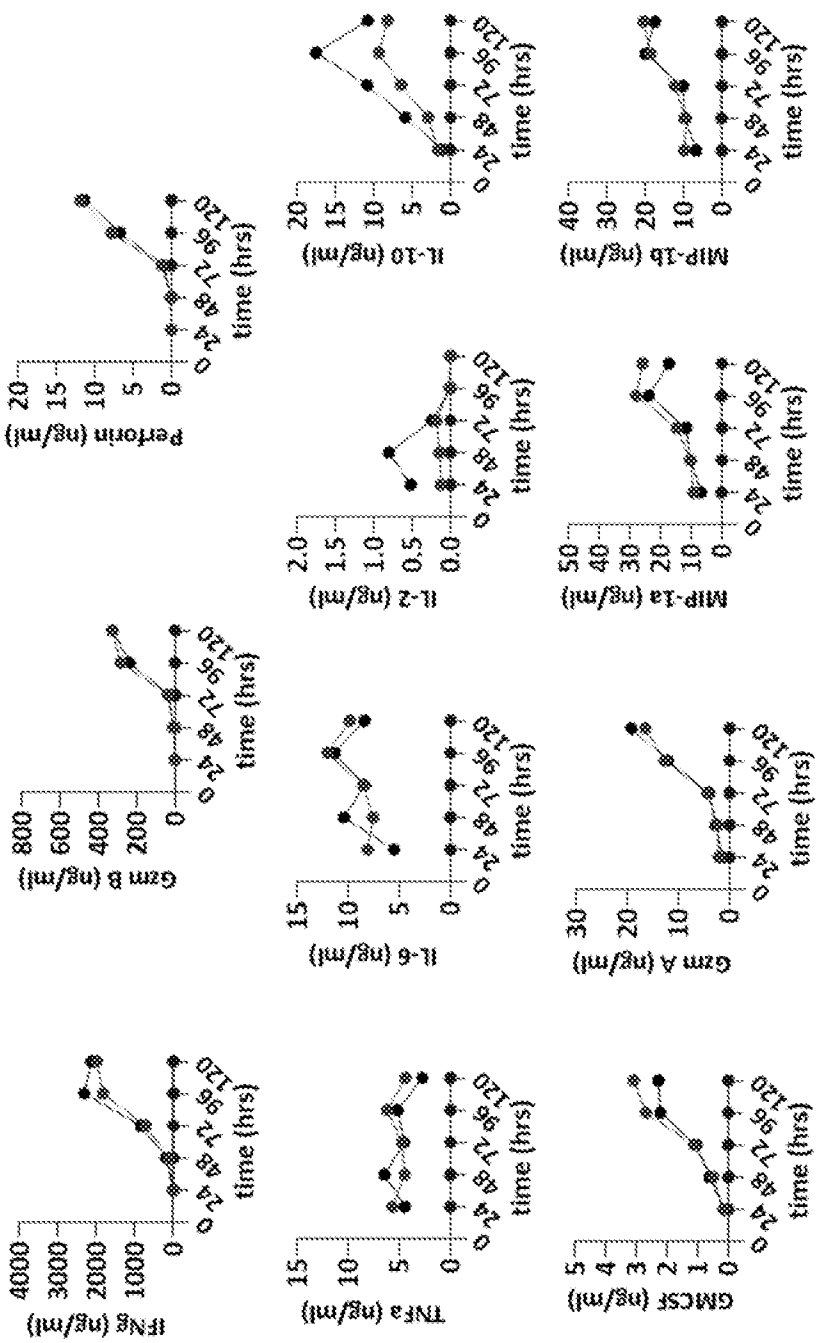

GMCSF (ng/ml)
Gzm A (ng/ml)
MIP-1a (ng/ml)
MIP-1b (ng/ml)
IL-6 (ng/ml)
IL-2 (ng/ml)
IL-10 (ng/ml)
TNFa (ng/ml)
Gzm B (ng/ml)
Perforin (ng/ml)
IFNg (ng/ml)
time (hrs)
0 24 48 72 96 120

FIG. 8

SEQUENCE LISTING

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Tyr

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20 25 30

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        35                  40                  45


Gly Arg Val Ile Pro Ser Asn Gly Gly Thr Ile Tyr Asn Leu Lys Phe
    50                  55                  60


Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Leu Ser Thr Ala Tyr
65                  70                  75                  80


Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
                85                  90                  95


Ala Arg Glu Asp Tyr Asn Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
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        35                  40                  45


Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
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50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Leu Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Glu Asp Tyr Asn Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys
115 120 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
130 135 140

```
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
145                 150                 155                 160

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
                165                 170                 175

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
            180                 185                 190

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
        195                 200                 205

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
    210                 215                 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
225                 230                 235                 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
                245                 250                 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
            260                 265                 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
        275                 280                 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
    290                 295                 300

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
305                 310                 315                 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
                325                 330                 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
            340                 345                 350
```

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
435 440 445

Ser Leu Ser Pro Gly Lys
450

<210> 34
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 34
Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
1 5 10 15

Asp Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Asp Phe
20 25 30

Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

```
Ser Gly Ser Gly Ser Asp Phe Thr Leu Thr Ile Asn Ser Val Glu Pro
65                  70                  75                  80


Glu Asp Val Gly Val Tyr Tyr Cys Gln Asn Gly His Ser Phe Pro Tyr
                85                  90                  95


Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110


Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175


Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190


Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205


Phe Asn Arg Gly Glu Cys
    210


<210> 35
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 35
Asp Tyr Tyr Met Asn
1               5
```

<210> 36
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 36
Arg Ile Ile Pro Ser Asn Gly Ala Thr Ile Tyr Asn Gln Lys Phe Lys
1 5 10 15

Gly

<210> 37
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 37
Glu Asp Tyr Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp Tyr
1 5 10 15

<210> 38
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 38
Arg Ala Ser Gln Ser Ile Ser His Tyr Leu His
1 5 10

<210> 39
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 39
Tyr Ala Ser Gln Ser Ile Ser
1   5

<210> 40
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 40
Gln Asn Gly His Ser Phe Pro Tyr Thr
1   5

<210> 41
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 41
Gly Tyr Thr Phe Thr Asp Tyr
1   5

<210> 42
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 42
Ile Pro Ser Asn Gly Ala
1   5

<210> 43
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 43
Glu Asp Tyr Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
1 5 10

<210> 44
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 44
Ser Gln Ser Ile Ser His Tyr
1 5

<210> 45
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 45
Tyr Ala Ser
1

<210> 46
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 46
Gly His Ser Phe Pro Tyr
1 5

<210> 47
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 47
Gly Tyr Thr Phe Thr Asp Tyr Tyr Met Asn
1 5 10

<210> 48
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 48
Arg Ile Ile Pro Ser Asn Gly Ala Thr Ile
1 5 10

<210> 49
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 49
Glu Asp Tyr Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp Tyr
1 5 10 15

<210> 50
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 50
Arg Ala Ser Gln Ser Ile Ser His Tyr Leu His
1 5 10

<210> 51
<211> 7

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 51
Tyr Ala Ser Gln Ser Ile Ser
1 5

<210> 52
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 52
Gln Asn Gly His Ser Phe Pro Tyr Thr
1 5

<210> 53
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 53
Thr Asp Tyr Tyr Met Asn
1 5

<210> 54
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 54
Trp Ile Gly Arg Ile Ile Pro Ser Asn Gly Ala Thr Ile
1 5 10

<210> 55
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 55
Ala Arg Glu Asp Tyr Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
1 5 10 15

<210> 56
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 56
Ser His Tyr Leu His Trp Tyr
1 5

<210> 57
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 57
Leu Leu Ile Lys Tyr Ala Ser Gln Ser Ile
1 5 10

<210> 58
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 58
Gln Asn Gly His Ser Phe Pro Tyr
1 5

<210> 59
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 59
Gly Tyr Thr Phe Thr Asp Tyr Tyr
1 5

<210> 60
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 60
Ile Ile Pro Ser Asn Gly Ala Thr
1 5

<210> 61
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 61
Ala Arg Glu Asp Tyr Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
1 5 10 15

Tyr

<210> 62
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 62
Gln Ser Ile Ser His Tyr
1 5

<210> 63
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 63
Tyr Ala Ser
1

<210> 64
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 64
Gln Asn Gly His Ser Phe Pro Tyr Thr
1 5

<210> 65
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 65
Glu Phe Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Gln Trp Ile
35 40 45

Gly Arg Ile Ile Pro Ser Asn Gly Ala Thr Ile Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Leu Ser Thr Ala Tyr
65 70 75 80

Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Asp Tyr Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 66
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 66
Asp Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
1 5 10 15

Asp Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser His Tyr
20 25 30

Leu His Trp Tyr Gln Gln Lys Leu His Glu Ser Pro Arg Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Ser Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Pro
65 70 75 80

Glu Asp Val Gly Val Tyr Tyr Cys Gln Asn Gly His Ser Phe Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 67
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 67
Glu Phe Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Gln Trp Ile
35 40 45

Gly Arg Ile Ile Pro Ser Asn Gly Ala Thr Ile Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Leu Ser Thr Ala Tyr
65 70 75 80

Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Asp Tyr Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys
115 120 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
130 135 140

```
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
145                 150                 155                 160

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
                165                 170                 175

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
            180                 185                 190

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
        195                 200                 205

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
    210                 215                 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
225                 230                 235                 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
                245                 250                 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
            260                 265                 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
        275                 280                 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
    290                 295                 300

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
305                 310                 315                 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
                325                 330                 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
            340                 345                 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
        355                 360                 365
```

```
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
    370                 375                 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
385                 390                 395                 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
                405                 410                 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
            420                 425                 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
        435                 440                 445

Ser Leu Ser Pro Gly Lys
    450
```

<210> 68
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 68

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Asp Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
1               5                   10                  15

Asp Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser His Tyr
            20                  25                  30

Leu His Trp Tyr Gln Gln Lys Leu His Glu Ser Pro Arg Leu Leu Ile
        35                  40                  45

Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Ser Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Pro
65                  70                  75                  80
```

```
Glu Asp Val Gly Val Tyr Tyr Cys Gln Asn Gly His Ser Phe Pro Tyr
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 69
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 69

```
Asp Tyr Tyr Met Asn
1               5
```

<210> 70
<211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 70
Arg Val Ile Pro Ser Asn Gly Gly Thr Ile Tyr Asn Gln Lys Phe Arg
1 5 10 15

Gly

<210> 71
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 71
Glu Asp Tyr Gly Asn Gln Gly Phe Phe Leu Asp Ala Met Asp Tyr
1 5 10 15

<210> 72
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 72
Arg Ala Ser Gln Ser Ile Ser His Phe Leu His
1 5 10

<210> 73
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 73

Tyr Ala Ser Gln Ser Ile Ser
1 5

<210> 74
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 74
Gln Ser Gly His Ser Phe Pro Tyr Thr
1 5

<210> 75
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 75
Gly Tyr Thr Phe Thr Asp Tyr
1 5

<210> 76
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 76
Ile Pro Ser Asn Gly Gly
1 5

<210> 77
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 77
Glu Asp Tyr Gly Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
1   5   10

<210> 78
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 78
Ser Gln Ser Ile Ser His Phe
1   5

<210> 79
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 79
Tyr Ala Ser
1

<210> 80
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 80
Gly His Ser Phe Pro Tyr
1   5

<210> 81
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 81
Gly Tyr Thr Phe Thr Asp Tyr Tyr Met Asn
1 5 10

<210> 82
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 82
Arg Val Ile Pro Ser Asn Gly Gly Thr Ile
1 5 10

<210> 83
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 83
Glu Asp Tyr Gly Asn Gln Gly Phe Phe Leu Asp Ala Met Asp Tyr
1 5 10 15

<210> 84
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 84
Arg Ala Ser Gln Ser Ile Ser His Phe Leu His
1 5 10

<210> 85
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 85
Tyr Ala Ser Gln Ser Ile Ser
1 5

<210> 86
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 86
Gln Ser Gly His Ser Phe Pro Tyr Thr
1 5

<210> 87
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 87
Thr Asp Tyr Tyr Met Asn
1 5

<210> 88
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 88
Trp Ile Gly Arg Val Ile Pro Ser Asn Gly Gly Thr Ile
1 5 10

<210> 89
<211> 16

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 89
Ala Arg Glu Asp Tyr Gly Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
1 5 10 15

<210> 90
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 90
Ser His Phe Leu His Trp Tyr
1 5

<210> 91
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 91
Leu Leu Ile Lys Tyr Ala Ser Gln Ser Ile
1 5 10

<210> 92
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 92
Gln Ser Gly His Ser Phe Pro Tyr
1 5

<210> 93
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 93
Gly Tyr Thr Phe Thr Asp Tyr Tyr
1 5

<210> 94
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 94
Val Ile Pro Ser Asn Gly Gly Thr
1 5

<210> 95
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 95
Ala Arg Glu Asp Tyr Gly Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
1 5 10 15

Tyr

<210> 96
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 96
Gln Ser Ile Ser His Phe
1 5

<210> 97
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 97
Tyr Ala Ser
1

<210> 98
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 98
Gln Ser Gly His Ser Phe Pro Tyr Thr
1 5

<210> 99
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 99
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

```
Gly Arg Val Ile Pro Ser Asn Gly Gly Thr Ile Tyr Asn Gln Lys Phe
    50                  55                  60

Arg Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Leu Ser Thr Ala Tyr
65                  70                  75                  80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Asp Tyr Gly Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 100
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 100

```
Asp Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
1               5                   10                  15

Asp Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser His Phe
            20                  25                  30

Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
        35                  40                  45

Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ser Pro Ser Lys Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Ser Asp Phe Thr Leu Thr Ile Asn Ser Val Glu Pro
65                  70                  75                  80

Glu Asp Val Gly Val Tyr Tyr Cys Gln Ser Gly His Ser Phe Pro Tyr
                85                  90                  95
```

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 101
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 101
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Arg Val Ile Pro Ser Asn Gly Gly Thr Ile Tyr Asn Gln Lys Phe
50 55 60

Arg Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Leu Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Asp Tyr Gly Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys
115 120 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
130 135 140

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
145 150 155 160

```
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
                165                 170                 175

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
            180                 185                 190

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
        195                 200                 205

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
    210                 215                 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
225                 230                 235                 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
                245                 250                 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
            260                 265                 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
        275                 280                 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
    290                 295                 300

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
305                 310                 315                 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
                325                 330                 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
            340                 345                 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
        355                 360                 365
```

```
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
    370                 375                 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
385                 390                 395                 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
                405                 410                 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
            420                 425                 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
        435                 440                 445

Ser Leu Ser Pro Gly Lys
    450
```

<210> 102
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 102

```
Asp Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
1               5                   10                  15

Asp Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser His Phe
            20                  25                  30

Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
        35                  40                  45

Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ser Pro Ser Lys Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Ser Asp Phe Thr Leu Thr Ile Asn Ser Val Glu Pro
65                  70                  75                  80
```

```
Glu Asp Val Gly Val Tyr Tyr Cys Gln Ser Gly His Ser Phe Pro Tyr
                85                  90                  95


Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110


Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175


Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190


Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205


Phe Asn Arg Gly Glu Cys
    210


<210> 103
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 103
Asp Tyr Tyr Met Asn
1               5


<210> 104
<211> 17
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 104
Arg Val Ile Pro Asn Asn Gly Gly Thr Arg Tyr Asn Gln Lys Phe Lys
1 5 10 15

Gly

<210> 105
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 105
Glu Asp Phe Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp Tyr
1 5 10 15

<210> 106
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 106
Arg Ala Ser Gln Thr Ile Ser Asp Tyr Leu His
1 5 10

<210> 107
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 107
Tyr Ala Ser Gln Ser Ile Ser
1 5

<210> 108
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 108
Gln Asn Gly His Ser Phe Pro Tyr Thr
1 5

<210> 109
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 109
Gly Tyr Thr Phe Thr Asp Tyr
1 5

<210> 110
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 110
Ile Pro Asn Asn Gly Gly
1 5

<210> 111
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 111

Glu Asp Phe Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
1   5   10

<210> 112
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 112
Ser Gln Thr Ile Ser Asp Tyr
1   5

<210> 113
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 113
Tyr Ala Ser
1

<210> 114
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 114
Gly His Ser Phe Pro Tyr
1   5

<210> 115
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 115
Gly Tyr Thr Phe Thr Asp Tyr Tyr Met Asn
1 5 10

<210> 116
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 116
Arg Val Ile Pro Asn Asn Gly Gly Thr Arg
1 5 10

<210> 117
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 117
Glu Asp Phe Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp Tyr
1 5 10 15

<210> 118
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 118
Arg Ala Ser Gln Thr Ile Ser Asp Tyr Leu His
1 5 10

<210> 119
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 119
Tyr Ala Ser Gln Ser Ile Ser
1 5

<210> 120
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 120
Gln Asn Gly His Ser Phe Pro Tyr Thr
1 5

<210> 121
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 121
Thr Asp Tyr Tyr Met Asn
1 5

<210> 122
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 122
Trp Ile Gly Arg Val Ile Pro Asn Asn Gly Gly Thr Arg
1 5 10

<210> 123
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 123
Ala Arg Glu Asp Phe Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
1 5 10 15

<210> 124
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 124
Ser Asp Tyr Leu His Trp Tyr
1 5

<210> 125
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 125
Leu Leu Ile Lys Tyr Ala Ser Gln Ser Ile
1 5 10

<210> 126
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 126
Gln Asn Gly His Ser Phe Pro Tyr
1 5

<210> 127
<211> 8

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 127
Gly Tyr Thr Phe Thr Asp Tyr Tyr
1 5

<210> 128
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 128
Val Ile Pro Asn Asn Gly Gly Thr
1 5

<210> 129
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 129
Ala Arg Glu Asp Phe Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
1 5 10 15

Tyr

<210> 130
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 130

Gln Thr Ile Ser Asp Tyr
1   5

<210> 131
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 131
Tyr Ala Ser
1

<210> 132
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 132
Gln Asn Gly His Ser Phe Pro Tyr Thr
1   5

<210> 133
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 133
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20   25   30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
        35   40   45

```
Gly Arg Val Ile Pro Asn Asn Gly Gly Thr Arg Tyr Asn Gln Lys Phe
    50                  55                  60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Leu Ser Thr Ala Tyr
65                  70                  75                  80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Asp Phe Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
        115                 120
```

<210> 134
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 134

```
Asp Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
1               5                   10                  15

Asp Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Thr Ile Ser Asp Tyr
            20                  25                  30

Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
        35                  40                  45

Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Ser Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Pro
65                  70                  75                  80

Glu Asp Val Gly Val Tyr Tyr Cys Gln Asn Gly His Ser Phe Pro Tyr
                85                  90                  95
```

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 135
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 135
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Arg Val Ile Pro Asn Asn Gly Gly Thr Arg Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Leu Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Asp Phe Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys
115 120 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
130 135 140

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
145 150 155 160

```
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
                165                 170                 175

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
            180                 185                 190

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
        195                 200                 205

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
    210                 215                 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
225                 230                 235                 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
                245                 250                 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
            260                 265                 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
        275                 280                 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
    290                 295                 300

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
305                 310                 315                 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
                325                 330                 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
            340                 345                 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
        355                 360                 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
    370                 375                 380
```

```
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
385                 390                 395                 400


Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
                405                 410                 415


Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
            420                 425                 430


Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
        435                 440                 445


Ser Leu Ser Pro Gly Lys
    450


<210> 136
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 136
Asp Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
1               5                   10                  15


Asp Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Thr Ile Ser Asp Tyr
            20                  25                  30


Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
        35                  40                  45


Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Ser Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Pro
65                  70                  75                  80


Glu Asp Val Gly Val Tyr Tyr Cys Gln Asn Gly His Ser Phe Pro Tyr
                85                  90                  95
```

```
Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala
            100                 105                 110


Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175


Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190


Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205


Phe Asn Arg Gly Glu Cys
    210


<210> 137
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 137
Asp Tyr Tyr Val Asn
1               5


<210> 138
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
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<223> Description of Artificial Sequence: Synthetic
peptide

<400> 138
Arg Val Ile Pro Asn Asn Gly Asn Val Ile Tyr Asn Gln Asn Phe Lys
1 5 10 15

Gly

<210> 139
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 139
Glu Asp Tyr Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp Tyr
1 5 10 15

<210> 140
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 140
Arg Ala Ser Gln Thr Ile Ser Asn Tyr Leu His
1 5 10

<210> 141
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 141
Tyr Ala Ser Gln Ser Ile Ser
1 5

<210> 142
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 142
Gln Asn Gly His Ser Phe Pro Tyr Thr
1 5

<210> 143
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 143
Gly Tyr Thr Phe Thr Asp Tyr
1 5

<210> 144
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 144
Ile Pro Asn Asn Gly Asn
1 5

<210> 145
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 145
Glu Asp Tyr Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
1 5 10

<210> 146
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 146
Ser Gln Thr Ile Ser Asn Tyr
1 5

<210> 147
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 147
Tyr Ala Ser
1

<210> 148
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 148
Gly His Ser Phe Pro Tyr
1 5

<210> 149
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 149

Gly Tyr Thr Phe Thr Asp Tyr Tyr Val Asn
1 5 10

<210> 150
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 150
Arg Val Ile Pro Asn Asn Gly Asn Val Ile
1 5 10

<210> 151
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 151
Glu Asp Tyr Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp Tyr
1 5 10 15

<210> 152
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 152
Arg Ala Ser Gln Thr Ile Ser Asn Tyr Leu His
1 5 10

<210> 153
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 153
Tyr Ala Ser Gln Ser Ile Ser
1 5

<210> 154
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 154
Gln Asn Gly His Ser Phe Pro Tyr Thr
1 5

<210> 155
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 155
Thr Asp Tyr Tyr Val Asn
1 5

<210> 156
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 156
Trp Ile Gly Arg Val Ile Pro Asn Asn Gly Asn Val Ile
1 5 10

<210> 157
<211> 16
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 157
Thr Arg Glu Asp Tyr Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
1 5 10 15

<210> 158
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 158
Ser Asn Tyr Leu His Trp Tyr
1 5

<210> 159
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 159
Leu Leu Ile Lys Tyr Ala Ser Gln Ser Ile
1 5 10

<210> 160
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 160
Gln Asn Gly His Ser Phe Pro Tyr
1 5

<210> 161
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 161
Gly Tyr Thr Phe Thr Asp Tyr Tyr
1 5

<210> 162
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 162
Val Ile Pro Asn Asn Gly Asn Val
1 5

<210> 163
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 163
Thr Arg Glu Asp Tyr Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
1 5 10 15

Tyr

<210> 164
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 164
Gln Thr Ile Ser Asn Tyr
1 5

<210> 165
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 165
Tyr Ala Ser
1

<210> 166
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 166
Gln Asn Gly His Ser Phe Pro Tyr Thr
1 5

<210> 167
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 167
Glu Phe Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Val Asn Trp Val Gln Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Arg Val Ile Pro Asn Asn Gly Asn Val Ile Tyr Asn Gln Asn Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Leu Ser Ser Ala Tyr
65 70 75 80

Leu Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Glu Asp Tyr Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 168
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 168
Asp Ile Val Met Thr Gln Thr Pro Ala Thr Leu Ser Val Thr Pro Gly
1 5 10 15

Asp Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Thr Ile Ser Asn Tyr
20 25 30

Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Ser Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Pro
65 70 75 80

Glu Asp Val Gly Val Tyr Tyr Cys Gln Asn Gly His Ser Phe Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 169
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 169
Glu Phe Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Val Asn Trp Val Gln Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Arg Val Ile Pro Asn Asn Gly Asn Val Ile Tyr Asn Gln Asn Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Leu Ser Ser Ala Tyr
65 70 75 80

Leu Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Glu Asp Tyr Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys
115 120 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
130 135 140

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
145 150 155 160

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
165 170 175

```
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
            180                 185                 190

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
        195                 200                 205

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
    210                 215                 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
225                 230                 235                 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
                245                 250                 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
            260                 265                 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
        275                 280                 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
    290                 295                 300

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
305                 310                 315                 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
                325                 330                 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
            340                 345                 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
        355                 360                 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
    370                 375                 380
```

```
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
385                 390                 395                 400


Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
                405                 410                 415


Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
            420                 425                 430


Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
        435                 440                 445


Ser Leu Ser Pro Gly Lys
    450


<210> 170
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 170
Asp Ile Val Met Thr Gln Thr Pro Ala Thr Leu Ser Val Thr Pro Gly
1               5                   10                  15


Asp Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Thr Ile Ser Asn Tyr
            20                  25                  30


Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
        35                  40                  45


Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Ser Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Pro
65                  70                  75                  80


Glu Asp Val Gly Val Tyr Tyr Cys Gln Asn Gly His Ser Phe Pro Tyr
                85                  90                  95
```

```
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110


Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175


Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190


Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205


Phe Asn Arg Gly Glu Cys
    210


<210> 171
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 171
Ser Tyr Trp Met His
1               5


<210> 172
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide
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<400> 172
Glu Ile Asn Pro Ser Asn Gly Asp Ser Tyr Tyr Asn Glu Lys Phe Lys
1   5   10   15

Arg

<210> 173
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 173
Ser Met Tyr Tyr Asp Gly Arg Ala Gly Ala Tyr
1   5   10

<210> 174
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 174
Ile Thr Ser Thr Asp Ile Asp Asp Asp Met Asn
1   5   10

<210> 175
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 175
Glu Gly Asn Thr Leu Arg Pro
1   5

<210> 176
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 176
Leu Gln Ser Asp Asn Met Pro Leu Thr
1 5

<210> 177
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 177
Gly Tyr Thr Phe Thr Ser Tyr
1 5

<210> 178
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 178
Asn Pro Ser Asn Gly Asp
1 5

<210> 179
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 179
Ser Met Tyr Tyr Asp Gly Arg Ala Gly Ala
1 5 10

<210> 180
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 180
Ser Thr Asp Ile Asp Asp Asp
1 5

<210> 181
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 181
Glu Gly Asn
1

<210> 182
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 182
Ser Asp Asn Met Pro Leu
1 5

<210> 183
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 183
Gly Tyr Thr Phe Thr Ser Tyr Trp Met His
1 5 10

<210> 184
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 184
Glu Ile Asn Pro Ser Asn Gly Asp Ser Tyr
1 5 10

<210> 185
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 185
Ser Met Tyr Tyr Asp Gly Arg Ala Gly Ala Tyr
1 5 10

<210> 186
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 186
Ile Thr Ser Thr Asp Ile Asp Asp Asp Met Asn
1 5 10

<210> 187
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 187

Glu Gly Asn Thr Leu Arg Pro
1 5

<210> 188
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 188
Leu Gln Ser Asp Asn Met Pro Leu Thr
1 5

<210> 189
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 189
Thr Ser Tyr Trp Met His
1 5

<210> 190
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 190
Trp Ile Gly Glu Ile Asn Pro Ser Asn Gly Asp Ser Tyr
1 5 10

<210> 191
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 191
Thr Arg Ser Met Tyr Tyr Asp Gly Arg Ala Gly Ala
1   5   10

<210> 192
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 192
Asp Asp Asp Met Asn Trp Tyr
1   5

<210> 193
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 193
Leu Leu Ile Ser Glu Gly Asn Thr Leu Arg
1   5   10

<210> 194
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 194
Leu Gln Ser Asp Asn Met Pro Leu
1   5

<210> 195
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 195
Gly Tyr Thr Phe Thr Ser Tyr Trp
1 5

<210> 196
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 196
Ile Asn Pro Ser Asn Gly Asp Ser
1 5

<210> 197
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 197
Thr Arg Ser Met Tyr Tyr Asp Gly Arg Ala Gly Ala Tyr
1 5 10

<210> 198
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 198
Thr Asp Ile Asp Asp Asp
1 5

<210> 199
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 199
Glu Gly Asn
1

<210> 200
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 200
Leu Gln Ser Asp Asn Met Pro Leu Thr
1 5

<210> 201
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 201
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met His Trp Val Asn Arg Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn Pro Ser Asn Gly Asp Ser Tyr Tyr Asn Glu Lys Phe
50 55 60

Lys Arg Lys Ala Thr Leu Thr Val Asp Ile Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Ser Met Tyr Tyr Asp Gly Arg Ala Gly Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 202
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 202
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ser Val Ala Thr Gly
1 5 10 15

Glu Lys Val Thr Ile Arg Cys Ile Thr Ser Thr Asp Ile Asp Asp Asp
20 25 30

Met Asn Trp Tyr Gln Gln Lys Pro Gly Glu Pro Pro Lys Leu Leu Ile
35 40 45

Ser Glu Gly Asn Thr Leu Arg Pro Gly Val Pro Ser Arg Phe Ser Ser
50 55 60

Ser Gly Tyr Gly Thr Asp Phe Val Phe Thr Ile Glu Asn Thr Leu Ser
65 70 75 80

Glu Asp Val Ala Asp Tyr Tyr Cys Leu Gln Ser Asp Asn Met Pro Leu
85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 203
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 203
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met His Trp Val Asn Arg Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn Pro Ser Asn Gly Asp Ser Tyr Tyr Asn Glu Lys Phe
50 55 60

Lys Arg Lys Ala Thr Leu Thr Val Asp Ile Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Ser Met Tyr Tyr Asp Gly Arg Ala Gly Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

```
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415
```

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 204
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 204
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ser Val Ala Thr Gly
1 5 10 15

Glu Lys Val Thr Ile Arg Cys Ile Thr Ser Thr Asp Ile Asp Asp Asp
20 25 30

Met Asn Trp Tyr Gln Gln Lys Pro Gly Glu Pro Pro Lys Leu Leu Ile
35 40 45

Ser Glu Gly Asn Thr Leu Arg Pro Gly Val Pro Ser Arg Phe Ser Ser
50 55 60

Ser Gly Tyr Gly Thr Asp Phe Val Phe Thr Ile Glu Asn Thr Leu Ser
65 70 75 80

Glu Asp Val Ala Asp Tyr Tyr Cys Leu Gln Ser Asp Asn Met Pro Leu
85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 205
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 205
Asn Tyr Trp Ile His
1 5

<210> 206
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 206
Asn Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Lys Phe Lys
1 5 10 15

Asp

<210> 207
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 207
Gly Leu Thr Gly Thr Gly Tyr Tyr
1 5

<210> 208
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 208
Arg Ala Ser Gln Asp Ile Ser Pro Tyr Leu Asn
1 5 10

<210> 209
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 209
Tyr Thr Ser Lys Leu His Ser
1 5

<210> 210
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 210
Gln Gln Asp Asn Thr Leu Pro Tyr Thr
1 5

<210> 211
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 211
Gly Tyr Thr Phe Thr Asn Tyr
1 5

<210> 212
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 212
Asp Pro Ser Asp Ser Glu
1 5

<210> 213
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 213
Gly Leu Thr Gly Thr Gly Tyr
1 5

<210> 214
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 214
Ser Gln Asp Ile Ser Pro Tyr
1 5

<210> 215
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 215
Tyr Thr Ser
1

<210> 216
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 216
Asp Asn Thr Leu Pro Tyr
1 5

<210> 217
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 217
Gly Tyr Thr Phe Thr Asn Tyr Trp Ile His
1 5 10

<210> 218
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 218
Asn Ile Asp Pro Ser Asp Ser Glu Thr His
1 5 10

<210> 219
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 219
Gly Leu Thr Gly Thr Gly Tyr Tyr
1 5

<210> 220
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 220
Arg Ala Ser Gln Asp Ile Ser Pro Tyr Leu Asn
1 5 10

<210> 221
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 221
Tyr Thr Ser Lys Leu His Ser
1 5

<210> 222
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 222
Gln Gln Asp Asn Thr Leu Pro Tyr Thr
1 5

<210> 223
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 223
Thr Asn Tyr Trp Ile His
1 5

<210> 224
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 224
Trp Ile Gly Asn Ile Asp Pro Ser Asp Ser Glu Thr His
1 5 10

<210> 225
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 225
Ala Ser Gly Leu Thr Gly Thr Gly Tyr
1 5

<210> 226
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 226
Ser Pro Tyr Leu Asn Trp Tyr
1 5

<210> 227
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 227
Leu Leu Ile Tyr Tyr Thr Ser Lys Leu His
1 5 10

<210> 228
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 228
Gln Gln Asp Asn Thr Leu Pro Tyr
1 5

<210> 229
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 229
Gly Tyr Thr Phe Thr Asn Tyr Trp
1 5

<210> 230
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 230
Ile Asp Pro Ser Asp Ser Glu Thr
1 5

<210> 231
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 231
Ala Ser Gly Leu Thr Gly Thr Gly Tyr Tyr
1 5 10

<210> 232
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 232
Gln Asp Ile Ser Pro Tyr
1 5

<210> 233
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 233

Tyr Thr Ser
1

<210> 234
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 234
Gln Gln Asp Asn Thr Leu Pro Tyr Thr
1 5

<210> 235
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 235
Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Trp Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Asn Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ile Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Ser Gly Leu Thr Gly Thr Gly Tyr Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Ser Ser
        115

<210> 236
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 236
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Pro Tyr
            20   25   30

Leu Asn Trp Tyr Gln Gln Lys Pro Glu Gly Thr Ile Lys Leu Leu Ile
        35   40   45

Tyr Tyr Thr Ser Lys Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65   70   75   80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Asp Asn Thr Leu Pro Tyr
                85   90   95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Leu Lys
            100   105

<210> 237
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 237

```
Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
            20                  25                  30

Trp Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45

Gly Asn Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Lys Phe
    50                  55                  60

Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

Met Gln Leu Ile Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Ser Gly Leu Thr Gly Thr Gly Tyr Tyr Trp Gly Gln Gly Thr Thr
            100                 105                 110

Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
        115                 120                 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
    210                 215                 220
```

```
Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
225                 230                 235                 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
            260                 265                 270

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
    290                 295                 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                 310                 315                 320

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
                325                 330                 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
            340                 345                 350

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        355                 360                 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385                 390                 395                 400

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
                405                 410                 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            420                 425                 430
```

```
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445


<210> 238
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 238
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Pro Tyr
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Glu Gly Thr Ile Lys Leu Leu Ile
        35                  40                  45


Tyr Tyr Thr Ser Lys Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65                  70                  75                  80


Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Asp Asn Thr Leu Pro Tyr
                85                  90                  95


Thr Phe Gly Ser Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala
            100                 105                 110


Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160
```

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 239
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 239
Asp Tyr Tyr Met Asn
1 5

<210> 240
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 240
Arg Val Ile Pro Asn Asn Gly Gly Thr Ile Tyr Asn Gln Lys Phe Lys
1 5 10 15

Asp

<210> 241
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 241
Glu Asp Tyr Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp Tyr
1 5 10 15

<210> 242
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 242
Arg Ala Ser Gln Thr Ile Ser His Phe Leu His
1 5 10

<210> 243
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 243
Tyr Ala Ser Gln Ser Ile Ser
1 5

<210> 244
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 244
Gln Ser Gly His Ser Phe Pro Tyr Thr
1 5

<210> 245
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 245
Gly Tyr Thr Phe Thr Asp Tyr
1 5

<210> 246
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 246
Ile Pro Asn Asn Gly Gly
1 5

<210> 247
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 247
Glu Asp Tyr Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
1 5 10

<210> 248
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 248
Ser Gln Thr Ile Ser His Phe
1 5

<210> 249
<211> 3

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 249
Tyr Ala Ser
1

<210> 250
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 250
Gly His Ser Phe Pro Tyr
1 5

<210> 251
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 251
Gly Tyr Thr Phe Thr Asp Tyr Tyr Met Asn
1 5 10

<210> 252
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 252
Arg Val Ile Pro Asn Asn Gly Gly Thr Ile
1 5 10

<210> 253
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 253
Glu Asp Tyr Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp Tyr
1 5 10 15

<210> 254
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 254
Arg Ala Ser Gln Thr Ile Ser His Phe Leu His
1 5 10

<210> 255
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 255
Tyr Ala Ser Gln Ser Ile Ser
1 5

<210> 256
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 256
Gln Ser Gly His Ser Phe Pro Tyr Thr
1 5

<210> 257
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 257
Thr Asp Tyr Tyr Met Asn
1 5

<210> 258
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 258
Trp Ile Gly Arg Val Ile Pro Asn Asn Gly Gly Thr Ile
1 5 10

<210> 259
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 259
Ala Arg Glu Asp Tyr Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
1 5 10 15

<210> 260
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 260

Ser His Phe Leu His Trp Tyr
1 5

<210> 261
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 261
Leu Leu Ile Lys Tyr Ala Ser Gln Ser Ile
1 5 10

<210> 262
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 262
Gln Ser Gly His Ser Phe Pro Tyr
1 5

<210> 263
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 263
Gly Tyr Thr Phe Thr Asp Tyr Tyr
1 5

<210> 264
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 264
Val Ile Pro Asn Asn Gly Gly Thr
1 5

<210> 265
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 265
Ala Arg Glu Asp Tyr Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
1 5 10 15

Tyr

<210> 266
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 266
Gln Thr Ile Ser His Phe
1 5

<210> 267
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 267
Tyr Ala Ser
1

<210> 268
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 268
Gln Ser Gly His Ser Phe Pro Tyr Thr
1 5

<210> 269
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 269
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Arg Val Ile Pro Asn Asn Gly Gly Thr Ile Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Leu Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Asp Tyr Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 270
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 270
Asp Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
1 5 10 15

Glu Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Thr Ile Ser His Phe
20 25 30

Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Gly Gly Ser Gly Ser Asp Phe Ile Leu Thr Ile Asn Ser Val Glu Pro
65 70 75 80

Glu Asp Val Gly Met Tyr Tyr Cys Gln Ser Gly His Ser Phe Pro Tyr
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 271
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 271
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

```
Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
        35                  40                  45

Gly Arg Val Ile Pro Asn Asn Gly Gly Thr Ile Tyr Asn Gln Lys Phe
    50                  55                  60

Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Leu Ser Thr Ala Tyr
65                  70                  75                  80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Asp Tyr Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys
        115                 120                 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
    130                 135                 140

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
145                 150                 155                 160

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
                165                 170                 175

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
            180                 185                 190

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
        195                 200                 205

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
    210                 215                 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
225                 230                 235                 240
```

```
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
                245                 250                 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
            260                 265                 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
        275                 280                 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
    290                 295                 300

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
305                 310                 315                 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
                325                 330                 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
            340                 345                 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
        355                 360                 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
    370                 375                 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
385                 390                 395                 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
                405                 410                 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
            420                 425                 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
        435                 440                 445

Ser Leu Ser Pro Gly Lys
    450
```

<210> 272
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 272
Asp Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
1 5 10 15

Glu Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Thr Ile Ser His Phe
20 25 30

Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Gly Gly Ser Gly Ser Asp Phe Ile Leu Thr Ile Asn Ser Val Glu Pro
65 70 75 80

Glu Asp Val Gly Met Tyr Tyr Cys Gln Ser Gly His Ser Phe Pro Tyr
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 273
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 273
Asp Tyr Tyr Met Asn
1 5

<210> 274
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 274
Arg Val Ile Pro Arg Asn Gly Ala Thr Thr Tyr Asn Gln Asn Phe Arg
1 5 10 15

Gly

<210> 275
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 275
Glu Asp Phe Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp Tyr
1   5   10   15

<210> 276
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 276
Arg Ala Ser Gln Ser Ile Ser His Tyr Leu His
1   5   10

<210> 277
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 277
Tyr Ala Ser Gln Ser Ile Ser
1   5

<210> 278
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 278
Gln Asn Gly His Ser Phe Pro Tyr Thr
1   5

<210> 279
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 279
Gly Tyr Ser Phe Thr Asp Tyr
1 5

<210> 280
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 280
Ile Pro Arg Asn Gly Ala
1 5

<210> 281
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 281
Glu Asp Phe Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
1 5 10

<210> 282
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 282
Ser Gln Ser Ile Ser His Tyr
1 5

<210> 283
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 283
Tyr Ala Ser
1

<210> 284
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 284
Gly His Ser Phe Pro Tyr
1 5

<210> 285
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 285
Gly Tyr Ser Phe Thr Asp Tyr Tyr Met Asn
1 5 10

<210> 286
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 286
Arg Val Ile Pro Arg Asn Gly Ala Thr Thr
1 5 10

<210> 287
<211> 15

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 287
Glu Asp Phe Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp Tyr
1 5 10 15

<210> 288
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 288
Arg Ala Ser Gln Ser Ile Ser His Tyr Leu His
1 5 10

<210> 289
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 289
Tyr Ala Ser Gln Ser Ile Ser
1 5

<210> 290
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 290
Gln Asn Gly His Ser Phe Pro Tyr Thr
1 5

<210> 291
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 291
Thr Asp Tyr Tyr Met Asn
1 5

<210> 292
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 292
Trp Ile Gly Arg Val Ile Pro Arg Asn Gly Ala Thr Thr
1 5 10

<210> 293
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 293
Ala Arg Glu Asp Phe Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
1 5 10 15

<210> 294
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 294
Ser His Tyr Leu His Trp Tyr
1 5

<210> 295
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 295
Leu Leu Ile Lys Tyr Ala Ser Gln Ser Ile
1 5 10

<210> 296
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 296
Gln Asn Gly His Ser Phe Pro Tyr
1 5

<210> 297
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 297
Gly Tyr Ser Phe Thr Asp Tyr Tyr
1 5

<210> 298
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 298

Val Ile Pro Arg Asn Gly Ala Thr
1 5

<210> 299
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 299
Ala Arg Glu Asp Phe Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
1 5 10 15

Tyr

<210> 300
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 300
Gln Ser Ile Ser His Tyr
1 5

<210> 301
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 301
Tyr Ala Ser
1

<210> 302
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 302
Gln Asn Gly His Ser Phe Pro Tyr Thr
1 5

<210> 303
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 303
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr
20 25 30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Gln Ser Leu Glu Trp Ile
35 40 45

Gly Arg Val Ile Pro Arg Asn Gly Ala Thr Thr Tyr Asn Gln Asn Phe
50 55 60

Arg Gly Lys Ala Thr Leu Thr Val Asp Ile Ser Leu Arg Thr Ala Tyr
65 70 75 80

Met His Leu Asn Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Asp Phe Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 304
<211> 107

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 304
Asp Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
1 5 10 15

Asp Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser His Tyr
20 25 30

Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Ser Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Pro
65 70 75 80

Glu Asp Val Gly Val Tyr Tyr Cys Gln Asn Gly His Ser Phe Pro Tyr
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Met Lys
100 105

<210> 305
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 305
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr
20 25 30

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Tyr Met Asn Trp Val Lys Gln Ser His Gly Gln Ser Leu Glu Trp Ile
        35                  40                  45

Gly Arg Val Ile Pro Arg Asn Gly Ala Thr Thr Tyr Asn Gln Asn Phe
    50                  55                  60

Arg Gly Lys Ala Thr Leu Thr Val Asp Ile Ser Leu Arg Thr Ala Tyr
65                  70                  75                  80

Met His Leu Asn Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Asp Phe Ser Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys
        115                 120                 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
    130                 135                 140

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
145                 150                 155                 160

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
                165                 170                 175

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
            180                 185                 190

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
        195                 200                 205

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
    210                 215                 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
225                 230                 235                 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
                245                 250                 255
```

```
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
            260                 265                 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
        275                 280                 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
    290                 295                 300

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
305                 310                 315                 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
                325                 330                 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
            340                 345                 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
        355                 360                 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
    370                 375                 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
385                 390                 395                 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
                405                 410                 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
            420                 425                 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
        435                 440                 445

Ser Leu Ser Pro Gly Lys
    450
```

<210> 306
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 306
Asp Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
1 5 10 15

Asp Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser His Tyr
20 25 30

Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Ser Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Pro
65 70 75 80

Glu Asp Val Gly Val Tyr Tyr Cys Gln Asn Gly His Ser Phe Pro Tyr
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Met Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180   185   190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195   200   205

Phe Asn Arg Gly Glu Cys
    210

<210> 307
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 307
Asn Tyr Trp Met His
1   5

<210> 308
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 308
Asn Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Lys Phe Lys
1   5   10   15

Asp

<210> 309
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 309

Gly Leu Thr Gly Thr Gly Tyr Tyr
1 5

<210> 310
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 310
Arg Ala Ser Gln Asp Ile Arg Pro Tyr Leu Asn
1 5 10

<210> 311
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 311
Phe Thr Ser Lys Leu His Ser
1 5

<210> 312
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 312
Gln Gln Asp Asn Thr Leu Pro Tyr Thr
1 5

<210> 313
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 313
Gly Tyr Thr Phe Thr Asn Tyr
1 5

<210> 314
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 314
Asp Pro Ser Asp Ser Glu
1 5

<210> 315
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 315
Gly Leu Thr Gly Thr Gly Tyr
1 5

<210> 316
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 316
Ser Gln Asp Ile Arg Pro Tyr
1 5

<210> 317
<211> 3
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 317
Phe Thr Ser
1

<210> 318
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 318
Asp Asn Thr Leu Pro Tyr
1 5

<210> 319
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 319
Gly Tyr Thr Phe Thr Asn Tyr Trp Met His
1 5 10

<210> 320
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 320
Asn Ile Asp Pro Ser Asp Ser Glu Thr His
1 5 10

<210> 321
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 321
Gly Leu Thr Gly Thr Gly Tyr Tyr
1 5

<210> 322
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 322
Arg Ala Ser Gln Asp Ile Arg Pro Tyr Leu Asn
1 5 10

<210> 323
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 323
Phe Thr Ser Lys Leu His Ser
1 5

<210> 324
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 324
Gln Gln Asp Asn Thr Leu Pro Tyr Thr
1 5

<210> 325
<211> 6

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 325
Thr Asn Tyr Trp Met His
1 5

<210> 326
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 326
Trp Ile Gly Asn Ile Asp Pro Ser Asp Ser Glu Thr His
1 5 10

<210> 327
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 327
Ala Ser Gly Leu Thr Gly Thr Gly Tyr
1 5

<210> 328
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 328
Arg Pro Tyr Leu Asn Trp Tyr
1 5

<210> 329
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 329
Leu Leu Ile Tyr Phe Thr Ser Lys Leu His
1 5 10

<210> 330
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 330
Gln Gln Asp Asn Thr Leu Pro Tyr
1 5

<210> 331
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 331
Gly Tyr Thr Phe Thr Asn Tyr Trp
1 5

<210> 332
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 332
Ile Asp Pro Ser Asp Ser Glu Thr
1 5

<210> 333
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 333
Ala Ser Gly Leu Thr Gly Thr Gly Tyr Tyr
1 5 10

<210> 334
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 334
Gln Asp Ile Arg Pro Tyr
1 5

<210> 335
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 335
Phe Thr Ser
1

<210> 336
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 336

Gln Gln Asp Asn Thr Leu Pro Tyr Thr
1   5

<210> 337
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 337
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1   5   10   15

Ser Val Met Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
            20   25   30

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Asn Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Lys Phe
    50   55   60

Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85   90   95

Ala Ser Gly Leu Thr Gly Thr Gly Tyr Tyr Trp Gly Gln Gly Thr Thr
            100   105   110

Leu Thr Val Ser Ser
        115

<210> 338
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 338
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Pro Tyr
            20   25   30

Leu Asn Trp Tyr Gln Gln Lys Pro Glu Gly Thr Ile Lys Leu Leu Ile
        35   40   45

Tyr Phe Thr Ser Lys Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65   70   75   80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Asp Asn Thr Leu Pro Tyr
                85   90   95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Leu Lys
            100   105

<210> 339
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 339
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1   5   10   15

Ser Val Met Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
            20   25   30

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Asn Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Lys Phe
    50   55   60

```
Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Ser Gly Leu Thr Gly Thr Gly Tyr Tyr Trp Gly Gln Gly Thr Thr
            100                 105                 110

Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
        115                 120                 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
    210                 215                 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
225                 230                 235                 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
            260                 265                 270
```

```
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
    290                 295                 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                 310                 315                 320

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
                325                 330                 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
            340                 345                 350

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        355                 360                 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385                 390                 395                 400

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
                405                 410                 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            420                 425                 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
```

<210> 340
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 340

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Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1               5                  10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Pro Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Glu Gly Thr Ile Lys Leu Leu Ile
        35                  40                  45

Tyr Phe Thr Ser Lys Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65                  70                  75                  80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Asp Asn Thr Leu Pro Tyr
                85                  90                  95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 341
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 341
Asp Tyr Tyr Met Asp
1 5

<210> 342
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 342
Tyr Ile Tyr Pro Asn Asn Gly Ile Thr Ser Tyr Asn Gln Lys Phe Lys
1 5 10 15

Gly

<210> 343
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 343
Ser Ile Tyr Tyr Asp His Gly Gly Gly Phe Pro Tyr
1 5 10

<210> 344
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 344
Lys Ala Ser Gln Asn Val Asp Lys Tyr Val Ala
1 5 10

<210> 345
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 345
Ser Ala Ser Tyr Arg Tyr Ser
1 5

<210> 346
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 346
Gln Gln Tyr Asn Thr Tyr Pro Ser
1 5

<210> 347
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 347
Gly Tyr Ile Phe Thr Asp Tyr
1 5

<210> 348
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 348
Tyr Pro Asn Asn Gly Ile
1 5

<210> 349
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 349
Ser Ile Tyr Tyr Asp His Gly Gly Gly Phe Pro
1 5 10

<210> 350
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 350
Ser Gln Asn Val Asp Lys Tyr
1 5

<210> 351
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 351
Ser Ala Ser
1

<210> 352
<211> 5

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 352
Tyr Asn Thr Tyr Pro
1 5

<210> 353
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 353
Gly Tyr Ile Phe Thr Asp Tyr Tyr Met Asp
1 5 10

<210> 354
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 354
Tyr Ile Tyr Pro Asn Asn Gly Ile Thr Ser
1 5 10

<210> 355
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 355
Ser Ile Tyr Tyr Asp His Gly Gly Gly Phe Pro Tyr
1 5 10

<210> 356
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 356
Lys Ala Ser Gln Asn Val Asp Lys Tyr Val Ala
1 5 10

<210> 357
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 357
Ser Ala Ser Tyr Arg Tyr Ser
1 5

<210> 358
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 358
Gln Gln Tyr Asn Thr Tyr Pro Ser
1 5

<210> 359
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 359
Thr Asp Tyr Tyr Met Asp
1 5

<210> 360
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 360
Trp Ile Gly Tyr Ile Tyr Pro Asn Asn Gly Ile Thr Ser
1 5 10

<210> 361
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 361
Ala Arg Ser Ile Tyr Tyr Asp His Gly Gly Gly Phe Pro
1 5 10

<210> 362
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 362
Asp Lys Tyr Val Ala Trp Tyr
1 5

<210> 363
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 363

Ala Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr
1   5   10

<210> 364
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 364
Gln Gln Tyr Asn Thr Tyr Pro
1   5

<210> 365
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 365
Gly Tyr Ile Phe Thr Asp Tyr Tyr
1   5

<210> 366
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 366
Ile Tyr Pro Asn Asn Gly Ile Thr
1   5

<210> 367
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 367
Ala Arg Ser Ile Tyr Tyr Asp His Gly Gly Gly Phe Pro Tyr
1   5   10

<210> 368
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 368
Gln Asn Val Asp Lys Tyr
1   5

<210> 369
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 369
Ser Ala Ser
1

<210> 370
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 370
Gln Gln Tyr Asn Thr Tyr Pro Ser
1   5

<210> 371
<211> 121
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 371
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Asp
1 5 10 15

Ser Met Lys Met Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asp Tyr
20 25 30

Tyr Met Asp Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Tyr Pro Asn Asn Gly Ile Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Arg Ala Thr Leu Thr Ile Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu His Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Ile Tyr Tyr Asp His Gly Gly Gly Phe Pro Tyr Trp Gly
100 105 110

Gln Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 372
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 372
Asp Ile Val Leu Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15

Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Asp Lys Tyr
20 25 30

```
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile
        35                  40                  45


Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Val Gln Ser
65                  70                  75                  80


Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Asn Thr Tyr Pro Ser
                85                  90                  95


Phe Gly Ser Gly Thr Lys Leu Glu Met Lys
            100                 105


<210> 373
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 373
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Asp
1               5                   10                  15


Ser Met Lys Met Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asp Tyr
            20                  25                  30


Tyr Met Asp Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
        35                  40                  45


Gly Tyr Ile Tyr Pro Asn Asn Gly Ile Thr Ser Tyr Asn Gln Lys Phe
    50                  55                  60


Lys Gly Arg Ala Thr Leu Thr Ile Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu His Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Arg Ser Ile Tyr Tyr Asp His Gly Gly Gly Phe Pro Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320
```

```
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445

Pro Gly Lys
    450
```

<210> 374
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 374

```
Asp Ile Val Leu Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly
1               5                   10                  15

Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Asp Lys Tyr
            20                  25                  30
```

```
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile
        35                  40                  45

Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Val Gln Ser
65                  70                  75                  80

Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Asn Thr Tyr Pro Ser
                85                  90                  95

Phe Gly Ser Gly Thr Lys Leu Glu Met Lys Arg Thr Val Ala Ala Pro
            100                 105                 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
        115                 120                 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
    130                 135                 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145                 150                 155                 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165                 170                 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180                 185                 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195                 200                 205

Asn Arg Gly Glu Cys
    210
```

<210> 375
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 375
Asp Tyr Tyr Met Asn
1 5

<210> 376
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 376
Arg Val Ile Pro Ser Asn Gly Gly Thr Ile Tyr Asn Leu Lys Phe Lys
1 5 10 15

Gly

<210> 377
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 377
Glu Asp Tyr Asn Asn Gln Gly Phe Phe Leu Asp Ala Met Asp Tyr
1 5 10 15

<210> 378
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 378
Arg Ala Ser Gln Ser Ile Ser Asp Phe Leu His
1 5 10

<210> 379
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 379
Tyr Ala Ser Gln Ser Ile Ser
1 5

<210> 380
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 380
Gln Asn Gly His Ser Phe Pro Tyr Thr
1 5

<210> 381
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 381
Gly Tyr Thr Phe Thr Asp Tyr
1 5

<210> 382
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 382

Ile Pro Ser Asn Gly Gly
1   5

<210> 383
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 383
Glu Asp Tyr Asn Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
1   5   10

<210> 384
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 384
Ser Gln Ser Ile Ser Asp Phe
1   5

<210> 385
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 385
Tyr Ala Ser
1

<210> 386
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 386
Gly His Ser Phe Pro Tyr
1 5

<210> 387
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 387
Gly Tyr Thr Phe Thr Asp Tyr Tyr Met Asn
1 5 10

<210> 388
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 388
Arg Val Ile Pro Ser Asn Gly Gly Thr Ile
1 5 10

<210> 389
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 389
Glu Asp Tyr Asn Asn Gln Gly Phe Phe Leu Asp Ala Met Asp Tyr
1 5 10 15

<210> 390
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 390
Arg Ala Ser Gln Ser Ile Ser Asp Phe Leu His
1 5 10

<210> 391
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 391
Tyr Ala Ser Gln Ser Ile Ser
1 5

<210> 392
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 392
Gln Asn Gly His Ser Phe Pro Tyr Thr
1 5

<210> 393
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 393
Thr Asp Tyr Tyr Met Asn
1 5

<210> 394
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 394
Trp Ile Gly Arg Val Ile Pro Ser Asn Gly Gly Thr Ile
1 5 10

<210> 395
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 395
Ala Arg Glu Asp Tyr Asn Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
1 5 10 15

<210> 396
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 396
Ser Asp Phe Leu His Trp Tyr
1 5

<210> 397
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 397
Leu Leu Ile Lys Tyr Ala Ser Gln Ser Ile
1 5 10

<210> 398
<211> 8

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 398
Gln Asn Gly His Ser Phe Pro Tyr
1 5

<210> 399
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 399
Gly Tyr Thr Phe Thr Asp Tyr Tyr
1 5

<210> 400
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 400
Val Ile Pro Ser Asn Gly Gly Thr
1 5

<210> 401
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 401
Ala Arg Glu Asp Tyr Asn Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
1 5 10 15

Tyr

<210> 402
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 402
Gln Ser Ile Ser Asp Phe
1 5

<210> 403
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 403
Tyr Ala Ser
1

<210> 404
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 404
Gln Asn Gly His Ser Phe Pro Tyr Thr
1 5

<210> 405
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 405
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Thr
1   5   10   15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20   25   30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
        35   40   45

Gly Arg Val Ile Pro Ser Asn Gly Gly Thr Ile Tyr Asn Leu Lys Phe
    50   55   60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Leu Ser Thr Ala Tyr
65   70   75   80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
                85   90   95

Ala Arg Glu Asp Tyr Asn Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
            100   105   110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
        115   120

<210> 406
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 406
Asp Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
1   5   10   15

Asp Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Asp Phe
            20   25   30

Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
        35   40   45

Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Ser Asp Phe Thr Leu Thr Ile Asn Ser Val Glu Pro
65   70   75   80

Glu Asp Val Gly Val Tyr Tyr Cys Gln Asn Gly His Ser Phe Pro Tyr
                85   90   95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 407
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 407
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Thr
1   5   10   15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20   25   30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
        35   40   45

Gly Arg Val Ile Pro Ser Asn Gly Gly Thr Ile Tyr Asn Leu Lys Phe
    50   55   60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Leu Ser Thr Ala Tyr
65   70   75   80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
                85   90   95

Ala Arg Glu Asp Tyr Asn Asn Gln Gly Phe Phe Leu Asp Ala Met Asp
            100   105   110

```
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys
        115                 120                 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
    130                 135                 140

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
145                 150                 155                 160

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
                165                 170                 175

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
            180                 185                 190

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
        195                 200                 205

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
    210                 215                 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
225                 230                 235                 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
                245                 250                 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
            260                 265                 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
        275                 280                 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
    290                 295                 300

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
305                 310                 315                 320
```

```
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
                325                 330                 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
            340                 345                 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
        355                 360                 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
    370                 375                 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
385                 390                 395                 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
                405                 410                 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
            420                 425                 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
        435                 440                 445

Ser Leu Ser Pro Gly Lys
    450
```

<210> 408
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 408

```
Asp Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
1               5                   10                  15

Asp Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Asp Phe
            20                  25                  30
```

```
Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
        35                  40                  45

Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Ser Asp Phe Thr Leu Thr Ile Asn Ser Val Glu Pro
65                  70                  75                  80

Glu Asp Val Gly Val Tyr Tyr Cys Gln Asn Gly His Ser Phe Pro Tyr
                85                  90                  95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 409
<211> 5
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 409
Asp Tyr Tyr Met Asp
1 5

<210> 410
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 410
Tyr Ile Tyr Pro Asn Asn Gly Asp Thr Arg Tyr Asn Gln Lys Phe Lys
1 5 10 15

Asp

<210> 411
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 411
Ser Ile Tyr Tyr Asp His Gly Gly Gly Phe Pro Tyr
1 5 10

<210> 412
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 412
Lys Ala Ser Gln Asn Val Gly Thr Tyr Val Ala
1 5 10

<210> 413
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 413
Ser Ala Ser Tyr Arg Tyr Ser
1 5

<210> 414
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 414
Gln Gln Tyr Asn Ser Tyr Pro Thr
1 5

<210> 415
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 415
Gly Tyr Thr Phe Thr Asp Tyr
1 5

<210> 416
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 416
Tyr Pro Asn Asn Gly Asp
1 5

<210> 417
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 417
Ser Ile Tyr Tyr Asp His Gly Gly Gly Phe Pro
1 5 10

<210> 418
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 418
Ser Gln Asn Val Gly Thr Tyr
1 5

<210> 419
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 419
Ser Ala Ser
1

<210> 420
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 420

Tyr Asn Ser Tyr Pro
1 5

<210> 421
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 421
Gly Tyr Thr Phe Thr Asp Tyr Tyr Met Asp
1 5 10

<210> 422
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 422
Tyr Ile Tyr Pro Asn Asn Gly Asp Thr Arg
1 5 10

<210> 423
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 423
Ser Ile Tyr Tyr Asp His Gly Gly Gly Phe Pro Tyr
1 5 10

<210> 424
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 424
Lys Ala Ser Gln Asn Val Gly Thr Tyr Val Ala
1   5   10

<210> 425
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 425
Ser Ala Ser Tyr Arg Tyr Ser
1   5

<210> 426
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 426
Gln Gln Tyr Asn Ser Tyr Pro Thr
1   5

<210> 427
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 427
Thr Asp Tyr Tyr Met Asp
1   5

<210> 428
<211> 13
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 428
Trp Ile Gly Tyr Ile Tyr Pro Asn Asn Gly Asp Thr Arg
1 5 10

<210> 429
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 429
Ala Arg Ser Ile Tyr Tyr Asp His Gly Gly Gly Phe Pro
1 5 10

<210> 430
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 430
Gly Thr Tyr Val Ala Trp Tyr
1 5

<210> 431
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 431
Ala Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr
1 5 10

<210> 432
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 432
Gln Gln Tyr Asn Ser Tyr Pro
1 5

<210> 433
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 433
Gly Tyr Thr Phe Thr Asp Tyr Tyr
1 5

<210> 434
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 434
Ile Tyr Pro Asn Asn Gly Asp Thr
1 5

<210> 435
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 435
Ala Arg Ser Ile Tyr Tyr Asp His Gly Gly Gly Phe Pro Tyr
1 5 10

<210> 436
<211> 6

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 436
Gln Asn Val Gly Thr Tyr
1 5

<210> 437
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 437
Ser Ala Ser
1

<210> 438
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 438
Gln Gln Tyr Asn Ser Tyr Pro Thr
1 5

<210> 439
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 439
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Asn
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20   25   30

Tyr Met Asp Trp Val Lys Gln Ser His Gly Thr Ser Leu Glu Trp Ile
        35   40   45

Gly Tyr Ile Tyr Pro Asn Asn Gly Asp Thr Arg Tyr Asn Gln Lys Phe
    50   55   60

Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80

Met Glu Leu His Ser Leu Thr Ser Glu Asp Ser Ala Val Phe Tyr Cys
                85   90   95

Ala Arg Ser Ile Tyr Tyr Asp His Gly Gly Gly Phe Pro Tyr Trp Gly
            100   105   110

Gln Gly Thr Leu Val Thr Val Ser Ala
        115   120

<210> 440
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 440
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly
1   5   10   15

Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Tyr
            20   25   30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile
        35   40   45

Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Gly
    50   55   60

```
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Asn Val Gln Ser
65                  70                  75                  80


Glu Asp Leu Ala Glu Tyr Leu Cys Gln Gln Tyr Asn Ser Tyr Pro Thr
                85                  90                  95


Phe Gly Gly Gly Thr Arg Leu Glu Ile Lys
            100                 105


<210> 441
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 441
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Asn
1               5                   10                  15


Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30


Tyr Met Asp Trp Val Lys Gln Ser His Gly Thr Ser Leu Glu Trp Ile
        35                  40                  45


Gly Tyr Ile Tyr Pro Asn Asn Gly Asp Thr Arg Tyr Asn Gln Lys Phe
    50                  55                  60


Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu His Ser Leu Thr Ser Glu Asp Ser Ala Val Phe Tyr Cys
                85                  90                  95


Ala Arg Ser Ile Tyr Tyr Asp His Gly Gly Gly Phe Pro Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125
```

```
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350
```

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 442
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 442
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15

Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Tyr
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile
35 40 45

Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

```
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Asn Val Gln Ser
65                  70                  75                  80

Glu Asp Leu Ala Glu Tyr Leu Cys Gln Gln Tyr Asn Ser Tyr Pro Thr
                85                  90                  95

Phe Gly Gly Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
            100                 105                 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
        115                 120                 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
    130                 135                 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145                 150                 155                 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165                 170                 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180                 185                 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195                 200                 205

Asn Arg Gly Glu Cys
    210


<210> 443
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 443
Thr Ser Gly Met Asn Val Gly
1               5
```

<210> 444
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 444
His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 445
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 445
Arg Gly Asn Tyr Gly Asn Tyr Glu Phe Ala Tyr
1 5 10

<210> 446
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 446
Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn
1 5 10

<210> 447
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 447

His Thr Ser Arg Leu His Ser
1   5

<210> 448
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 448
Gln Gln Gly Asn Thr Leu Pro Trp Thr
1   5

<210> 449
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 449
Gly Phe Ser Leu Ser Thr Ser Gly Met
1   5

<210> 450
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 450
Trp Trp Asp Asp Asp
1   5

<210> 451
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 451
Arg Gly Asn Tyr Gly Asn Tyr Glu Phe Ala
1   5   10

<210> 452
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 452
Ser Gln Asp Ile Arg Asn Tyr
1   5

<210> 453
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 453
His Thr Ser
1

<210> 454
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 454
Gly Asn Thr Leu Pro Trp
1   5

<210> 455
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 455
Gly Phe Ser Leu Ser Thr Ser Gly Met Asn Val Gly
1 5 10

<210> 456
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 456
His Ile Trp Trp Asp Asp Asp Lys Tyr
1 5

<210> 457
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 457
Arg Gly Asn Tyr Gly Asn Tyr Glu Phe Ala Tyr
1 5 10

<210> 458
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 458
Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn
1 5 10

<210> 459
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 459
His Thr Ser Arg Leu His Ser
1 5

<210> 460
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 460
Gln Gln Gly Asn Thr Leu Pro Trp Thr
1 5

<210> 461
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 461
Ser Thr Ser Gly Met Asn Val Gly
1 5

<210> 462
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 462
Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Tyr
1 5 10

<210> 463
<211> 12

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 463
Ala Arg Arg Gly Asn Tyr Gly Asn Tyr Glu Phe Ala
1 5 10

<210> 464
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 464
Arg Asn Tyr Leu Asn Trp Tyr
1 5

<210> 465
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 465
Leu Leu Ile Tyr His Thr Ser Arg Leu His
1 5 10

<210> 466
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 466
Gln Gln Gly Asn Thr Leu Pro Trp
1 5

<210> 467
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 467
Gly Phe Ser Leu Ser Thr Ser Gly Met Asn
1 5 10

<210> 468
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 468
Ile Trp Trp Asp Asp Asp Lys
1 5

<210> 469
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 469
Ala Arg Arg Gly Asn Tyr Gly Asn Tyr Glu Phe Ala Tyr
1 5 10

<210> 470
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 470
Gln Asp Ile Arg Asn Tyr
1 5

<210> 471
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 471
His Thr Ser
1

<210> 472
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 472
Gln Gln Gly Asn Thr Leu Pro Trp Thr
1 5

<210> 473
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 473
Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Ile Leu Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

Gly Met Asn Val Gly Trp Ile Arg Gln Pro Ser Gly Lys Gly Leu Glu
35 40 45

Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ser
50 55 60

```
Leu Lys Ser Gln Leu Thr Ile Ser Lys Asp Thr Ser Arg Asn Gln Val
65                  70                  75                  80


Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr
                85                  90                  95


Cys Ala Arg Arg Gly Asn Tyr Gly Asn Tyr Glu Phe Ala Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Thr Leu Thr Val Ser Ser
        115                 120


<210> 474
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 474
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1               5                   10                  15


Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
        35                  40                  45


Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65                  70                  75                  80


Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
                85                  90                  95


Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
            100                 105
```

<210> 475
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 475
Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Ile Leu Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

Gly Met Asn Val Gly Trp Ile Arg Gln Pro Ser Gly Lys Gly Leu Glu
35 40 45

Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Gln Leu Thr Ile Ser Lys Asp Thr Ser Arg Asn Gln Val
65 70 75 80

Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Arg Gly Asn Tyr Gly Asn Tyr Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

```
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380
```

```
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400


Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415


Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430


His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445


Pro Gly Lys
    450


<210> 476
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 476
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1               5                   10                  15


Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
        35                  40                  45


Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65                  70                  75                  80


Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
                85                  90                  95
```

```
Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala
            100                 105                 110


Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175


Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190


Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205


Phe Asn Arg Gly Glu Cys
    210


<210> 477
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 477
Val Tyr Thr Ile His
1               5


<210> 478
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide
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<400> 478
Trp Phe Tyr Pro Gly Ser Gly Asn Ile Lys Tyr Asn Glu Lys Phe Lys
1   5   10   15

Asp

<210> 479
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 479
His Glu Asp Asn His Tyr Tyr Asp Gly Asn Ser Trp Phe Ala Tyr
1   5   10   15

<210> 480
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 480
Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala
1   5   10

<210> 481
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 481
Asn Ala Lys Thr Leu Ala Asp
1   5

<210> 482
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 482
Gln His Phe Trp Asn Thr Pro Tyr Thr
1 5

<210> 483
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 483
Gly Tyr Thr Phe Thr Val Tyr
1 5

<210> 484
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 484
Tyr Pro Gly Ser Gly Asn
1 5

<210> 485
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 485
His Glu Asp Asn His Tyr Tyr Asp Gly Asn Ser Trp Phe Ala
1 5 10

<210> 486
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 486
Ser Gly Asn Ile His Asn Tyr
1 5

<210> 487
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 487
Asn Ala Lys
1

<210> 488
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 488
Phe Trp Asn Thr Pro Tyr
1 5

<210> 489
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 489
Gly Tyr Thr Phe Thr Val Tyr Thr Ile His
1 5 10

<210> 490
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 490
Trp Phe Tyr Pro Gly Ser Gly Asn Ile Lys
1 5 10

<210> 491
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 491
His Glu Asp Asn His Tyr Tyr Asp Gly Asn Ser Trp Phe Ala Tyr
1 5 10 15

<210> 492
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 492
Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala
1 5 10

<210> 493
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 493

Asn Ala Lys Thr Leu Ala Asp
1 5

<210> 494
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 494
Gln His Phe Trp Asn Thr Pro Tyr Thr
1 5

<210> 495
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 495
Thr Val Tyr Thr Ile His
1 5

<210> 496
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 496
Trp Ile Gly Trp Phe Tyr Pro Gly Ser Gly Asn Ile Lys
1 5 10

<210> 497
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 497
Ala Arg His Glu Asp Asn His Tyr Tyr Asp Gly Asn Ser Trp Phe Ala
1   5   10   15

<210> 498
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 498
His Asn Tyr Leu Ala Trp Phe
1   5

<210> 499
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 499
Leu Leu Val Tyr Asn Ala Lys Thr Leu Ala
1   5   10

<210> 500
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 500
Gln His Phe Trp Asn Thr Pro Tyr
1   5

<210> 501
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 501
Gly Tyr Thr Phe Thr Val Tyr Thr
1 5

<210> 502
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 502
Phe Tyr Pro Gly Ser Gly Asn Ile
1 5

<210> 503
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 503
Ala Arg His Glu Asp Asn His Tyr Tyr Asp Gly Asn Ser Trp Phe Ala
1 5 10 15

Tyr

<210> 504
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 504
Gly Asn Ile His Asn Tyr
1 5

<210> 505
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 505
Asn Ala Lys
1

<210> 506
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 506
Gln His Phe Trp Asn Thr Pro Tyr Thr
1 5

<210> 507
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 507
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Val Tyr
20 25 30

Thr Ile His Trp Val Lys Gln Arg Ser Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Phe Tyr Pro Gly Ser Gly Asn Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser His Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg His Glu Asp Asn His Tyr Tyr Asp Gly Asn Ser Trp Phe Ala
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
115 120

<210> 508
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 508
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Gln Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr
20 25 30

Leu Ala Trp Phe Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
35 40 45

Tyr Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Thr
65 70 75 80

Glu Asp Phe Gly Asn Tyr Tyr Cys Gln His Phe Trp Asn Thr Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 509
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 509
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Val Tyr
20 25 30

Thr Ile His Trp Val Lys Gln Arg Ser Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Phe Tyr Pro Gly Ser Gly Asn Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser His Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg His Glu Asp Asn His Tyr Tyr Asp Gly Asn Ser Trp Phe Ala
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys
115 120 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
130 135 140

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
145 150 155 160

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
165 170 175

```
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
            180                 185                 190

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
        195                 200                 205

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
    210                 215                 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
225                 230                 235                 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
                245                 250                 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
            260                 265                 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
        275                 280                 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
    290                 295                 300

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
305                 310                 315                 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
                325                 330                 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
            340                 345                 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
        355                 360                 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
    370                 375                 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
385                 390                 395                 400
```

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
435 440 445

Ser Leu Ser Pro Gly Lys
450

<210> 510
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 510
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Gln Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr
20 25 30

Leu Ala Trp Phe Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
35 40 45

Tyr Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Thr
65 70 75 80

Glu Asp Phe Gly Asn Tyr Tyr Cys Gln His Phe Trp Asn Thr Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

```
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175


Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190


Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205


Phe Asn Arg Gly Glu Cys
    210


<210> 511
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 511
Ile Tyr Ser Ile His
1               5


<210> 512
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 512
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Met Ile Trp Gly Gly Gly Asp Thr Asp Tyr Asn Ser Ala Leu Lys Ser
1 5 10 15

<210> 513
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 513
Asn Pro His Tyr Tyr Gly Gly Thr Tyr Glu Tyr Phe Asp Val
1 5 10

<210> 514
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 514
Ser Ala Ser Gln Gly Ile Ser Asn Tyr Leu Asn
1 5 10

<210> 515
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 515
Asp Thr Ser Ile Leu Tyr Ser
1 5

<210> 516
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 516
Gln Gln Tyr Ser Asn Leu Pro Tyr Thr
1   5

<210> 517
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 517
Gly Phe Ser Leu Ser Ile Tyr
1   5

<210> 518
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 518
Trp Gly Gly Gly Asp
1   5

<210> 519
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 519
Asn Pro His Tyr Tyr Gly Gly Thr Tyr Glu Tyr Phe Asp
1   5   10

<210> 520
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 520
Ser Gln Gly Ile Ser Asn Tyr
1 5

<210> 521
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 521
Asp Thr Ser
1

<210> 522
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 522
Tyr Ser Asn Leu Pro Tyr
1 5

<210> 523
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 523
Gly Phe Ser Leu Ser Ile Tyr Ser Ile His
1 5 10

<210> 524
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 524
Met Ile Trp Gly Gly Gly Asp Thr Asp
1 5

<210> 525
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 525
Asn Pro His Tyr Tyr Gly Gly Thr Tyr Glu Tyr Phe Asp Val
1 5 10

<210> 526
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 526
Ser Ala Ser Gln Gly Ile Ser Asn Tyr Leu Asn
1 5 10

<210> 527
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 527
Asp Thr Ser Ile Leu Tyr Ser
1 5

<210> 528
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 528
Gln Gln Tyr Ser Asn Leu Pro Tyr Thr
1 5

<210> 529
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 529
Ser Ile Tyr Ser Ile His
1 5

<210> 530
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 530
Trp Leu Gly Met Ile Trp Gly Gly Gly Asp Thr Asp
1 5 10

<210> 531
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 531
Ala Arg Asn Pro His Tyr Tyr Gly Gly Thr Tyr Glu Tyr Phe Asp
1 5 10 15

<210> 532
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 532
Ser Asn Tyr Leu Asn Trp Tyr
1 5

<210> 533
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 533
Leu Leu Ile Tyr Asp Thr Ser Ile Leu Tyr
1 5 10

<210> 534
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 534
Gln Gln Tyr Ser Asn Leu Pro Tyr
1 5

<210> 535
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 535
Gly Phe Ser Leu Ser Ile Tyr Ser
1 5

<210> 536
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 536
Ile Trp Gly Gly Gly Asp Thr
1 5

<210> 537
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 537
Ala Arg Asn Pro His Tyr Tyr Gly Gly Thr Tyr Glu Tyr Phe Asp Val
1 5 10 15

<210> 538
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 538
Gln Gly Ile Ser Asn Tyr
1 5

<210> 539
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 539

Asp Thr Ser
1

<210> 540
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 540
Gln Gln Tyr Ser Asn Leu Pro Tyr Thr
1 5

<210> 541
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 541
Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln
1 5 10 15

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Ile Tyr
20 25 30

Ser Ile His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Met Ile Trp Gly Gly Gly Asp Thr Asp Tyr Asn Ser Ala Leu Lys
50 55 60

Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Glu Ser Gln Val Phe Leu
65 70 75 80

Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

Arg Asn Pro His Tyr Tyr Gly Gly Thr Tyr Glu Tyr Phe Asp Val Trp
100 105 110

Gly Thr Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 542
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 542
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Ser Ala Ser Gln Gly Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr Asp Thr Ser Ile Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Pro
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Asn Leu Pro Tyr
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 543
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 543

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Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln
1               5                   10                  15

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Ile Tyr
            20                  25                  30

Ser Ile His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45

Gly Met Ile Trp Gly Gly Gly Asp Thr Asp Tyr Asn Ser Ala Leu Lys
    50                  55                  60

Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Glu Ser Gln Val Phe Leu
65                  70                  75                  80

Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys Ala
                85                  90                  95

Arg Asn Pro His Tyr Tyr Gly Gly Thr Tyr Glu Tyr Phe Asp Val Trp
            100                 105                 110

Gly Thr Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
        115                 120                 125

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
    130                 135                 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145                 150                 155                 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
                165                 170                 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
            180                 185                 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
        195                 200                 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
    210                 215                 220
```

```
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
225                 230                 235                 240

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                245                 250                 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            260                 265                 270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        275                 280                 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
    290                 295                 300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
305                 310                 315                 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                325                 330                 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            340                 345                 350

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
        355                 360                 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    370                 375                 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385                 390                 395                 400

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                405                 410                 415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            420                 425                 430
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Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
435 440 445

Ser Pro Gly Lys
450

<210> 544
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 544
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Ser Ala Ser Gln Gly Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr Asp Thr Ser Ile Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Pro
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Asn Leu Pro Tyr
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 545
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 545
Glu Tyr Thr Ile His
1 5

<210> 546
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 546
Trp Phe Tyr Pro Gly Thr Gly Ser Ile Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Asp

<210> 547
<211> 15

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 547
His Glu Asp Asn His Tyr Tyr Asp Gly Asn Ser Trp Phe Ala Tyr
1 5 10 15

<210> 548
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 548
Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala
1 5 10

<210> 549
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 549
Asn Ala Lys Thr Leu Ala Asp
1 5

<210> 550
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 550
Gln His Phe Trp Ser Thr Pro Tyr Thr
1 5

<210> 551
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 551
Gly Tyr Thr Phe Thr Glu Tyr
1 5

<210> 552
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 552
Tyr Pro Gly Thr Gly Ser
1 5

<210> 553
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 553
His Glu Asp Asn His Tyr Tyr Asp Gly Asn Ser Trp Phe Ala
1 5 10

<210> 554
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 554
Ser Gly Asn Ile His Asn Tyr
1 5

<210> 555
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 555
Asn Ala Lys
1

<210> 556
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 556
Phe Trp Ser Thr Pro Tyr
1 5

<210> 557
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 557
Gly Tyr Thr Phe Thr Glu Tyr Thr Ile His
1 5 10

<210> 558
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 558

Trp Phe Tyr Pro Gly Thr Gly Ser Ile Lys
1 5 10

<210> 559
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 559
His Glu Asp Asn His Tyr Tyr Asp Gly Asn Ser Trp Phe Ala Tyr
1 5 10 15

<210> 560
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 560
Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala
1 5 10

<210> 561
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 561
Asn Ala Lys Thr Leu Ala Asp
1 5

<210> 562
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 562
Gln His Phe Trp Ser Thr Pro Tyr Thr
1 5

<210> 563
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 563
Thr Glu Tyr Thr Ile His
1 5

<210> 564
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 564
Trp Ile Gly Trp Phe Tyr Pro Gly Thr Gly Ser Ile Lys
1 5 10

<210> 565
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 565
Ala Arg His Glu Asp Asn His Tyr Tyr Asp Gly Asn Ser Trp Phe Ala
1 5 10 15

<210> 566
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 566
His Asn Tyr Leu Ala Trp Phe
1 5

<210> 567
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 567
Leu Leu Val Tyr Asn Ala Lys Thr Leu Ala
1 5 10

<210> 568
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 568
Gln His Phe Trp Ser Thr Pro Tyr
1 5

<210> 569
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 569
Gly Tyr Thr Phe Thr Glu Tyr Thr
1 5

<210> 570
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 570
Phe Tyr Pro Gly Thr Gly Ser Ile
1 5

<210> 571
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 571
Ala Arg His Glu Asp Asn His Tyr Tyr Asp Gly Asn Ser Trp Phe Ala
1 5 10 15

Tyr

<210> 572
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 572
Gly Asn Ile His Asn Tyr
1 5

<210> 573
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 573
Asn Ala Lys
1

<210> 574
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 574
Gln His Phe Trp Ser Thr Pro Tyr Thr
1 5

<210> 575
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 575
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Glu Tyr
20 25 30

Thr Ile His Trp Val Lys Gln Arg Ser Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Phe Tyr Pro Gly Thr Gly Ser Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser His Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Lys Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg His Glu Asp Asn His Tyr Tyr Asp Gly Asn Ser Trp Phe Ala
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
115 120

<210> 576
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 576
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr
20 25 30

Leu Ala Trp Phe Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
35 40 45

Tyr Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Ala
65 70 75 80

Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp Ser Thr Pro Tyr
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 577
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 577
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

```
Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Glu Tyr
            20                  25                  30

Thr Ile His Trp Val Lys Gln Arg Ser Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45

Gly Trp Phe Tyr Pro Gly Thr Gly Ser Ile Lys Tyr Asn Glu Lys Phe
    50                  55                  60

Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser His Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Lys Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
                85                  90                  95

Ala Arg His Glu Asp Asn His Tyr Tyr Asp Gly Asn Ser Trp Phe Ala
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys
        115                 120                 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
    130                 135                 140

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
145                 150                 155                 160

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
                165                 170                 175

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
            180                 185                 190

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
        195                 200                 205

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
    210                 215                 220
```

```
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
225                 230                 235                 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
                245                 250                 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
            260                 265                 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
        275                 280                 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
    290                 295                 300

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
305                 310                 315                 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
                325                 330                 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
            340                 345                 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
        355                 360                 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
    370                 375                 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
385                 390                 395                 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
                405                 410                 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
            420                 425                 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
        435                 440                 445
```

Ser Leu Ser Pro Gly Lys
    450

<210> 578
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 578
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
1   5   10   15

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr
            20   25   30

Leu Ala Trp Phe Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
        35   40   45

Tyr Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Ala
65   70   75   80

Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp Ser Thr Pro Tyr
                85   90   95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
            100   105   110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115   120   125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130   135   140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145   150   155   160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 579
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 579
Glu Tyr Thr Ile His
1 5

<210> 580
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 580
Trp Phe Tyr Pro Gly Asn Gly Asn Met Arg Tyr Asn Glu Lys Phe Lys
1 5 10 15

Asp

<210> 581
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 581
Tyr Glu Asp Asn His Tyr Tyr Asp Gly Ala Ser Trp Phe Ala Tyr
1 5 10 15

<210> 582
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 582
Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala
1 5 10

<210> 583
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 583
Asn Ala Lys Thr Leu Ala Asp
1 5

<210> 584
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 584
Gln His Phe Trp Ser Thr Pro Phe Thr
1 5

<210> 585
<211> 7

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 585
Gly Tyr Thr Phe Thr Glu Tyr
1 5

<210> 586
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 586
Tyr Pro Gly Asn Gly Asn
1 5

<210> 587
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 587
Tyr Glu Asp Asn His Tyr Tyr Asp Gly Ala Ser Trp Phe Ala
1 5 10

<210> 588
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 588
Ser Gly Asn Ile His Asn Tyr
1 5

<210> 589
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 589
Asn Ala Lys
1

<210> 590
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 590
Phe Trp Ser Thr Pro Phe
1 5

<210> 591
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 591
Gly Tyr Thr Phe Thr Glu Tyr Thr Ile His
1 5 10

<210> 592
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 592
Trp Phe Tyr Pro Gly Asn Gly Asn Met Arg
1 5 10

<210> 593
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 593
Tyr Glu Asp Asn His Tyr Tyr Asp Gly Ala Ser Trp Phe Ala Tyr
1 5 10 15

<210> 594
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 594
Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala
1 5 10

<210> 595
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 595
Asn Ala Lys Thr Leu Ala Asp
1 5

<210> 596
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 596

Gln His Phe Trp Ser Thr Pro Phe Thr
1 5

<210> 597
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 597
Thr Glu Tyr Thr Ile His
1 5

<210> 598
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 598
Trp Ile Gly Trp Phe Tyr Pro Gly Asn Gly Asn Met Arg
1 5 10

<210> 599
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 599
Ala Arg Tyr Glu Asp Asn His Tyr Tyr Asp Gly Ala Ser Trp Phe Ala
1 5 10 15

<210> 600
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 600
His Asn Tyr Leu Ala Trp Phe
1   5

<210> 601
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 601
Leu Leu Val Tyr Asn Ala Lys Thr Leu Ala
1   5   10

<210> 602
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 602
Gln His Phe Trp Ser Thr Pro Phe
1   5

<210> 603
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 603
Gly Tyr Thr Phe Thr Glu Tyr Thr
1   5

<210> 604
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 604
Phe Tyr Pro Gly Asn Gly Asn Met
1 5

<210> 605
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 605
Ala Arg Tyr Glu Asp Asn His Tyr Tyr Asp Gly Ala Ser Trp Phe Ala
1 5 10 15

Tyr

<210> 606
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 606
Gly Asn Ile His Asn Tyr
1 5

<210> 607
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 607
Asn Ala Lys
1

<210> 608
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 608
Gln His Phe Trp Ser Thr Pro Phe Thr
1 5

<210> 609
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 609
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Glu Tyr
20 25 30

Thr Ile His Trp Val Lys Gln Lys Ser Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Phe Tyr Pro Gly Asn Gly Asn Met Arg Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Lys Ala Thr Leu Thr Ala Asp Arg Ser Ser His Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Tyr Glu Asp Asn His Tyr Tyr Asp Gly Ala Ser Trp Phe Ala
100 105 110

Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 610
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 610
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr
20 25 30

Leu Ala Trp Phe Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
35 40 45

Tyr Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Gly Thr Tyr Tyr Cys Gln His Phe Trp Ser Thr Pro Phe
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Met Lys
100 105

<210> 611
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 611
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

```
Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Glu Tyr
            20                  25                  30

Thr Ile His Trp Val Lys Gln Lys Ser Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45

Gly Trp Phe Tyr Pro Gly Asn Gly Asn Met Arg Tyr Asn Glu Lys Phe
    50                  55                  60

Lys Asp Lys Ala Thr Leu Thr Ala Asp Arg Ser Ser His Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
                85                  90                  95

Ala Arg Tyr Glu Asp Asn His Tyr Tyr Asp Gly Ala Ser Trp Phe Ala
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys
        115                 120                 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
    130                 135                 140

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
145                 150                 155                 160

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
                165                 170                 175

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
            180                 185                 190

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
        195                 200                 205

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
    210                 215                 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
225                 230                 235                 240
```

```
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
                245                 250                 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
            260                 265                 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
        275                 280                 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
    290                 295                 300

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
305                 310                 315                 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
                325                 330                 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
            340                 345                 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
        355                 360                 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
    370                 375                 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
385                 390                 395                 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
                405                 410                 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
            420                 425                 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
        435                 440                 445
```

Ser Leu Ser Pro Gly Lys
    450

<210> 612
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 612
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
1   5   10   15

Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr
            20   25   30

Leu Ala Trp Phe Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
        35   40   45

Tyr Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn Ser Leu Gln Pro
65   70   75   80

Glu Asp Phe Gly Thr Tyr Tyr Cys Gln His Phe Trp Ser Thr Pro Phe
                85   90   95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Met Lys Arg Thr Val Ala Ala
            100   105   110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115   120   125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130   135   140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145   150   155   160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 613
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 613
Asp Asp Tyr Ile Tyr
1 5

<210> 614
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 614
Trp Ile Asp Pro Glu Asn Gly Ala Thr Glu Tyr Ala Ser Lys Phe Gln
1 5 10 15

Gly

<210> 615
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 615
His Asp Tyr Gly Tyr Ala Met Asp Tyr
1 5

<210> 616
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 616
Thr Ala Ser Ser Ser Val Ser Ser Ser Tyr Leu His
1 5 10

<210> 617
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 617
Ser Thr Ser Asn Leu Ala Ser
1 5

<210> 618
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 618
His Gln Tyr His Arg Ser Pro Leu Thr
1 5

<210> 619
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 619
Gly Phe Asn Phe Lys Asp Asp
1 5

<210> 620
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 620
Asp Pro Glu Asn Gly Ala
1 5

<210> 621
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 621
His Asp Tyr Gly Tyr Ala Met Asp
1 5

<210> 622
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 622
Ser Ser Ser Val Ser Ser Ser Tyr
1 5

<210> 623
<211> 3

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 623
Ser Thr Ser
1

<210> 624
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 624
Tyr His Arg Ser Pro Leu
1 5

<210> 625
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 625
Gly Phe Asn Phe Lys Asp Asp Tyr Ile Tyr
1 5 10

<210> 626
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 626
Trp Ile Asp Pro Glu Asn Gly Ala Thr Glu
1 5 10

<210> 627
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 627
His Asp Tyr Gly Tyr Ala Met Asp Tyr
1 5

<210> 628
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 628
Thr Ala Ser Ser Ser Val Ser Ser Ser Tyr Leu His
1 5 10

<210> 629
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 629
Ser Thr Ser Asn Leu Ala Ser
1 5

<210> 630
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 630
His Gln Tyr His Arg Ser Pro Leu Thr
1 5

<210> 631
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 631
Lys Asp Asp Tyr Ile Tyr
1 5

<210> 632
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 632
Trp Ile Gly Trp Ile Asp Pro Glu Asn Gly Ala Thr Glu
1 5 10

<210> 633
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 633
Ser Leu His Asp Tyr Gly Tyr Ala Met Asp
1 5 10

<210> 634
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 634

Ser Ser Ser Tyr Leu His Trp Tyr
1 5

<210> 635
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 635
Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala
1 5 10

<210> 636
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 636
His Gln Tyr His Arg Ser Pro Leu
1 5

<210> 637
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 637
Gly Phe Asn Phe Lys Asp Asp Tyr
1 5

<210> 638
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 638
Ile Asp Pro Glu Asn Gly Ala Thr
1   5

<210> 639
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 639
Ser Leu His Asp Tyr Gly Tyr Ala Met Asp Tyr
1   5   10

<210> 640
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 640
Ser Ser Val Ser Ser Ser Tyr
1   5

<210> 641
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 641
Ser Thr Ser
1

<210> 642
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 642
His Gln Tyr His Arg Ser Pro Leu Thr
1 5

<210> 643
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 643
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Gly Ser Gly Phe Asn Phe Lys Asp Asp
20 25 30

Tyr Ile Tyr Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Ala Thr Glu Tyr Ala Ser Lys Phe
50 55 60

Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Ile Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ser Leu His Asp Tyr Gly Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Ser Val Thr Val Ser Ser
115

<210> 644
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 644
Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Leu Gly
1 5 10 15

Glu Arg Val Thr Leu Thr Cys Thr Ala Ser Ser Ser Val Ser Ser Ser
20 25 30

Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Leu Trp
35 40 45

Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Asn Met Glu
65 70 75 80

Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Tyr His Arg Ser Pro
85 90 95

Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 645
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 645
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Gly Ser Gly Phe Asn Phe Lys Asp Asp
20 25 30

Tyr Ile Tyr Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

```
Gly Trp Ile Asp Pro Glu Asn Gly Ala Thr Glu Tyr Ala Ser Lys Phe
    50                  55                  60

Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Ile Ala Tyr
65                  70                  75                  80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ser Leu His Asp Tyr Gly Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
    210                 215                 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255
```

```
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    290                 295                 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
                325                 330                 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
        355                 360                 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370                 375                 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385                 390                 395                 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                405                 410                 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            420                 425                 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
```

<210> 646
<211> 215
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 646

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Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Leu Gly
1               5                  10                  15

Glu Arg Val Thr Leu Thr Cys Thr Ala Ser Ser Ser Val Ser Ser Ser
            20                  25                  30

Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Leu Trp
        35                  40                  45

Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Asn Met Glu
65                  70                  75                  80

Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Tyr His Arg Ser Pro
                85                  90                  95

Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala
            100                 105                 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165                 170                 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180                 185                 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
        195                 200                 205
```

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 647
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 647
Ile Tyr Ser Ile His
1 5

<210> 648
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 648
Met Ile Trp Gly Gly Gly Ser Thr Asp Tyr Asn Ser Thr Leu Asn Ser
1 5 10 15

<210> 649
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 649
Asn Pro His His Tyr Gly Gly Ser Thr Gly Ala Met Asp Tyr
1 5 10

<210> 650
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 650
Lys Ala Ser Gln Asp Ile Lys Lys Tyr Met Ala
1 5 10

<210> 651
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 651
Tyr Thr Ser Ser Leu Gln Pro
1 5

<210> 652
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 652
Leu Gln Tyr Asp Asn Leu Phe Thr
1 5

<210> 653
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 653
Gly Phe Ser Leu Ser Ile Tyr
1 5

<210> 654
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 654
Trp Gly Gly Gly Ser
1 5

<210> 655
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 655
Asn Pro His His Tyr Gly Gly Ser Thr Gly Ala Met Asp
1 5 10

<210> 656
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 656
Ser Gln Asp Ile Lys Lys Tyr
1 5

<210> 657
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 657
Tyr Thr Ser
1

<210> 658
<211> 5

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 658
Tyr Asp Asn Leu Phe
1 5

<210> 659
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 659
Gly Phe Ser Leu Ser Ile Tyr Ser Ile His
1 5 10

<210> 660
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 660
Met Ile Trp Gly Gly Gly Ser Thr Asp
1 5

<210> 661
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 661
Asn Pro His His Tyr Gly Gly Ser Thr Gly Ala Met Asp Tyr
1 5 10

<210> 662
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 662
Lys Ala Ser Gln Asp Ile Lys Lys Tyr Met Ala
1 5 10

<210> 663
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 663
Tyr Thr Ser Ser Leu Gln Pro
1 5

<210> 664
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 664
Leu Gln Tyr Asp Asn Leu Phe Thr
1 5

<210> 665
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 665
Ser Ile Tyr Ser Ile His
1 5

<210> 666
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 666
Trp Leu Gly Met Ile Trp Gly Gly Gly Ser Thr Asp
1 5 10

<210> 667
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 667
Ala Arg Asn Pro His His Tyr Gly Gly Ser Thr Gly Ala Met Asp
1 5 10 15

<210> 668
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 668
Lys Lys Tyr Met Ala Trp Tyr
1 5

<210> 669
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 669

Leu Leu Ile His Tyr Thr Ser Ser Leu Gln
1 5 10

<210> 670
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 670
Leu Gln Tyr Asp Asn Leu Phe
1 5

<210> 671
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 671
Gly Phe Ser Leu Ser Ile Tyr Ser
1 5

<210> 672
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 672
Ile Trp Gly Gly Gly Ser Thr
1 5

<210> 673
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 673
Ala Arg Asn Pro His His Tyr Gly Gly Ser Thr Gly Ala Met Asp Tyr
1   5   10   15

<210> 674
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 674
Gln Asp Ile Lys Lys Tyr
1   5

<210> 675
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 675
Tyr Thr Ser
1

<210> 676
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 676
Leu Gln Tyr Asp Asn Leu Phe Thr
1   5

<210> 677
<211> 122
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 677
Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln
1 5 10 15

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Ile Tyr
20 25 30

Ser Ile His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Met Ile Trp Gly Gly Gly Ser Thr Asp Tyr Asn Ser Thr Leu Asn
50 55 60

Ser Arg Leu Ser Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu
65 70 75 80

Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

Arg Asn Pro His His Tyr Gly Gly Ser Thr Gly Ala Met Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 678
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 678
Asp Val Gln Met Ile Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Gly Thr Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Lys Lys Tyr
20 25 30

Met Ala Trp Tyr Gln His Lys Pro Gly Lys Gly Pro Arg Leu Leu Ile
35 40 45

His Tyr Thr Ser Ser Leu Gln Pro Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Arg Asp Tyr Tyr Phe Ser Ile Ser Asn Leu Glu Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Leu Gln Tyr Asp Asn Leu Phe Thr
85 90 95

Phe Gly Ser Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 679
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 679
Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln
1 5 10 15

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Ile Tyr
20 25 30

Ser Ile His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Met Ile Trp Gly Gly Gly Ser Thr Asp Tyr Asn Ser Thr Leu Asn
50 55 60

Ser Arg Leu Ser Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu
65 70 75 80

Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

```
Arg Asn Pro His His Tyr Gly Gly Ser Thr Gly Ala Met Asp Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
        115                 120                 125

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
    130                 135                 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145                 150                 155                 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
                165                 170                 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
            180                 185                 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
        195                 200                 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
    210                 215                 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
225                 230                 235                 240

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                245                 250                 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            260                 265                 270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        275                 280                 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
    290                 295                 300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
305                 310                 315                 320
```

```
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                325                 330                 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            340                 345                 350

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
        355                 360                 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    370                 375                 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385                 390                 395                 400

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                405                 410                 415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            420                 425                 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        435                 440                 445

Ser Pro Gly Lys
    450
```

<210> 680
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 680

```
Asp Val Gln Met Ile Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1               5                   10                  15

Gly Thr Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Lys Lys Tyr
            20                  25                  30
```

```
Met Ala Trp Tyr Gln His Lys Pro Gly Lys Gly Pro Arg Leu Leu Ile
        35                  40                  45

His Tyr Thr Ser Ser Leu Gln Pro Gly Ile Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Arg Asp Tyr Tyr Phe Ser Ile Ser Asn Leu Glu Pro
65                  70                  75                  80

Glu Asp Ile Ala Thr Tyr Phe Cys Leu Gln Tyr Asp Asn Leu Phe Thr
                85                  90                  95

Phe Gly Ser Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala Pro
            100                 105                 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
        115                 120                 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
    130                 135                 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145                 150                 155                 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165                 170                 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180                 185                 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195                 200                 205

Asn Arg Gly Glu Cys
    210
```

<210> 681
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 681
Thr Ser Gly Met Asn Val Gly
1 5

<210> 682
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 682
His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 683
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 683
Arg Gly Asn Tyr Gly Asn Tyr Glu Phe Ala Tyr
1 5 10

<210> 684
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 684
Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn
1 5 10

<210> 685
<211> 7

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 685
His Thr Ser Arg Leu His Ser
1 5

<210> 686
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 686
Gln Gln Gly Asn Thr Leu Pro Trp Thr
1 5

<210> 687
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 687
Gly Phe Ser Leu Ser Thr Ser Gly Met
1 5

<210> 688
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 688
Trp Trp Asp Asp Asp
1 5

<210> 689
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 689
Arg Gly Asn Tyr Gly Asn Tyr Glu Phe Ala
1 5 10

<210> 690
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 690
Ser Gln Asp Ile Arg Asn Tyr
1 5

<210> 691
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 691
His Thr Ser
1

<210> 692
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 692
Gly Asn Thr Leu Pro Trp
1 5

<210> 693
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 693
Gly Phe Ser Leu Ser Thr Ser Gly Met Asn Val Gly
1 5 10

<210> 694
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 694
His Ile Trp Trp Asp Asp Asp Lys Tyr
1 5

<210> 695
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 695
Arg Gly Asn Tyr Gly Asn Tyr Glu Phe Ala Tyr
1 5 10

<210> 696
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 696

Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn
1 5 10

<210> 697
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 697
His Thr Ser Arg Leu His Ser
1 5

<210> 698
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 698
Gln Gln Gly Asn Thr Leu Pro Trp Thr
1 5

<210> 699
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 699
Ser Thr Ser Gly Met Asn Val Gly
1 5

<210> 700
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 700
Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Tyr
1 5 10

<210> 701
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 701
Ala Arg Arg Gly Asn Tyr Gly Asn Tyr Glu Phe Ala
1 5 10

<210> 702
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 702
Arg Asn Tyr Leu Asn Trp Tyr
1 5

<210> 703
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 703
Leu Leu Ile Tyr His Thr Ser Arg Leu His
1 5 10

<210> 704
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 704
Gln Gln Gly Asn Thr Leu Pro Trp
1 5

<210> 705
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 705
Gly Phe Ser Leu Ser Thr Ser Gly Met Asn
1 5 10

<210> 706
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 706
Ile Trp Trp Asp Asp Asp Lys
1 5

<210> 707
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 707
Ala Arg Arg Gly Asn Tyr Gly Asn Tyr Glu Phe Ala Tyr
1 5 10

<210> 708
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 708
Gln Asp Ile Arg Asn Tyr
1 5

<210> 709
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 709
His Thr Ser
1

<210> 710
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 710
Gln Gln Gly Asn Thr Leu Pro Trp Thr
1 5

<210> 711
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 711
Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

```
Gly Met Asn Val Gly Trp Ile Arg Gln Pro Ser Gly Lys Gly Leu Glu
        35                  40                  45


Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ser
    50                  55                  60


Leu Lys Ser Gln Leu Thr Ile Ser Lys Asp Thr Ser Arg Asn Gln Val
65                  70                  75                  80


Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr
                85                  90                  95


Cys Ala Arg Arg Gly Asn Tyr Gly Asn Tyr Glu Phe Ala Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 712
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 712
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1               5                   10                  15


Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
        35                  40                  45


Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Asp Gln
65                  70                  75                  80
```

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 713
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 713
Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

Gly Met Asn Val Gly Trp Ile Arg Gln Pro Ser Gly Lys Gly Leu Glu
35 40 45

Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Gln Leu Thr Ile Ser Lys Asp Thr Ser Arg Asn Gln Val
65 70 75 80

Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Arg Gly Asn Tyr Gly Asn Tyr Glu Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

```
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350
```

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 714
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 714
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

```
Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Asp Gln
65                  70                  75                  80


Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
                85                  90                  95


Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala
            100                 105                 110


Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175


Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190


Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205


Phe Asn Arg Gly Glu Cys
    210


<210> 715
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 715
Ser Phe Trp Met His
1               5
```

<210> 716
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 716
Asn Val Asp Pro Ser Asp Ser Gln Thr His Tyr Asn Gln Lys Phe Lys
1 5 10 15

Asp

<210> 717
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 717
Ser Thr Tyr Tyr Arg Tyr Asp Gly Pro Phe Thr Tyr
1 5 10

<210> 718
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 718
Arg Ala Ser Gln Ser Ile Asn Asn Asn Leu His
1 5 10

<210> 719
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 719
Tyr Thr Ser Gln Ser Ile Ser
1 5

<210> 720
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 720
Gln Gln Ser Asn Ser Trp Pro Leu Thr
1 5

<210> 721
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 721
Gly Tyr Thr Phe Thr Ser Phe
1 5

<210> 722
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 722
Asp Pro Ser Asp Ser Gln
1 5

<210> 723
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 723
Ser Thr Tyr Tyr Arg Tyr Asp Gly Pro Phe Thr
1 5 10

<210> 724
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 724
Ser Gln Ser Ile Asn Asn Asn
1 5

<210> 725
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 725
Tyr Thr Ser
1

<210> 726
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 726
Ser Asn Ser Trp Pro Leu
1 5

<210> 727
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 727
Gly Tyr Thr Phe Thr Ser Phe Trp Met His
1 5 10

<210> 728
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 728
Asn Val Asp Pro Ser Asp Ser Gln Thr His
1 5 10

<210> 729
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 729
Ser Thr Tyr Tyr Arg Tyr Asp Gly Pro Phe Thr Tyr
1 5 10

<210> 730
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 730
Arg Ala Ser Gln Ser Ile Asn Asn Asn Leu His
1 5 10

<210> 731
<211> 7

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 731
Tyr Thr Ser Gln Ser Ile Ser
1 5

<210> 732
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 732
Gln Gln Ser Asn Ser Trp Pro Leu Thr
1 5

<210> 733
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 733
Thr Ser Phe Trp Met His
1 5

<210> 734
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 734
Trp Ile Gly Asn Val Asp Pro Ser Asp Ser Gln Thr His
1 5 10

<210> 735
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 735
Ala Arg Ser Thr Tyr Tyr Arg Tyr Asp Gly Pro Phe Thr
1 5 10

<210> 736
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 736
Asn Asn Asn Leu His Trp Tyr
1 5

<210> 737
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 737
Leu Leu Ile Lys Tyr Thr Ser Gln Ser Ile
1 5 10

<210> 738
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 738
Gln Gln Ser Asn Ser Trp Pro Leu
1 5

<210> 739
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 739
Gly Tyr Thr Phe Thr Ser Phe Trp
1 5

<210> 740
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 740
Val Asp Pro Ser Asp Ser Gln Thr
1 5

<210> 741
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 741
Ala Arg Ser Thr Tyr Tyr Arg Tyr Asp Gly Pro Phe Thr Tyr
1 5 10

<210> 742
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 742

Gln Ser Ile Asn Asn Asn
1 5

<210> 743
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 743
Tyr Thr Ser
1

<210> 744
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 744
Gln Gln Ser Asn Ser Trp Pro Leu Thr
1 5

<210> 745
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 745
Gln Val Gln Leu Gln Gln Pro Gly Ala Asp Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Phe
20 25 30

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

```
Gly Asn Val Asp Pro Ser Asp Ser Gln Thr His Tyr Asn Gln Lys Phe
    50                  55                  60

Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Asn Thr Ala Tyr
65                  70                  75                  80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ser Thr Tyr Tyr Arg Tyr Asp Gly Pro Phe Thr Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 746
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 746

```
Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
1               5                   10                  15

Asp Ser Val Ser Leu Ser Cys Arg Ala Ser Gln Ser Ile Asn Asn Asn
            20                  25                  30

Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
        35                  40                  45

Lys Tyr Thr Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Pro Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Thr
65                  70                  75                  80

Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Asn Ser Trp Pro Leu
                85                  90                  95
```

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 747
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 747
Gln Val Gln Leu Gln Gln Pro Gly Ala Asp Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Phe
20 25 30

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Asn Val Asp Pro Ser Asp Ser Gln Thr His Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Asn Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Thr Tyr Tyr Arg Tyr Asp Gly Pro Phe Thr Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

```
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380
```

```
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400


Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415


Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430


His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445


Pro Gly Lys
    450


<210> 748
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 748
Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
1               5                   10                  15


Asp Ser Val Ser Leu Ser Cys Arg Ala Ser Gln Ser Ile Asn Asn Asn
            20                  25                  30


Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
        35                  40                  45


Lys Tyr Thr Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Pro Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Thr
65                  70                  75                  80


Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Asn Ser Trp Pro Leu
                85                  90                  95
```

```
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110


Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175


Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190


Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205


Phe Asn Arg Gly Glu Cys
    210


<210> 749
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 749
Ser Tyr Trp Met Asn
1               5


<210> 750
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
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<223> Description of Artificial Sequence: Synthetic
peptide

<400> 750
Ala Val Asn Pro Ser Asn Ser Tyr Thr Glu Tyr Ala Gln Lys Phe Lys
1 5 10 15

Asp

<210> 751
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 751
Ser Gly Leu Tyr Asn Thr Asn His Leu Ala Trp Phe Ala Tyr
1 5 10

<210> 752
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 752
Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala
1 5 10

<210> 753
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 753
Asn Ala Glu Thr Leu Ala Asp
1 5

<210> 754
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 754
Gln His Phe Trp Asn Asn Pro Leu Thr
1 5

<210> 755
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 755
Gly Tyr Thr Phe Thr Ser Tyr
1 5

<210> 756
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 756
Asn Pro Ser Asn Ser Tyr
1 5

<210> 757
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 757
Ser Gly Leu Tyr Asn Thr Asn His Leu Ala Trp Phe Ala
1 5 10

<210> 758
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 758
Ser Gly Asn Ile His Asn Tyr
1 5

<210> 759
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 759
Asn Ala Glu
1

<210> 760
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 760
Phe Trp Asn Asn Pro Leu
1 5

<210> 761
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 761

Gly Tyr Thr Phe Thr Ser Tyr Trp Met Asn
1 5 10

<210> 762
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 762
Ala Val Asn Pro Ser Asn Ser Tyr Thr Glu
1 5 10

<210> 763
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 763
Ser Gly Leu Tyr Asn Thr Asn His Leu Ala Trp Phe Ala Tyr
1 5 10

<210> 764
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 764
Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala
1 5 10

<210> 765
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 765
Asn Ala Glu Thr Leu Ala Asp
1   5

<210> 766
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 766
Gln His Phe Trp Asn Asn Pro Leu Thr
1   5

<210> 767
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 767
Thr Ser Tyr Trp Met Asn
1   5

<210> 768
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 768
Trp Ile Gly Ala Val Asn Pro Ser Asn Ser Tyr Thr Glu
1   5   10

<210> 769
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 769
Ala Arg Ser Gly Leu Tyr Asn Thr Asn His Leu Ala Trp Phe Ala
1 5 10 15

<210> 770
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 770
His Asn Tyr Leu Ala Trp Tyr
1 5

<210> 771
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 771
Leu Leu Val Phe Asn Ala Glu Thr Leu Ala
1 5 10

<210> 772
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 772
Gln His Phe Trp Asn Asn Pro Leu
1 5

<210> 773
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 773
Gly Tyr Thr Phe Thr Ser Tyr Trp
1 5

<210> 774
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 774
Val Asn Pro Ser Asn Ser Tyr Thr
1 5

<210> 775
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 775
Ala Arg Ser Gly Leu Tyr Asn Thr Asn His Leu Ala Trp Phe Ala Tyr
1 5 10 15

<210> 776
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 776
Gly Asn Ile His Asn Tyr
1 5

<210> 777
<211> 3

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 777
Asn Ala Glu
1

<210> 778
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 778
Gln His Phe Trp Asn Asn Pro Leu Thr
1 5

<210> 779
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 779
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Ala Lys Pro Gly Thr
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Ala Val Asn Pro Ser Asn Ser Tyr Thr Glu Tyr Ala Gln Lys Phe
50 55 60

Lys Asp Lys Ala Ile Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Ser Leu Ser Gly Leu Thr Ser Glu Ala Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Leu Tyr Asn Thr Asn His Leu Ala Trp Phe Ala Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
115 120

<210> 780
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 780
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
35 40 45

Phe Asn Ala Glu Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Gly Thr Tyr Tyr Cys Gln His Phe Trp Asn Asn Pro Leu
85 90 95

Thr Leu Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 781
<211> 453

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 781
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Ala Lys Pro Gly Thr
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Ala Val Asn Pro Ser Asn Ser Tyr Thr Glu Tyr Ala Gln Lys Phe
50 55 60

Lys Asp Lys Ala Ile Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Ser Leu Ser Gly Leu Thr Ser Glu Ala Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Leu Tyr Asn Thr Asn His Leu Ala Trp Phe Ala Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
165 170 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
180 185 190

```
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
225                 230                 235                 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400
```

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
435 440 445

Leu Ser Pro Gly Lys
450

<210> 782
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 782
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
35 40 45

Phe Asn Ala Glu Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Gly Thr Tyr Tyr Cys Gln His Phe Trp Asn Asn Pro Leu
85 90 95

Thr Leu Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala
100 105 110

```
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175


Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190


Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205


Phe Asn Arg Gly Glu Cys
    210


<210> 783
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 783
Ala Tyr Trp Ile Asn
1               5


<210> 784
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 784
Ser Ile Asn Pro Ser Asn Gly Tyr Thr Glu Tyr Ser Gln Lys Phe Lys
1               5                   10                  15
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Asp

<210> 785
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 785
Ser Gly Leu Tyr Tyr Thr Asn His Leu Ala Trp Cys Pro Tyr
1 5 10

<210> 786
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 786
Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala
1 5 10

<210> 787
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 787
Asn Ala Glu Thr Leu Ala Asp
1 5

<210> 788
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 788
Gln His Phe Trp Asn Ser Pro Leu Thr
1 5

<210> 789
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 789
Gly Tyr Thr Phe Ala Ala Tyr
1 5

<210> 790
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 790
Asn Pro Ser Asn Gly Tyr
1 5

<210> 791
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 791
Ser Gly Leu Tyr Tyr Thr Asn His Leu Ala Trp Cys Pro
1 5 10

<210> 792
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 792
Ser Gly Asn Ile His Asn Tyr
1 5

<210> 793
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 793
Asn Ala Glu
1

<210> 794
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 794
Phe Trp Asn Ser Pro Leu
1 5

<210> 795
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 795
Gly Tyr Thr Phe Ala Ala Tyr Trp Ile Asn
1 5 10

<210> 796
<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 796
Ser Ile Asn Pro Ser Asn Gly Tyr Thr Glu
1 5 10

<210> 797
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 797
Ser Gly Leu Tyr Tyr Thr Asn His Leu Ala Trp Cys Pro Tyr
1 5 10

<210> 798
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 798
Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala
1 5 10

<210> 799
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 799
Asn Ala Glu Thr Leu Ala Asp
1 5

<210> 800
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 800
Gln His Phe Trp Asn Ser Pro Leu Thr
1 5

<210> 801
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 801
Ala Ala Tyr Trp Ile Asn
1 5

<210> 802
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 802
Trp Ile Gly Ser Ile Asn Pro Ser Asn Gly Tyr Thr Glu
1 5 10

<210> 803
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 803
Ser Arg Ser Gly Leu Tyr Tyr Thr Asn His Leu Ala Trp Cys Pro
1 5 10 15

<210> 804
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 804
His Asn Tyr Leu Ala Trp Tyr
1 5

<210> 805
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 805
Val Leu Val Tyr Asn Ala Glu Thr Leu Ala
1 5 10

<210> 806
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 806
Gln His Phe Trp Asn Ser Pro Leu
1 5

<210> 807
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 807

Gly Tyr Thr Phe Ala Ala Tyr Trp
1 5

<210> 808
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 808
Ile Asn Pro Ser Asn Gly Tyr Thr
1 5

<210> 809
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 809
Ser Arg Ser Gly Leu Tyr Tyr Thr Asn His Leu Ala Trp Cys Pro Tyr
1 5 10 15

<210> 810
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 810
Gly Asn Ile His Asn Tyr
1 5

<210> 811
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 811
Asn Ala Glu
1

<210> 812
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 812
Gln His Phe Trp Asn Ser Pro Leu Thr
1 5

<210> 813
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 813
Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Lys Pro Gly Thr
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ala Ala Tyr
20 25 30

Trp Ile Asn Trp Leu Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Ser Ile Asn Pro Ser Asn Gly Tyr Thr Glu Tyr Ser Gln Lys Phe
50 55 60

Lys Asp Lys Ala Ile Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ser Arg Ser Gly Leu Tyr Tyr Thr Asn His Leu Ala Trp Cys Pro Tyr
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 814
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 814
Asp Ile Val Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Val Leu Val
35 40 45

Tyr Asn Ala Glu Thr Leu Ala Asp Ser Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Gly Asn Tyr Tyr Cys Gln His Phe Trp Asn Ser Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 815
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 815

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Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Lys Pro Gly Thr
1               5                  10                  15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ala Ala Tyr
            20                  25                  30

Trp Ile Asn Trp Leu Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45

Gly Ser Ile Asn Pro Ser Asn Gly Tyr Thr Glu Tyr Ser Gln Lys Phe
    50                  55                  60

Lys Asp Lys Ala Ile Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95

Ser Arg Ser Gly Leu Tyr Tyr Thr Asn His Leu Ala Trp Cys Pro Tyr
            100                 105                 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205
```

```
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
225                 230                 235                 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430
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Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
435 440 445

Leu Ser Pro Gly Lys
450

<210> 816
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 816
Asp Ile Val Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Val Leu Val
35 40 45

Tyr Asn Ala Glu Thr Leu Ala Asp Ser Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Gly Asn Tyr Tyr Cys Gln His Phe Trp Asn Ser Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 817
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 817
Ser Gly Tyr Tyr Trp Asn
1 5

<210> 818
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 818
Tyr Ile Ser Tyr Asp Gly Ser Asn Asn Tyr Asn Pro Ser Leu Lys Asn
1 5 10 15

<210> 819
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 819
Asn His Gly Asp Ala Met Asp Tyr
1 5

<210> 820
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 820
Lys Ala Ser Gln Asn Val Gly Thr Ala Val Ala
1 5 10

<210> 821
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 821
Ser Ala Ser Tyr Arg Tyr Thr
1 5

<210> 822
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 822
Gln Gln Tyr Ser Ser Tyr Leu Thr
1 5

<210> 823
<211> 8

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 823
Gly Tyr Ser Ile Thr Ser Gly Tyr
1 5

<210> 824
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 824
Ser Tyr Asp Gly Ser
1 5

<210> 825
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 825
Asn His Gly Asp Ala Met Asp
1 5

<210> 826
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 826
Ser Gln Asn Val Gly Thr Ala
1 5

<210> 827
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 827
Ser Ala Ser
1

<210> 828
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 828
Tyr Ser Ser Tyr Leu
1 5

<210> 829
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 829
Gly Tyr Ser Ile Thr Ser Gly Tyr Tyr Trp Asn
1 5 10

<210> 830
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 830
Tyr Ile Ser Tyr Asp Gly Ser Asn Asn
1 5

<210> 831
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 831
Asn His Gly Asp Ala Met Asp Tyr
1 5

<210> 832
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 832
Lys Ala Ser Gln Asn Val Gly Thr Ala Val Ala
1 5 10

<210> 833
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 833
Ser Ala Ser Tyr Arg Tyr Thr
1 5

<210> 834
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 834

Gln Gln Tyr Ser Ser Tyr Leu Thr
1 5

<210> 835
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 835
Thr Ser Gly Tyr Tyr Trp Asn
1 5

<210> 836
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 836
Trp Met Gly Tyr Ile Ser Tyr Asp Gly Ser Asn Asn
1 5 10

<210> 837
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 837
Val Arg Asn His Gly Asp Ala Met Asp
1 5

<210> 838
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 838
Gly Thr Ala Val Ala Trp Tyr
1 5

<210> 839
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 839
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr
1 5 10

<210> 840
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 840
Gln Gln Tyr Ser Ser Tyr Leu
1 5

<210> 841
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 841
Gly Tyr Ser Ile Thr Ser Gly Tyr Tyr
1 5

<210> 842
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 842
Ile Ser Tyr Asp Gly Ser Asn
1 5

<210> 843
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 843
Val Arg Asn His Gly Asp Ala Met Asp Tyr
1 5 10

<210> 844
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 844
Gln Asn Val Gly Thr Ala
1 5

<210> 845
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 845
Ser Ala Ser
1

<210> 846
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 846
Gln Gln Tyr Ser Ser Tyr Leu Thr
1 5

<210> 847
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 847
Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Gly
20 25 30

Tyr Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
35 40 45

Met Gly Tyr Ile Ser Tyr Asp Gly Ser Asn Asn Tyr Asn Pro Ser Leu
50 55 60

Lys Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65 70 75 80

Leu Lys Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Val Arg Asn His Gly Asp Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
100 105 110

Val Thr Val Ser Ser
115

<210> 848
<211> 106

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 848
Asp Ile Val Leu Thr Gln Ser Gln Lys Phe Met Ser Thr Thr Val Gly
1 5 10 15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr His Phe Thr Leu Thr Ile Ser Asn Met Gln Ser
65 70 75 80

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Ser Tyr Leu Thr
85 90 95

Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 849
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 849
Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Gly
20 25 30

```
Tyr Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
        35                  40                  45

Met Gly Tyr Ile Ser Tyr Asp Gly Ser Asn Asn Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65                  70                  75                  80

Leu Lys Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
                85                  90                  95

Val Arg Asn His Gly Asp Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
            100                 105                 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
        115                 120                 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
    210                 215                 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
225                 230                 235                 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255
```

```
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
            260                 265                 270

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
    290                 295                 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                 310                 315                 320

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
                325                 330                 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
            340                 345                 350

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        355                 360                 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385                 390                 395                 400

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
                405                 410                 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            420                 425                 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
```

<210> 850
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 850
Asp Ile Val Leu Thr Gln Ser Gln Lys Phe Met Ser Thr Thr Val Gly
1 5 10 15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr His Phe Thr Leu Thr Ile Ser Asn Met Gln Ser
65 70 75 80

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Ser Tyr Leu Thr
85 90 95

Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
210

<210> 851
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 851
Asn Thr Tyr Ile Ser
1 5

<210> 852
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 852
Trp Ile Tyr Thr Gly Thr Gly Gly Thr Trp Tyr Asn Gln Lys Phe Thr
1 5 10 15

Asp

<210> 853
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 853
Thr Asn Trp Asp Trp Tyr Phe Asp Val
1 5

<210> 854
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 854
Arg Ala Ser Glu Asn Ile Tyr Ser Tyr Leu Ala
1 5 10

<210> 855
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 855
Tyr Ala Lys Thr Leu Thr Asp
1 5

<210> 856
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 856
Gln His His Tyr Gly Arg Pro Tyr Thr
1 5

<210> 857
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 857
Gly Phe Thr Phe Thr Asn Thr
1 5

<210> 858
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 858
Tyr Thr Gly Thr Gly Gly
1 5

<210> 859
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 859
Thr Asn Trp Asp Trp Tyr Phe Asp
1 5

<210> 860
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 860
Ser Glu Asn Ile Tyr Ser Tyr
1 5

<210> 861
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 861

Tyr Ala Lys
1

<210> 862
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 862
His Tyr Gly Arg Pro Tyr
1 5

<210> 863
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 863
Gly Phe Thr Phe Thr Asn Thr Tyr Ile Ser
1 5 10

<210> 864
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 864
Trp Ile Tyr Thr Gly Thr Gly Gly Thr Trp
1 5 10

<210> 865
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 865
Thr Asn Trp Asp Trp Tyr Phe Asp Val
1 5

<210> 866
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 866
Arg Ala Ser Glu Asn Ile Tyr Ser Tyr Leu Ala
1 5 10

<210> 867
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 867
Tyr Ala Lys Thr Leu Thr Asp
1 5

<210> 868
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 868
Gln His His Tyr Gly Arg Pro Tyr Thr
1 5

<210> 869
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 869
Thr Asn Thr Tyr Ile Ser
1 5

<210> 870
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 870
Trp Ile Ala Trp Ile Tyr Thr Gly Thr Gly Gly Thr Trp
1 5 10

<210> 871
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 871
Ala Arg Thr Asn Trp Asp Trp Tyr Phe Asp
1 5 10

<210> 872
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 872
Tyr Ser Tyr Leu Ala Trp Tyr
1 5

<210> 873
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 873
Leu Leu Val Tyr Tyr Ala Lys Thr Leu Thr
1 5 10

<210> 874
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 874
Gln His His Tyr Gly Arg Pro Tyr
1 5

<210> 875
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 875
Gly Phe Thr Phe Thr Asn Thr Tyr
1 5

<210> 876
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 876
Ile Tyr Thr Gly Thr Gly Gly Thr
1 5

<210> 877
<211> 11

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 877
Ala Arg Thr Asn Trp Asp Trp Tyr Phe Asp Val
1 5 10

<210> 878
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 878
Glu Asn Ile Tyr Ser Tyr
1 5

<210> 879
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 879
Tyr Ala Lys
1

<210> 880
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 880
Gln His His Tyr Gly Arg Pro Tyr Thr
1 5

<210> 881
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 881
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Thr Ser Gly Phe Thr Phe Thr Asn Thr
20 25 30

Tyr Ile Ser Trp Leu Lys Gln Lys Pro Arg Gln Ser Leu Glu Trp Ile
35 40 45

Ala Trp Ile Tyr Thr Gly Thr Gly Gly Thr Trp Tyr Asn Gln Lys Phe
50 55 60

Thr Asp Lys Ala Gln Leu Thr Val Asp Thr Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Val Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys
85 90 95

Ala Arg Thr Asn Trp Asp Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr
100 105 110

Ser Val Thr Val Ser Ser
115

<210> 882
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 882
Asp Ile Val Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
1 5 10 15

```
Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr Ser Tyr
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
        35                  40                  45

Tyr Tyr Ala Lys Thr Leu Thr Asp Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His His Tyr Gly Arg Pro Tyr
                85                  90                  95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
            100                 105
```

<210> 883
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 883

```
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Leu Ser Cys Lys Thr Ser Gly Phe Thr Phe Thr Asn Thr
            20                  25                  30

Tyr Ile Ser Trp Leu Lys Gln Lys Pro Arg Gln Ser Leu Glu Trp Ile
        35                  40                  45

Ala Trp Ile Tyr Thr Gly Thr Gly Gly Thr Trp Tyr Asn Gln Lys Phe
    50                  55                  60

Thr Asp Lys Ala Gln Leu Thr Val Asp Thr Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
```

```
Met Gln Val Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys
                85                  90                  95

Ala Arg Thr Asn Trp Asp Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr
            100                 105                 110

Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
    210                 215                 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285
```

```
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    290                 295                 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
                325                 330                 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
        355                 360                 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370                 375                 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385                 390                 395                 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                405                 410                 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            420                 425                 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445


<210> 884
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 884
Asp Ile Val Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15
```

```
Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr Ser Tyr
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
        35                  40                  45

Tyr Tyr Ala Lys Thr Leu Thr Asp Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His His Tyr Gly Arg Pro Tyr
                85                  90                  95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 885
<211> 5

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 885
Asp Tyr Tyr Met Ala
1 5

<210> 886
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 886
His Ile Asn Tyr Asp Gly Ser Ile Thr Tyr Tyr Leu Asp Ser Leu Lys
1 5 10 15

Ser

<210> 887
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 887
Glu Asp Tyr Ser Asn Tyr Gly Phe Ala Tyr
1 5 10

<210> 888
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 888

His Ala Ser Gln Asn Ile Asn Val Trp Leu Ser
1 5 10

<210> 889
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 889
Lys Ala Ser Asn Leu His Thr
1 5

<210> 890
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 890
Gln Gln Gly Gln Ser Tyr Pro Leu Thr
1 5

<210> 891
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 891
Gly Phe Thr Phe Ser Asp Tyr
1 5

<210> 892
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 892
Asn Tyr Asp Gly Ser Ile
1   5

<210> 893
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 893
Glu Asp Tyr Ser Asn Tyr Gly Phe Ala
1   5

<210> 894
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 894
Ser Gln Asn Ile Asn Val Trp
1   5

<210> 895
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 895
Lys Ala Ser
1

<210> 896
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 896
Gly Gln Ser Tyr Pro Leu
1 5

<210> 897
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 897
Gly Phe Thr Phe Ser Asp Tyr Tyr Met Ala
1 5 10

<210> 898
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 898
His Ile Asn Tyr Asp Gly Ser Ile Thr Tyr
1 5 10

<210> 899
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 899
Glu Asp Tyr Ser Asn Tyr Gly Phe Ala Tyr
1 5 10

<210> 900
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 900
His Ala Ser Gln Asn Ile Asn Val Trp Leu Ser
1 5 10

<210> 901
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 901
Lys Ala Ser Asn Leu His Thr
1 5

<210> 902
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 902
Gln Gln Gly Gln Ser Tyr Pro Leu Thr
1 5

<210> 903
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 903
Ser Asp Tyr Tyr Met Ala
1 5

<210> 904
<211> 13

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 904
Trp Val Ala His Ile Asn Tyr Asp Gly Ser Ile Thr Tyr
1 5 10

<210> 905
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 905
Ala Arg Glu Asp Tyr Ser Asn Tyr Gly Phe Ala
1 5 10

<210> 906
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 906
Asn Val Trp Leu Ser Trp Tyr
1 5

<210> 907
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 907
Leu Leu Ile Tyr Lys Ala Ser Asn Leu His
1 5 10

<210> 908
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 908
Gln Gln Gly Gln Ser Tyr Pro Leu
1 5

<210> 909
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 909
Gly Phe Thr Phe Ser Asp Tyr Tyr
1 5

<210> 910
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 910
Ile Asn Tyr Asp Gly Ser Ile Thr
1 5

<210> 911
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 911
Ala Arg Glu Asp Tyr Ser Asn Tyr Gly Phe Ala Tyr
1 5 10

<210> 912
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 912
Gln Asn Ile Asn Val Trp
1 5

<210> 913
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 913
Lys Ala Ser
1

<210> 914
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 914
Gln Gln Gly Gln Ser Tyr Pro Leu Thr
1 5

<210> 915
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 915

Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Ser
1 5 10 15

Ser Met Lys Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Tyr Met Ala Trp Val Arg Gln Val Pro Glu Lys Gly Leu Glu Trp Val
35 40 45

Ala His Ile Asn Tyr Asp Gly Ser Ile Thr Tyr Tyr Leu Asp Ser Leu
50 55 60

Lys Ser Arg Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Ile Leu Tyr
65 70 75 80

Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Glu Asp Tyr Ser Asn Tyr Gly Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ala
115

<210> 916
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 916
Asn Thr Gln Met Asn Gln Thr Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Thr Ile Thr Ile Thr Cys His Ala Ser Gln Asn Ile Asn Val Trp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Asn Ile Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Asn Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Gly Gln Ser Tyr Pro Leu
                85   90   95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Met Lys
            100   105

<210> 917
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 917
Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Ser
1   5   10   15

Ser Met Lys Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20   25   30

Tyr Met Ala Trp Val Arg Gln Val Pro Glu Lys Gly Leu Glu Trp Val
        35   40   45

Ala His Ile Asn Tyr Asp Gly Ser Ile Thr Tyr Tyr Leu Asp Ser Leu
    50   55   60

Lys Ser Arg Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Ile Leu Tyr
65   70   75   80

Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
                85   90   95

Ala Arg Glu Asp Tyr Ser Asn Tyr Gly Phe Ala Tyr Trp Gly Gln Gly
            100   105   110

```
Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
```

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
340 345 350

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys

<210> 918
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 918
Asn Thr Gln Met Asn Gln Thr Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Thr Ile Thr Ile Thr Cys His Ala Ser Gln Asn Ile Asn Val Trp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Asn Ile Pro Lys Leu Leu Ile
35 40 45

```
Tyr Lys Ala Ser Asn Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Gly Gln Ser Tyr Pro Leu
                85                  90                  95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Met Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 919
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 919
Ser Tyr Trp Met Asn
1 5

<210> 920
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 920
Ala Val Asn Pro Thr Asn Tyr Tyr Thr Glu Tyr Ile Gln Lys Phe Lys
1 5 10 15

Asp

<210> 921
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 921
Ser Gly Leu Tyr Asn Thr Asn His Leu Ala Trp Phe Ala Tyr
1 5 10

<210> 922
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 922
Arg Ala Ser Glu Asn Ile His Asn Tyr Leu Ala
1 5 10

<210> 923
<211> 7

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 923
Asn Ala Lys Thr Leu Ala Asn
1 5

<210> 924
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 924
Gln His Phe Trp Thr Thr Pro Leu Thr
1 5

<210> 925
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 925
Gly Tyr Thr Phe Thr Ser Tyr
1 5

<210> 926
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 926
Asn Pro Thr Asn Tyr Tyr
1 5

<210> 927
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 927
Ser Gly Leu Tyr Asn Thr Asn His Leu Ala Trp Phe Ala
1 5 10

<210> 928
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 928
Ser Glu Asn Ile His Asn Tyr
1 5

<210> 929
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 929
Asn Ala Lys
1

<210> 930
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 930
Phe Trp Thr Thr Pro Leu
1 5

<210> 931
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 931
Gly Tyr Thr Phe Thr Ser Tyr Trp Met Asn
1 5 10

<210> 932
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 932
Ala Val Asn Pro Thr Asn Tyr Tyr Thr Glu
1 5 10

<210> 933
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 933
Ser Gly Leu Tyr Asn Thr Asn His Leu Ala Trp Phe Ala Tyr
1 5 10

<210> 934
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 934

Arg Ala Ser Glu Asn Ile His Asn Tyr Leu Ala
1 5 10

<210> 935
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 935
Asn Ala Lys Thr Leu Ala Asn
1 5

<210> 936
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 936
Gln His Phe Trp Thr Thr Pro Leu Thr
1 5

<210> 937
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 937
Thr Ser Tyr Trp Met Asn
1 5

<210> 938
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 938
Trp Ile Gly Ala Val Asn Pro Thr Asn Tyr Tyr Thr Glu
1   5   10

<210> 939
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 939
Ala Arg Ser Gly Leu Tyr Asn Thr Asn His Leu Ala Trp Phe Ala
1   5   10   15

<210> 940
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 940
His Asn Tyr Leu Ala Trp Tyr
1   5

<210> 941
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 941
Leu Leu Val Tyr Asn Ala Lys Thr Leu Ala
1   5   10

<210> 942
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 942
Gln His Phe Trp Thr Thr Pro Leu
1 5

<210> 943
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 943
Gly Tyr Thr Phe Thr Ser Tyr Trp
1 5

<210> 944
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 944
Val Asn Pro Thr Asn Tyr Tyr Thr
1 5

<210> 945
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 945
Ala Arg Ser Gly Leu Tyr Asn Thr Asn His Leu Ala Trp Phe Ala Tyr
1 5 10 15

<210> 946
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 946
Glu Asn Ile His Asn Tyr
1 5

<210> 947
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 947
Asn Ala Lys
1

<210> 948
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 948
Gln His Phe Trp Thr Thr Pro Leu Thr
1 5

<210> 949
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 949
Glu Val Gln Leu Gln Gln Ser Gly Ala Ala Leu Ala Lys Pro Gly Thr
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

```
Trp Met Asn Trp Val Arg Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45

Gly Ala Val Asn Pro Thr Asn Tyr Tyr Thr Glu Tyr Ile Gln Lys Phe
    50                  55                  60

Lys Asp Lys Ala Ile Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

Met His Leu Ser Gly Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ser Gly Leu Tyr Asn Thr Asn His Leu Ala Trp Phe Ala Tyr
            100                 105                 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 950
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 950

```
Asp Ile Lys Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile His Asn Tyr
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Ile Gln Gly Lys Ser Pro Gln Leu Leu Val
        35                  40                  45

Tyr Asn Ala Lys Thr Leu Ala Asn Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Ala Ser Gly Thr Gln Phe Ser Leu Thr Ile Asn Ser Leu Gln Pro
65                  70                  75                  80
```

Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp Thr Thr Pro Leu
85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 951
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 951
Glu Val Gln Leu Gln Gln Ser Gly Ala Ala Leu Ala Lys Pro Gly Thr
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Ala Val Asn Pro Thr Asn Tyr Tyr Thr Glu Tyr Ile Gln Lys Phe
50 55 60

Lys Asp Lys Ala Ile Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met His Leu Ser Gly Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Leu Tyr Asn Thr Asn His Leu Ala Trp Phe Ala Tyr
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
130 135 140

```
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
225                 230                 235                 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350
```

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
355 360 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
370 375 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385 390 395 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
435 440 445

Leu Ser Pro Gly Lys
450

<210> 952
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 952
Asp Ile Lys Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile His Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Ile Gln Gly Lys Ser Pro Gln Leu Leu Val
35 40 45

Tyr Asn Ala Lys Thr Leu Ala Asn Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Ala Ser Gly Thr Gln Phe Ser Leu Thr Ile Asn Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp Thr Thr Pro Leu
85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 953
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 953
Ser Tyr Trp Met His
1 5

<210> 954
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 954
Asn Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Lys Phe Lys
1 5 10 15

Asp

<210> 955
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 955
Val Tyr Tyr Ser Tyr Tyr Ser Tyr Asp Ala Thr Tyr Phe Asp Tyr
1 5 10 15

<210> 956
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 956
Arg Ala Ser Glu Asn Ile Tyr Ser Tyr Leu Ala
1 5 10

<210> 957
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 957
Asn Ala Lys Thr Leu Ala Glu
1   5

<210> 958
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 958
Gln His His Tyr Thr Thr Pro Leu Thr
1   5

<210> 959
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 959
Gly Tyr Ser Phe Asn Ser Tyr
1   5

<210> 960
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 960
Asp Pro Ser Asp Ser Glu
1   5

<210> 961
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 961
Val Tyr Tyr Ser Tyr Tyr Ser Tyr Asp Ala Thr Tyr Phe Asp
1 5 10

<210> 962
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 962
Ser Glu Asn Ile Tyr Ser Tyr
1 5

<210> 963
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 963
Asn Ala Lys
1

<210> 964
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 964
His Tyr Thr Thr Pro Leu
1 5

<210> 965
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 965
Gly Tyr Ser Phe Asn Ser Tyr Trp Met His
1 5 10

<210> 966
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 966
Asn Ile Asp Pro Ser Asp Ser Glu Thr His
1 5 10

<210> 967
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 967
Val Tyr Tyr Ser Tyr Tyr Ser Tyr Asp Ala Thr Tyr Phe Asp Tyr
1 5 10 15

<210> 968
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 968
Arg Ala Ser Glu Asn Ile Tyr Ser Tyr Leu Ala
1 5 10

<210> 969
<211> 7

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 969
Asn Ala Lys Thr Leu Ala Glu
1 5

<210> 970
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 970
Gln His His Tyr Thr Thr Pro Leu Thr
1 5

<210> 971
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 971
Asn Ser Tyr Trp Met His
1 5

<210> 972
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 972
Trp Ile Gly Asn Ile Asp Pro Ser Asp Ser Glu Thr His
1 5 10

<210> 973
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 973
Ala Arg Val Tyr Tyr Ser Tyr Tyr Ser Tyr Asp Ala Thr Tyr Phe Asp
1 5 10 15

<210> 974
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 974
Tyr Ser Tyr Leu Ala Trp Tyr
1 5

<210> 975
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 975
Leu Leu Val Tyr Asn Ala Lys Thr Leu Ala
1 5 10

<210> 976
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 976
Gln His His Tyr Thr Thr Pro Leu
1 5

<210> 977
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 977
Gly Tyr Ser Phe Asn Ser Tyr Trp
1 5

<210> 978
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 978
Ile Asp Pro Ser Asp Ser Glu Thr
1 5

<210> 979
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 979
Ala Arg Val Tyr Tyr Ser Tyr Tyr Ser Tyr Asp Ala Thr Tyr Phe Asp
1 5 10 15

Tyr

<210> 980
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 980
Glu Asn Ile Tyr Ser Tyr
1 5

<210> 981
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 981
Asn Ala Lys
1

<210> 982
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 982
Gln His His Tyr Thr Thr Pro Leu Thr
1 5

<210> 983
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 983
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Ser Phe Asn Ser Tyr
20 25 30

```
Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Asn Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Lys Phe
    50                  55                  60


Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80


Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Val Tyr Tyr Ser Tyr Tyr Ser Tyr Asp Ala Thr Tyr Phe Asp
            100                 105                 110


Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
        115                 120


<210> 984
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 984
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr Ser Tyr
            20                  25                  30


Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
        35                  40                  45


Tyr Asn Ala Lys Thr Leu Ala Glu Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn Ser Leu Gln Pro
65                  70                  75                  80
```

Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His His Tyr Thr Thr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 985
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 985
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Ser Phe Asn Ser Tyr
20 25 30

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Asn Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Val Tyr Tyr Ser Tyr Tyr Ser Tyr Asp Ala Thr Tyr Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys
115 120 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
130 135 140

```
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
145                 150                 155                 160

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
                165                 170                 175

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
            180                 185                 190

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
        195                 200                 205

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
    210                 215                 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
225                 230                 235                 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
                245                 250                 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
            260                 265                 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
        275                 280                 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
    290                 295                 300

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
305                 310                 315                 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
                325                 330                 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
            340                 345                 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
        355                 360                 365
```

```
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
    370                 375                 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
385                 390                 395                 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
                405                 410                 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
            420                 425                 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
        435                 440                 445

Ser Leu Ser Pro Gly Lys
    450
```

<210> 986
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 986

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Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr Ser Tyr
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
        35                  40                  45

Tyr Asn Ala Lys Thr Leu Ala Glu Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn Ser Leu Gln Pro
65                  70                  75                  80
```

Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His His Tyr Thr Thr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 987
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 987
Ser Tyr Ser Val His
1 5

<210> 988
<211> 16

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 988
Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Phe Met Ser
1 5 10 15

<210> 989
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 989
His Ser Tyr Tyr Ser Phe Asp Ala Phe Asp Tyr
1 5 10

<210> 990
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 990
Lys Ala Ser Gln Asn Val Asn Thr Asp Val Ala
1 5 10

<210> 991
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 991
Ser Ala Ser Tyr Arg Tyr Ser
1 5

<210> 992
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 992
Gln Gln Cys Asn Ser Tyr Pro Leu Thr
1 5

<210> 993
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 993
Gly Phe Ser Leu Thr Ser Tyr
1 5

<210> 994
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 994
Trp Ala Gly Gly Ser
1 5

<210> 995
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 995
His Ser Tyr Tyr Ser Phe Asp Ala Phe Asp
1 5 10

<210> 996
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 996
Ser Gln Asn Val Asn Thr Asp
1 5

<210> 997
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 997
Ser Ala Ser
1

<210> 998
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 998
Cys Asn Ser Tyr Pro Leu
1 5

<210> 999
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 999

Gly Phe Ser Leu Thr Ser Tyr Ser Val His
1 5 10

<210> 1000
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1000
Val Ile Trp Ala Gly Gly Ser Thr Asn
1 5

<210> 1001
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1001
His Ser Tyr Tyr Ser Phe Asp Ala Phe Asp Tyr
1 5 10

<210> 1002
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1002
Lys Ala Ser Gln Asn Val Asn Thr Asp Val Ala
1 5 10

<210> 1003
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1003
Ser Ala Ser Tyr Arg Tyr Ser
1 5

<210> 1004
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1004
Gln Gln Cys Asn Ser Tyr Pro Leu Thr
1 5

<210> 1005
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1005
Thr Ser Tyr Ser Val His
1 5

<210> 1006
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1006
Trp Leu Gly Val Ile Trp Ala Gly Gly Ser Thr Asn
1 5 10

<210> 1007
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1007
Ala Lys His Ser Tyr Tyr Ser Phe Asp Ala Phe Asp
1 5 10

<210> 1008
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1008
Asn Thr Asp Val Ala Trp Tyr
1 5

<210> 1009
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1009
Ala Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr
1 5 10

<210> 1010
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1010
Gln Gln Cys Asn Ser Tyr Pro Leu
1 5

<210> 1011
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1011
Gly Phe Ser Leu Thr Ser Tyr Ser
1 5

<210> 1012
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1012
Ile Trp Ala Gly Gly Ser Thr
1 5

<210> 1013
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1013
Ala Lys His Ser Tyr Tyr Ser Phe Asp Ala Phe Asp Tyr
1 5 10

<210> 1014
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1014
Gln Asn Val Asn Thr Asp
1 5

<210> 1015
<211> 3

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1015
Ser Ala Ser
1

<210> 1016
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1016
Gln Gln Cys Asn Ser Tyr Pro Leu Thr
1 5

<210> 1017
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1017
Asp Val Gln Leu Gln Glu Ser Gly Pro Ile Leu Val Ala Pro Ser Gln
1 5 10 15

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Tyr
20 25 30

Ser Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Phe Met
50 55 60

Ser Arg Leu Thr Ile Ser Lys Asp Asn Ser Glu Ser Gln Val Phe Leu
65 70 75 80

Lys Met Ile Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

Lys His Ser Tyr Tyr Ser Phe Asp Ala Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Leu Thr Val Ser Ser
115

<210> 1018
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1018
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15

Asp Arg Val Arg Val Thr Cys Lys Ala Ser Gln Asn Val Asn Thr Asp
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile
35 40 45

Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Val Gln Ser
65 70 75 80

Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Cys Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 1019
<211> 449

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1019
Asp Val Gln Leu Gln Glu Ser Gly Pro Ile Leu Val Ala Pro Ser Gln
1 5 10 15

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Tyr
20 25 30

Ser Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Phe Met
50 55 60

Ser Arg Leu Thr Ile Ser Lys Asp Asn Ser Glu Ser Gln Val Phe Leu
65 70 75 80

Lys Met Ile Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

Lys His Ser Tyr Tyr Ser Phe Asp Ala Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

```
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
```

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys

<210> 1020
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1020
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15

Asp Arg Val Arg Val Thr Cys Lys Ala Ser Gln Asn Val Asn Thr Asp
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile
35 40 45

Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Val Gln Ser
65 70 75 80

Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Cys Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 1021
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1021
Ser Gly Tyr Tyr Trp Asn
1 5

<210> 1022
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1022
Tyr Ile Asn Tyr Asp Gly Arg Asn Asn Tyr Asn Pro Ser Leu Lys Asn
1 5 10 15

<210> 1023
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1023
Asp Gln Gly Tyr Ser Lys Phe Tyr Phe Asp Tyr
1 5 10

<210> 1024
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1024
Lys Ala Ser Glu Asp Ile Tyr Asn Arg Leu Ala
1 5 10

<210> 1025
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1025
Gly Ala Thr Ser Leu Glu Thr
1 5

<210> 1026
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1026

Gln Gln Tyr Trp Ser Phe Pro Arg Thr
1 5

<210> 1027
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1027
Gly Tyr Ser Ile Thr Ser Gly Tyr
1 5

<210> 1028
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1028
Asn Tyr Asp Gly Arg
1 5

<210> 1029
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1029
Asp Gln Gly Tyr Ser Lys Phe Tyr Phe Asp
1 5 10

<210> 1030
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1030
Ser Glu Asp Ile Tyr Asn Arg
1 5

<210> 1031
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1031
Gly Ala Thr
1

<210> 1032
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1032
Tyr Trp Ser Phe Pro Arg
1 5

<210> 1033
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1033
Gly Tyr Ser Ile Thr Ser Gly Tyr Tyr Trp Asn
1 5 10

<210> 1034
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1034
Tyr Ile Asn Tyr Asp Gly Arg Asn Asn
1 5

<210> 1035
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1035
Asp Gln Gly Tyr Ser Lys Phe Tyr Phe Asp Tyr
1 5 10

<210> 1036
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1036
Lys Ala Ser Glu Asp Ile Tyr Asn Arg Leu Ala
1 5 10

<210> 1037
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1037
Gly Ala Thr Ser Leu Glu Thr
1 5

<210> 1038
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1038
Gln Gln Tyr Trp Ser Phe Pro Arg Thr
1 5

<210> 1039
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1039
Thr Ser Gly Tyr Tyr Trp Asn
1 5

<210> 1040
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1040
Trp Met Gly Tyr Ile Asn Tyr Asp Gly Arg Asn Asn
1 5 10

<210> 1041
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1041
Ser Arg Asp Gln Gly Tyr Ser Lys Phe Tyr Phe Asp
1 5 10

<210> 1042
<211> 7

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1042
Tyr Asn Arg Leu Ala Trp Tyr
1 5

<210> 1043
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1043
Leu Leu Ile Ser Gly Ala Thr Ser Leu Glu
1 5 10

<210> 1044
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1044
Gln Gln Tyr Trp Ser Phe Pro Arg
1 5

<210> 1045
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1045
Gly Tyr Ser Ile Thr Ser Gly Tyr Tyr
1 5

<210> 1046
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1046
Ile Asn Tyr Asp Gly Arg Asn
1 5

<210> 1047
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1047
Ser Arg Asp Gln Gly Tyr Ser Lys Phe Tyr Phe Asp Tyr
1 5 10

<210> 1048
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1048
Glu Asp Ile Tyr Asn Arg
1 5

<210> 1049
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1049
Gly Ala Thr
1

<210> 1050
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1050
Gln Gln Tyr Trp Ser Phe Pro Arg Thr
1 5

<210> 1051
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1051
Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Gly
20 25 30

Tyr Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
35 40 45

Met Gly Tyr Ile Asn Tyr Asp Gly Arg Asn Asn Tyr Asn Pro Ser Leu
50 55 60

Lys Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn His Phe Phe
65 70 75 80

Leu Lys Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ser Arg Asp Gln Gly Tyr Ser Lys Phe Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Leu Thr Val Ser Ser
        115   120

<210> 1052
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 1052
Asp Ile Gln Met Thr Gln Ser Ser Ser Ser Phe Ser Val Ser Leu Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Glu Asp Ile Tyr Asn Arg
            20   25   30

Leu Ala Trp Tyr Gln Gln Arg Pro Gly Asn Ala Pro Arg Leu Leu Ile
        35   40   45

Ser Gly Ala Thr Ser Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Gly Gly Ser Gly Lys Asp Tyr Thr Leu Ser Ile Thr Ser Leu Gln Thr
65   70   75   80

Glu Asp Val Ala Asn Tyr Tyr Cys Gln Gln Tyr Trp Ser Phe Pro Arg
                85   90   95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 1053
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 1053
Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1   5   10   15

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Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Tyr Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
        35                  40                  45

Met Gly Tyr Ile Asn Tyr Asp Gly Arg Asn Asn Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn His Phe Phe
65                  70                  75                  80

Leu Lys Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
                85                  90                  95

Ser Arg Asp Gln Gly Tyr Ser Lys Phe Tyr Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220
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```
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445
```

Gly Lys
450

<210> 1054
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1054
Asp Ile Gln Met Thr Gln Ser Ser Ser Ser Phe Ser Val Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Glu Asp Ile Tyr Asn Arg
20 25 30

Leu Ala Trp Tyr Gln Gln Arg Pro Gly Asn Ala Pro Arg Leu Leu Ile
35 40 45

Ser Gly Ala Thr Ser Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Gly Gly Ser Gly Lys Asp Tyr Thr Leu Ser Ile Thr Ser Leu Gln Thr
65 70 75 80

Glu Asp Val Ala Asn Tyr Tyr Cys Gln Gln Tyr Trp Ser Phe Pro Arg
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 1055
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1055
Thr Tyr Ala Val His
1 5

<210> 1056
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1056
Val Ile Trp Ser Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Ile Ser
1 5 10 15

<210> 1057
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1057
His Ser Tyr Tyr His Tyr Asn Ala Met Asp Asn
1 5 10

<210> 1058
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1058
Lys Ala Ser Gln Asn Val Gly Thr Ala Val Ala
1 5 10

<210> 1059
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1059
Ser Ala Ser Asn Arg Tyr Thr
1 5

<210> 1060
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1060
Gln Gln Tyr Ser Ser Tyr Pro Phe Thr
1 5

<210> 1061
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1061
Gly Phe Ser Leu Thr Thr Tyr
1 5

<210> 1062
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1062
Trp Ser Gly Gly Ser
1 5

<210> 1063
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1063
His Ser Tyr Tyr His Tyr Asn Ala Met Asp
1 5 10

<210> 1064
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1064
Ser Gln Asn Val Gly Thr Ala
1 5

<210> 1065
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1065
Ser Ala Ser
1

<210> 1066
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1066
Tyr Ser Ser Tyr Pro Phe
1 5

<210> 1067
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1067
Gly Phe Ser Leu Thr Thr Tyr Ala Val His
1 5 10

<210> 1068
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1068
Val Ile Trp Ser Gly Gly Ser Thr Asp
1 5

<210> 1069
<211> 11

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1069
His Ser Tyr Tyr His Tyr Asn Ala Met Asp Asn
1 5 10

<210> 1070
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1070
Lys Ala Ser Gln Asn Val Gly Thr Ala Val Ala
1 5 10

<210> 1071
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1071
Ser Ala Ser Asn Arg Tyr Thr
1 5

<210> 1072
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1072
Gln Gln Tyr Ser Ser Tyr Pro Phe Thr
1 5

<210> 1073
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1073
Thr Thr Tyr Ala Val His
1 5

<210> 1074
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1074
Trp Leu Gly Val Ile Trp Ser Gly Gly Ser Thr Asp
1 5 10

<210> 1075
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1075
Ala Arg His Ser Tyr Tyr His Tyr Asn Ala Met Asp
1 5 10

<210> 1076
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1076
Gly Thr Ala Val Ala Trp Tyr
1 5

<210> 1077
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1077
Leu Leu Ile Tyr Ser Ala Ser Asn Arg Tyr
1 5 10

<210> 1078
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1078
Gln Gln Tyr Ser Ser Tyr Pro Phe
1 5

<210> 1079
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1079
Gly Phe Ser Leu Thr Thr Tyr Ala
1 5

<210> 1080
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1080

Ile Trp Ser Gly Gly Ser Thr
1 5

<210> 1081
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1081
Ala Arg His Ser Tyr Tyr His Tyr Asn Ala Met Asp Asn
1 5 10

<210> 1082
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1082
Gln Asn Val Gly Thr Ala
1 5

<210> 1083
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1083
Ser Ala Ser
1

<210> 1084
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1084
Gln Gln Tyr Ser Ser Tyr Pro Phe Thr
1 5

<210> 1085
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1085
Gln Val Gln Leu Lys Gly Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Thr Tyr
20 25 30

Ala Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ser Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Ile
50 55 60

Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65 70 75 80

Lys Met Asn Ser Leu Gln Ala Asp Asp Thr Ala Ile Tyr Tyr Cys Ala
85 90 95

Arg His Ser Tyr Tyr His Tyr Asn Ala Met Asp Asn Trp Gly Gln Gly
100 105 110

Thr Ser Val Thr Val Ser Ser
115

<210> 1086
<211> 107
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1086
Asp Ile Lys Met Thr Gln Ser Gln Lys Phe Met Ser Thr Thr Val Gly
1 5 10 15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Met Gln Ser
65 70 75 80

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Ser Tyr Pro Phe
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 1087
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1087
Gln Val Gln Leu Lys Gly Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Thr Tyr
20 25 30

Ala Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

```
Gly Val Ile Trp Ser Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Ile
    50                  55                  60

Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65                  70                  75                  80

Lys Met Asn Ser Leu Gln Ala Asp Asp Thr Ala Ile Tyr Tyr Cys Ala
                85                  90                  95

Arg His Ser Tyr Tyr His Tyr Asn Ala Met Asp Asn Trp Gly Gln Gly
            100                 105                 110

Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
```

```
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445

Lys
```

<210> 1088
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1088
Asp Ile Lys Met Thr Gln Ser Gln Lys Phe Met Ser Thr Thr Val Gly
1 5 10 15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Met Gln Ser
65 70 75 80

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Ser Tyr Pro Phe
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 1089
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1089
Ser Gly Tyr Tyr Trp Asn
1 5

<210> 1090
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1090
Tyr Ile Ser Tyr Asp Gly Ser Asn Asn Tyr Asn Pro Ser Leu Lys Asn
1 5 10 15

<210> 1091
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1091
Asn His Gly Asp Ala Met Asp His
1 5

<210> 1092
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1092
Lys Ala Ser Gln Asn Val Gly Thr Asp Val Ala
1 5 10

<210> 1093
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1093
Ser Ala Ser Tyr Arg Tyr Ser
1 5

<210> 1094
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1094
Gln Gln Tyr Lys Ser Tyr Pro Leu Thr
1 5

<210> 1095
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1095
Gly Tyr Ser Ile Thr Ser Gly Tyr
1 5

<210> 1096
<211> 5

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1096
Ser Tyr Asp Gly Ser
1 5

<210> 1097
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1097
Asn His Gly Asp Ala Met Asp
1 5

<210> 1098
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1098
Ser Gln Asn Val Gly Thr Asp
1 5

<210> 1099
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1099
Ser Ala Ser
1

<210> 1100
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1100
Tyr Lys Ser Tyr Pro Leu
1 5

<210> 1101
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1101
Gly Tyr Ser Ile Thr Ser Gly Tyr Tyr Trp Asn
1 5 10

<210> 1102
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1102
Tyr Ile Ser Tyr Asp Gly Ser Asn Asn
1 5

<210> 1103
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1103
Asn His Gly Asp Ala Met Asp His
1 5

<210> 1104
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1104
Lys Ala Ser Gln Asn Val Gly Thr Asp Val Ala
1 5 10

<210> 1105
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1105
Ser Ala Ser Tyr Arg Tyr Ser
1 5

<210> 1106
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1106
Gln Gln Tyr Lys Ser Tyr Pro Leu Thr
1 5

<210> 1107
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1107

Thr Ser Gly Tyr Tyr Trp Asn
1 5

<210> 1108
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1108
Trp Met Gly Tyr Ile Ser Tyr Asp Gly Ser Asn Asn
1 5 10

<210> 1109
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1109
Val Arg Asn His Gly Asp Ala Met Asp
1 5

<210> 1110
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1110
Gly Thr Asp Val Ala Trp Tyr
1 5

<210> 1111
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1111
Ala Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr
1 5 10

<210> 1112
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1112
Gln Gln Tyr Lys Ser Tyr Pro Leu
1 5

<210> 1113
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1113
Gly Tyr Ser Ile Thr Ser Gly Tyr Tyr
1 5

<210> 1114
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1114
Ile Ser Tyr Asp Gly Ser Asn
1 5

<210> 1115
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1115
Val Arg Asn His Gly Asp Ala Met Asp His
1 5 10

<210> 1116
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1116
Gln Asn Val Gly Thr Asp
1 5

<210> 1117
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1117
Ser Ala Ser
1

<210> 1118
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1118
Gln Gln Tyr Lys Ser Tyr Pro Leu Thr
1 5

<210> 1119
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1119
Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Gly
20 25 30

Tyr Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
35 40 45

Met Gly Tyr Ile Ser Tyr Asp Gly Ser Asn Asn Tyr Asn Pro Ser Leu
50 55 60

Lys Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65 70 75 80

Leu Lys Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Val Arg Asn His Gly Asp Ala Met Asp His Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Ser Ser
115

<210> 1120
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1120
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15

Asp Arg Val Arg Val Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asp
20 25 30

```
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile
        35                  40                  45

Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asp Val Gln Ser
65                  70                  75                  80

Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Lys Ser Tyr Pro Leu
                85                  90                  95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
            100                 105
```

<210> 1121
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1121

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Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15

Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Tyr Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
        35                  40                  45

Met Gly Tyr Ile Ser Tyr Asp Gly Ser Asn Asn Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65                  70                  75                  80

Leu Lys Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
                85                  90                  95
```

```
Val Arg Asn His Gly Asp Ala Met Asp His Trp Gly Gln Gly Thr Thr
            100                 105                 110

Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
        115                 120                 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
    210                 215                 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
225                 230                 235                 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
            260                 265                 270

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
    290                 295                 300
```

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 1122
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1122
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15

Asp Arg Val Arg Val Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asp
20 25 30

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Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile
        35                  40                  45

Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asp Val Gln Ser
65                  70                  75                  80

Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Lys Ser Tyr Pro Leu
                85                  90                  95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
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<210> 1123
<211> 5
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1123
Arg Tyr Ser Val His
1 5

<210> 1124
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1124
Met Ile Trp Gly Gly Gly Ser Thr Asp Tyr Asn Ser Ala Leu Lys Ser
1 5 10 15

<210> 1125
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1125
Ile Tyr Phe Asp Asn Tyr Val Gly Phe Ala Tyr
1 5 10

<210> 1126
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1126
Lys Ala Ser Gln Asp Val Gly Thr Val Val Ala
1 5 10

<210> 1127
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1127
Trp Thr Ser Thr Arg His Thr
1 5

<210> 1128
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1128
Gln Gln Tyr Ser Ser Tyr Pro Tyr Thr
1 5

<210> 1129
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1129
Gly Phe Ser Leu Ser Arg Tyr
1 5

<210> 1130
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1130
Trp Gly Gly Gly Ser
1 5

<210> 1131
<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1131
Ile Tyr Phe Asp Asn Tyr Val Gly Phe Ala
1 5 10

<210> 1132
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1132
Ser Gln Asp Val Gly Thr Val
1 5

<210> 1133
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1133
Trp Thr Ser
1

<210> 1134
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1134
Tyr Ser Ser Tyr Pro Tyr
1 5

<210> 1135
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1135
Gly Phe Ser Leu Ser Arg Tyr Ser Val His
1 5 10

<210> 1136
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1136
Met Ile Trp Gly Gly Gly Ser Thr Asp
1 5

<210> 1137
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1137
Ile Tyr Phe Asp Asn Tyr Val Gly Phe Ala Tyr
1 5 10

<210> 1138
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1138
Lys Ala Ser Gln Asp Val Gly Thr Val Val Ala
1 5 10

<210> 1139
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1139
Trp Thr Ser Thr Arg His Thr
1 5

<210> 1140
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1140
Gln Gln Tyr Ser Ser Tyr Pro Tyr Thr
1 5

<210> 1141
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1141
Ser Arg Tyr Ser Val His
1 5

<210> 1142
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1142

Trp Leu Gly Met Ile Trp Gly Gly Gly Ser Thr Asp
1 5 10

<210> 1143
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1143
Ala Arg Ile Tyr Phe Asp Asn Tyr Val Gly Phe Ala
1 5 10

<210> 1144
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1144
Gly Thr Val Val Ala Trp Tyr
1 5

<210> 1145
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1145
Leu Leu Ile Phe Trp Thr Ser Thr Arg His
1 5 10

<210> 1146
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1146
Gln Gln Tyr Ser Ser Tyr Pro Tyr
1 5

<210> 1147
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1147
Gly Phe Ser Leu Ser Arg Tyr Ser
1 5

<210> 1148
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1148
Ile Trp Gly Gly Gly Ser Thr
1 5

<210> 1149
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1149
Ala Arg Ile Tyr Phe Asp Asn Tyr Val Gly Phe Ala Tyr
1 5 10

<210> 1150
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1150
Gln Asp Val Gly Thr Val
1 5

<210> 1151
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1151
Trp Thr Ser
1

<210> 1152
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1152
Gln Gln Tyr Ser Ser Tyr Pro Tyr Thr
1 5

<210> 1153
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1153
Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln
1 5 10 15

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Arg Tyr
20 25 30

Ser Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Val Trp Leu
35 40 45

Gly Met Ile Trp Gly Gly Gly Ser Thr Asp Tyr Asn Ser Ala Leu Lys
50 55 60

Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu
65 70 75 80

Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

Arg Ile Tyr Phe Asp Asn Tyr Val Gly Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Leu Thr Val Ser Ser
115

<210> 1154
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1154
Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Gly Thr Val
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45

Phe Trp Thr Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Val Gln Ser
65 70 75 80

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 1155
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1155
Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln
1 5 10 15

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Arg Tyr
20 25 30

Ser Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Val Trp Leu
35 40 45

Gly Met Ile Trp Gly Gly Gly Ser Thr Asp Tyr Asn Ser Ala Leu Lys
50 55 60

Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu
65 70 75 80

Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

Arg Ile Tyr Phe Asp Asn Tyr Val Gly Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

```
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
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Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys

<210> 1156
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1156
Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Gly Thr Val
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45

Phe Trp Thr Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Val Gln Ser
65 70 75 80

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Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Ser Tyr Pro Tyr
                85                  90                  95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210


<210> 1157
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1157
Asn Tyr Ala Val His
1               5


<210> 1158
<211> 16
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<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1158
Val Ile Trp Thr Asp Gly Ser Thr Asp Tyr Asn Ala Gly Phe Ile Ser
1 5 10 15

<210> 1159
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1159
Asn Asn Gly Tyr Phe Pro Ala Phe Phe Ala Tyr
1 5 10

<210> 1160
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1160
Arg Ser Ser Gln Thr Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
1 5 10 15

<210> 1161
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1161
Lys Val Ser Asn Arg Phe Ser
1 5

<210> 1162
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1162
Phe Gln Gly Ser His Ala Pro Phe Thr
1 5

<210> 1163
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1163
Gly Phe Ser Leu Thr Asn Tyr
1 5

<210> 1164
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1164
Trp Thr Asp Gly Ser
1 5

<210> 1165
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1165
Asn Asn Gly Tyr Phe Pro Ala Phe Phe Ala
1 5 10

<210> 1166
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1166
Ser Gln Thr Ile Val His Ser Asn Gly Asn Thr Tyr
1 5 10

<210> 1167
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1167
Lys Val Ser
1

<210> 1168
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1168
Gly Ser His Ala Pro Phe
1 5

<210> 1169
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1169

Gly Phe Ser Leu Thr Asn Tyr Ala Val His
1 5 10

<210> 1170
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1170
Val Ile Trp Thr Asp Gly Ser Thr Asp
1 5

<210> 1171
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1171
Asn Asn Gly Tyr Phe Pro Ala Phe Phe Ala Tyr
1 5 10

<210> 1172
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1172
Arg Ser Ser Gln Thr Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
1 5 10 15

<210> 1173
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1173
Lys Val Ser Asn Arg Phe Ser
1 5

<210> 1174
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1174
Phe Gln Gly Ser His Ala Pro Phe Thr
1 5

<210> 1175
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1175
Thr Asn Tyr Ala Val His
1 5

<210> 1176
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1176
Trp Leu Gly Val Ile Trp Thr Asp Gly Ser Thr Asp
1 5 10

<210> 1177
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1177
Ala Arg Asn Asn Gly Tyr Phe Pro Ala Phe Phe Ala
1 5 10

<210> 1178
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1178
Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr
1 5 10

<210> 1179
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1179
Leu Leu Met Tyr Lys Val Ser Asn Arg Phe
1 5 10

<210> 1180
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1180
Phe Gln Gly Ser His Ala Pro Phe
1 5

<210> 1181
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1181
Gly Phe Ser Leu Thr Asn Tyr Ala
1 5

<210> 1182
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1182
Ile Trp Thr Asp Gly Ser Thr
1 5

<210> 1183
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1183
Ala Arg Asn Asn Gly Tyr Phe Pro Ala Phe Phe Ala Tyr
1 5 10

<210> 1184
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1184
Gln Thr Ile Val His Ser Asn Gly Asn Thr Tyr
1 5 10

<210> 1185
<211> 3

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1185
Lys Val Ser
1

<210> 1186
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1186
Phe Gln Gly Ser His Ala Pro Phe Thr
1 5

<210> 1187
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1187
Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln
1 5 10 15

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

Ala Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Thr Asp Gly Ser Thr Asp Tyr Asn Ala Gly Phe Ile
50 55 60

Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65 70 75 80

Lys Met Asn Ser Leu Gln Ala Asp Asp Thr Ala Ile Tyr Tyr Cys Ala
85 90 95

Arg Asn Asn Gly Tyr Phe Pro Ala Phe Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 1188
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1188
Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Thr Ile Val His Ser
20 25 30

Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Met Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Gly Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly
85 90 95

Ser His Ala Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 1189
<211> 449

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1189
Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln
1 5 10 15

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

Ala Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Thr Asp Gly Ser Thr Asp Tyr Asn Ala Gly Phe Ile
50 55 60

Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65 70 75 80

Lys Met Asn Ser Leu Gln Ala Asp Asp Thr Ala Ile Tyr Tyr Cys Ala
85 90 95

Arg Asn Asn Gly Tyr Phe Pro Ala Phe Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

```
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
```

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys

<210> 1190
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1190
Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Thr Ile Val His Ser
20 25 30

Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Met Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Gly Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly
85 90 95

Ser His Ala Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
        115   120   125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
    130   135   140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145   150   155   160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
                165   170   175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
            180   185   190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
        195   200   205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210   215

<210> 1191
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1191
Ser Gly Tyr Tyr Trp Asn
1   5

<210> 1192
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1192
Tyr Ile Asn Tyr Asp Gly Arg Asn Asn Tyr Asn Pro Ser Leu Arg Asn
1   5   10   15

<210> 1193
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1193
Asp Gln Gly Tyr Ser Lys Phe Tyr Phe Asp Tyr
1 5 10

<210> 1194
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1194
Lys Ala Ser Glu Asp Ile Tyr Asn Arg Leu Ala
1 5 10

<210> 1195
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1195
Gly Ala Thr Ser Leu Glu Thr
1 5

<210> 1196
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1196

Gln Gln Tyr Trp Ser Phe Pro Arg Thr
1 5

<210> 1197
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1197
Gly Tyr Ser Ile Thr Ser Gly Tyr
1 5

<210> 1198
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1198
Asn Tyr Asp Gly Arg
1 5

<210> 1199
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1199
Asp Gln Gly Tyr Ser Lys Phe Tyr Phe Asp
1 5 10

<210> 1200
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1200
Ser Glu Asp Ile Tyr Asn Arg
1 5

<210> 1201
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1201
Gly Ala Thr
1

<210> 1202
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1202
Tyr Trp Ser Phe Pro Arg
1 5

<210> 1203
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1203
Gly Tyr Ser Ile Thr Ser Gly Tyr Tyr Trp Asn
1 5 10

<210> 1204
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1204
Tyr Ile Asn Tyr Asp Gly Arg Asn Asn
1 5

<210> 1205
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1205
Asp Gln Gly Tyr Ser Lys Phe Tyr Phe Asp Tyr
1 5 10

<210> 1206
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1206
Lys Ala Ser Glu Asp Ile Tyr Asn Arg Leu Ala
1 5 10

<210> 1207
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1207
Gly Ala Thr Ser Leu Glu Thr
1 5

<210> 1208
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1208
Gln Gln Tyr Trp Ser Phe Pro Arg Thr
1 5

<210> 1209
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1209
Thr Ser Gly Tyr Tyr Trp Asn
1 5

<210> 1210
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1210
Trp Met Gly Tyr Ile Asn Tyr Asp Gly Arg Asn Asn
1 5 10

<210> 1211
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1211
Ala Arg Asp Gln Gly Tyr Ser Lys Phe Tyr Phe Asp
1 5 10

<210> 1212
<211> 7

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1212
Tyr Asn Arg Leu Ala Trp Tyr
1 5

<210> 1213
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1213
Leu Leu Ile Ser Gly Ala Thr Ser Leu Glu
1 5 10

<210> 1214
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1214
Gln Gln Tyr Trp Ser Phe Pro Arg
1 5

<210> 1215
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1215
Gly Tyr Ser Ile Thr Ser Gly Tyr Tyr
1 5

<210> 1216
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1216
Ile Asn Tyr Asp Gly Arg Asn
1 5

<210> 1217
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1217
Ala Arg Asp Gln Gly Tyr Ser Lys Phe Tyr Phe Asp Tyr
1 5 10

<210> 1218
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1218
Glu Asp Ile Tyr Asn Arg
1 5

<210> 1219
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1219
Gly Ala Thr
1

<210> 1220
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1220
Gln Gln Tyr Trp Ser Phe Pro Arg Thr
1 5

<210> 1221
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1221
Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Gly
20 25 30

Tyr Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
35 40 45

Met Gly Tyr Ile Asn Tyr Asp Gly Arg Asn Asn Tyr Asn Pro Ser Leu
50 55 60

Arg Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn His Phe Phe
65 70 75 80

Leu Lys Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Asp Gln Gly Tyr Ser Lys Phe Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Leu Thr Val Ser Ser
        115   120

<210> 1222
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 1222
Asp Ile Gln Met Thr Gln Ser Ser Ser Ser Phe Ser Val Ser Leu Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Glu Asp Ile Tyr Asn Arg
            20   25   30

Leu Ala Trp Tyr Gln Gln Arg Pro Gly Asn Ala Pro Arg Leu Leu Ile
        35   40   45

Ser Gly Ala Thr Ser Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Lys Asp Tyr Thr Leu Ser Ile Thr Ser Leu Gln Thr
65   70   75   80

Glu Asp Val Ala Asn Tyr Tyr Cys Gln Gln Tyr Trp Ser Phe Pro Arg
                85   90   95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 1223
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 1223
Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1   5   10   15

```
Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Tyr Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
        35                  40                  45

Met Gly Tyr Ile Asn Tyr Asp Gly Arg Asn Asn Tyr Asn Pro Ser Leu
    50                  55                  60

Arg Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn His Phe Phe
65                  70                  75                  80

Leu Lys Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Gln Gly Tyr Ser Lys Phe Tyr Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220
```

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Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445
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Gly Lys
    450

<210> 1224
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 1224
Asp Ile Gln Met Thr Gln Ser Ser Ser Ser Phe Ser Val Ser Leu Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Glu Asp Ile Tyr Asn Arg
            20   25   30

Leu Ala Trp Tyr Gln Gln Arg Pro Gly Asn Ala Pro Arg Leu Leu Ile
        35   40   45

Ser Gly Ala Thr Ser Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Lys Asp Tyr Thr Leu Ser Ile Thr Ser Leu Gln Thr
65   70   75   80

Glu Asp Val Ala Asn Tyr Tyr Cys Gln Gln Tyr Trp Ser Phe Pro Arg
                85   90   95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
            100   105   110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115   120   125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130   135   140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145   150   155   160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 1225
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1225
Ala Tyr Tyr Met His
1 5

<210> 1226
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1226
Glu Ile Asn Pro Ser Ala Gly Gly Thr Thr Tyr Asn Gln Lys Phe Lys
1 5 10 15

Ala

<210> 1227
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1227
Trp Thr Asn Pro Phe Asp Tyr
1 5

<210> 1228
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1228
Lys Ala Ser Gln Asn Val Gly Thr Ala Val Ala
1 5 10

<210> 1229
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1229
Ser Ala Ser Tyr Arg Tyr Thr
1 5

<210> 1230
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1230
Gln Gln Tyr Asn Asn Tyr Leu Thr
1 5

<210> 1231
<211> 7

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1231
Gly Tyr Ser Phe Thr Ala Tyr
1 5

<210> 1232
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1232
Asn Pro Ser Ala Gly Gly
1 5

<210> 1233
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1233
Trp Thr Asn Pro Phe Asp
1 5

<210> 1234
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1234
Ser Gln Asn Val Gly Thr Ala
1 5

<210> 1235
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1235
Ser Ala Ser
1

<210> 1236
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1236
Tyr Asn Asn Tyr Leu
1 5

<210> 1237
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1237
Gly Tyr Ser Phe Thr Ala Tyr Tyr Met His
1 5 10

<210> 1238
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1238
Glu Ile Asn Pro Ser Ala Gly Gly Thr Thr
1 5 10

<210> 1239
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1239
Trp Thr Asn Pro Phe Asp Tyr
1 5

<210> 1240
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1240
Lys Ala Ser Gln Asn Val Gly Thr Ala Val Ala
1 5 10

<210> 1241
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1241
Ser Ala Ser Tyr Arg Tyr Thr
1 5

<210> 1242
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1242

Gln Gln Tyr Asn Asn Tyr Leu Thr
1 5

<210> 1243
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1243
Thr Ala Tyr Tyr Met His
1 5

<210> 1244
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1244
Trp Ile Gly Glu Ile Asn Pro Ser Ala Gly Gly Thr Thr
1 5 10

<210> 1245
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1245
Ala Arg Trp Thr Asn Pro Phe Asp
1 5

<210> 1246
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1246
Gly Thr Ala Val Ala Trp Tyr
1   5

<210> 1247
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1247
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr
1   5   10

<210> 1248
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1248
Gln Gln Tyr Asn Asn Tyr Leu
1   5

<210> 1249
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1249
Gly Tyr Ser Phe Thr Ala Tyr Tyr
1   5

<210> 1250
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1250
Ile Asn Pro Ser Ala Gly Gly Thr
1 5

<210> 1251
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1251
Ala Arg Trp Thr Asn Pro Phe Asp Tyr
1 5

<210> 1252
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1252
Gln Asn Val Gly Thr Ala
1 5

<210> 1253
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1253
Ser Ala Ser
1

<210> 1254
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1254
Gln Gln Tyr Asn Asn Tyr Leu Thr
1 5

<210> 1255
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1255
Gln Val Gln Leu Lys Glu Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
1 5 10 15

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ala Tyr
20 25 30

Tyr Met His Trp Val Lys Gln Ser Pro Glu Lys Ser Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn Pro Ser Ala Gly Gly Thr Thr Tyr Asn Gln Lys Phe
50 55 60

Lys Ala Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Phe
65 70 75 80

Ile Gln Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Trp Thr Asn Pro Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu
100 105 110

Thr Val Ser Ser
115

<210> 1256
<211> 106

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1256
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Thr Val Gly
1 5 10 15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr His Phe Thr Leu Thr Ile Ser Asn Ile Gln Ser
65 70 75 80

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Asn Asn Tyr Leu Thr
85 90 95

Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 1257
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1257
Gln Val Gln Leu Lys Glu Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
1 5 10 15

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ala Tyr
20 25 30

```
Tyr Met His Trp Val Lys Gln Ser Pro Glu Lys Ser Leu Glu Trp Ile
        35                  40                  45

Gly Glu Ile Asn Pro Ser Ala Gly Gly Thr Thr Tyr Asn Gln Lys Phe
    50                  55                  60

Lys Ala Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Phe
65                  70                  75                  80

Ile Gln Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Trp Thr Asn Pro Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu
            100                 105                 110

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        115                 120                 125

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    130                 135                 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145                 150                 155                 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                165                 170                 175

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            180                 185                 190

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        195                 200                 205

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    210                 215                 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
225                 230                 235                 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255
```

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Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            260                 265                 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    290                 295                 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305                 310                 315                 320

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
                325                 330                 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            340                 345                 350

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
        355                 360                 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    370                 375                 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385                 390                 395                 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            420                 425                 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
```

<210> 1258
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1258
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Thr Val Gly
1 5 10 15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr His Phe Thr Leu Thr Ile Ser Asn Ile Gln Ser
65 70 75 80

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Asn Asn Tyr Leu Thr
85 90 95

Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
210

<210> 1259
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1259
Ser Tyr Trp Ile Asn
1 5

<210> 1260
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1260
Asn Ile Tyr Pro Gly Ser Ser Ser Thr Asn Tyr Asn Glu Lys Phe Lys
1 5 10 15

Ser

<210> 1261
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1261
Glu Leu Gly Pro Tyr Tyr Arg Tyr Ser Ala Met Val Tyr
1 5 10

<210> 1262
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1262
Lys Ala Ser Gln Asn Val Gly Thr Ala Val Ala
1 5 10

<210> 1263
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1263
Ser Ala Ser Asn Arg Tyr Thr
1 5

<210> 1264
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1264
Gln Gln Tyr Ser Ser Tyr Pro Phe Thr
1 5

<210> 1265
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1265
Gly Tyr Thr Phe Thr Ser Tyr
1 5

<210> 1266
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1266
Tyr Pro Gly Ser Ser Ser
1 5

<210> 1267
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1267
Glu Leu Gly Pro Tyr Tyr Arg Tyr Ser Ala Met Val
1 5 10

<210> 1268
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1268
Ser Gln Asn Val Gly Thr Ala
1 5

<210> 1269
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1269

Ser Ala Ser
1

<210> 1270
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1270
Tyr Ser Ser Tyr Pro Phe
1 5

<210> 1271
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1271
Gly Tyr Thr Phe Thr Ser Tyr Trp Ile Asn
1 5 10

<210> 1272
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1272
Asn Ile Tyr Pro Gly Ser Ser Ser Thr Asn
1 5 10

<210> 1273
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1273
Glu Leu Gly Pro Tyr Tyr Arg Tyr Ser Ala Met Val Tyr
1   5   10

<210> 1274
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1274
Lys Ala Ser Gln Asn Val Gly Thr Ala Val Ala
1   5   10

<210> 1275
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1275
Ser Ala Ser Asn Arg Tyr Thr
1   5

<210> 1276
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1276
Gln Gln Tyr Ser Ser Tyr Pro Phe Thr
1   5

<210> 1277
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1277
Thr Ser Tyr Trp Ile Asn
1 5

<210> 1278
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1278
Trp Ile Gly Asn Ile Tyr Pro Gly Ser Ser Ser Thr Asn
1 5 10

<210> 1279
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1279
Ala Arg Glu Leu Gly Pro Tyr Tyr Arg Tyr Ser Ala Met Val
1 5 10

<210> 1280
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1280
Gly Thr Ala Val Ala Trp Tyr
1 5

<210> 1281
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1281
Leu Leu Ile Tyr Ser Ala Ser Asn Arg Tyr
1 5 10

<210> 1282
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1282
Gln Gln Tyr Ser Ser Tyr Pro Phe
1 5

<210> 1283
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1283
Gly Tyr Thr Phe Thr Ser Tyr Trp
1 5

<210> 1284
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1284
Ile Tyr Pro Gly Ser Ser Ser Thr
1 5

<210> 1285
<211> 15

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1285
Ala Arg Glu Leu Gly Pro Tyr Tyr Arg Tyr Ser Ala Met Val Tyr
1 5 10 15

<210> 1286
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1286
Gln Asn Val Gly Thr Ala
1 5

<210> 1287
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1287
Ser Ala Ser
1

<210> 1288
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1288
Gln Gln Tyr Ser Ser Tyr Pro Phe Thr
1 5

<210> 1289
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1289
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Asn Ile Tyr Pro Gly Ser Ser Ser Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Ser Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser Ala Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Gly Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Leu Gly Pro Tyr Tyr Arg Tyr Ser Ala Met Val Tyr Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1290
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1290
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Thr Val Gly
1 5 10 15

```
Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala
            20                  25                  30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Met Gln Ser
65                  70                  75                  80

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Ser Tyr Pro Phe
                85                  90                  95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
            100                 105
```

<210> 1291
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1291

```
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30

Trp Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45

Gly Asn Ile Tyr Pro Gly Ser Ser Ser Thr Asn Tyr Asn Glu Lys Phe
    50                  55                  60

Lys Ser Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser Ala Ala Tyr
65                  70                  75                  80
```

```
Met Gln Leu Ser Ser Leu Thr Ser Gly Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Leu Gly Pro Tyr Tyr Arg Tyr Ser Ala Met Val Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
        115                 120                 125

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
    130                 135                 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145                 150                 155                 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
                165                 170                 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
            180                 185                 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
        195                 200                 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
    210                 215                 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
225                 230                 235                 240

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                245                 250                 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            260                 265                 270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        275                 280                 285
```

```
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
    290                 295                 300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
305                 310                 315                 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                325                 330                 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            340                 345                 350

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
        355                 360                 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    370                 375                 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385                 390                 395                 400

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                405                 410                 415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            420                 425                 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        435                 440                 445

Ser Pro Gly Lys
    450
```

<210> 1292
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1292

```
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Thr Val Gly
1               5                  10                  15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala
            20                  25                  30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Met Gln Ser
65                  70                  75                  80

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Ser Tyr Pro Phe
                85                  90                  95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 1293
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1293
Asn Tyr Trp Met His
1 5

<210> 1294
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1294
Asn Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Lys Phe Lys
1 5 10 15

Asp

<210> 1295
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1295
Gly Leu Thr Gly Thr Gly His Tyr
1 5

<210> 1296
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1296
Arg Ala Ser Gln Asp Ile Asn Ile Tyr Leu Asn
1 5 10

<210> 1297
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1297
His Thr Ser Arg Leu His Ser
1 5

<210> 1298
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1298
Gln Gln Asp Asn Thr Leu Pro Tyr Thr
1 5

<210> 1299
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1299
Gly Tyr Thr Phe Thr Asn Tyr
1 5

<210> 1300
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1300
Asp Pro Ser Asp Ser Glu
1 5

<210> 1301
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1301
Gly Leu Thr Gly Thr Gly His
1 5

<210> 1302
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1302
Ser Gln Asp Ile Asn Ile Tyr
1 5

<210> 1303
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1303
His Thr Ser
1

<210> 1304
<211> 6

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1304
Asp Asn Thr Leu Pro Tyr
1 5

<210> 1305
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1305
Gly Tyr Thr Phe Thr Asn Tyr Trp Met His
1 5 10

<210> 1306
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1306
Asn Ile Asp Pro Ser Asp Ser Glu Thr His
1 5 10

<210> 1307
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1307
Gly Leu Thr Gly Thr Gly His Tyr
1 5

<210> 1308
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1308
Arg Ala Ser Gln Asp Ile Asn Ile Tyr Leu Asn
1 5 10

<210> 1309
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1309
His Thr Ser Arg Leu His Ser
1 5

<210> 1310
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1310
Gln Gln Asp Asn Thr Leu Pro Tyr Thr
1 5

<210> 1311
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1311
Thr Asn Tyr Trp Met His
1 5

<210> 1312
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1312
Trp Ile Gly Asn Ile Asp Pro Ser Asp Ser Glu Thr His
1 5 10

<210> 1313
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1313
Ala Ser Gly Leu Thr Gly Thr Gly His
1 5

<210> 1314
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1314
Asn Ile Tyr Leu Asn Trp Tyr
1 5

<210> 1315
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1315

Cys Leu Ile Tyr His Thr Ser Arg Leu His
1 5 10

<210> 1316
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1316
Gln Gln Asp Asn Thr Leu Pro Tyr
1 5

<210> 1317
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1317
Gly Tyr Thr Phe Thr Asn Tyr Trp
1 5

<210> 1318
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1318
Ile Asp Pro Ser Asp Ser Glu Thr
1 5

<210> 1319
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1319
Ala Ser Gly Leu Thr Gly Thr Gly His Tyr
1   5   10

<210> 1320
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1320
Gln Asp Ile Asn Ile Tyr
1   5

<210> 1321
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1321
His Thr Ser
1

<210> 1322
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1322
Gln Gln Asp Asn Thr Leu Pro Tyr Thr
1   5

<210> 1323
<211> 117
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1323
Glu Val Lys Leu Val Glu Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Asn Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Ser Gly Leu Thr Gly Thr Gly His Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Ser Ser
115

<210> 1324
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1324
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Asn Ile Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Glu Gly Ser Ile Lys Cys Leu Ile
        35   40   45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65   70   75   80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Asp Asn Thr Leu Pro Tyr
                85   90   95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 1325
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 1325
Glu Val Lys Leu Val Glu Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
            20   25   30

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Asn Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Lys Phe
    50   55   60

Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85   90   95

```
Ala Ser Gly Leu Thr Gly Thr Gly His Tyr Trp Gly Gln Gly Thr Thr
            100                 105                 110

Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
        115                 120                 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
    210                 215                 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
225                 230                 235                 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
            260                 265                 270

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
    290                 295                 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                 310                 315                 320
```

```
Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
                325                 330                 335


Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
            340                 345                 350


Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        355                 360                 365


Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380


Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385                 390                 395                 400


Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
                405                 410                 415


Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            420                 425                 430


His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
```

<210> 1326
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1326

```
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Asn Ile Tyr
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Glu Gly Ser Ile Lys Cys Leu Ile
        35                  40                  45
```

```
Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65                  70                  75                  80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Asp Asn Thr Leu Pro Tyr
                85                  90                  95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 1327
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1327
Asp Tyr Ser Met Asp
1 5

<210> 1328
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1328
Tyr Ile Tyr Thr Tyr Ser Gly Gly Ala Gly Tyr Asn Arg Lys Phe Lys
1 5 10 15

Ser

<210> 1329
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1329
Asp Ser Ser Asp Tyr Glu Phe Ala Tyr
1 5

<210> 1330
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1330
Lys Ala Ser Gln Asp Ile Lys Ser Tyr Leu Ser
1 5 10

<210> 1331
<211> 7

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1331
Arg Ala Asn Arg Leu Val Asp
1 5

<210> 1332
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1332
Leu Gln Tyr Asp Glu Phe Arg Thr
1 5

<210> 1333
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1333
Gly Tyr Thr Phe Thr Asp Tyr
1 5

<210> 1334
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1334
Tyr Thr Tyr Ser Gly Gly
1 5

<210> 1335
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1335
Asp Ser Ser Asp Tyr Glu Phe Ala
1 5

<210> 1336
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1336
Ser Gln Asp Ile Lys Ser Tyr
1 5

<210> 1337
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1337
Arg Ala Asn
1

<210> 1338
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1338
Tyr Asp Glu Phe Arg
1 5

<210> 1339
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1339
Gly Tyr Thr Phe Thr Asp Tyr Ser Met Asp
1 5 10

<210> 1340
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1340
Tyr Ile Tyr Thr Tyr Ser Gly Gly Ala Gly
1 5 10

<210> 1341
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1341
Asp Ser Ser Asp Tyr Glu Phe Ala Tyr
1 5

<210> 1342
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1342

Lys Ala Ser Gln Asp Ile Lys Ser Tyr Leu Ser
1 5 10

<210> 1343
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1343
Arg Ala Asn Arg Leu Val Asp
1 5

<210> 1344
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1344
Leu Gln Tyr Asp Glu Phe Arg Thr
1 5

<210> 1345
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1345
Thr Asp Tyr Ser Met Asp
1 5

<210> 1346
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1346
Trp Ile Gly Tyr Ile Tyr Thr Tyr Ser Gly Gly Ala Gly
1   5   10

<210> 1347
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1347
Ala Arg Asp Ser Ser Asp Tyr Glu Phe Ala
1   5   10

<210> 1348
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1348
Lys Ser Tyr Leu Ser Trp Phe
1   5

<210> 1349
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1349
Thr Leu Ile Tyr Arg Ala Asn Arg Leu Val
1   5   10

<210> 1350
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1350
Leu Gln Tyr Asp Glu Phe Arg
1 5

<210> 1351
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1351
Gly Tyr Thr Phe Thr Asp Tyr Ser
1 5

<210> 1352
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1352
Ile Tyr Thr Tyr Ser Gly Gly Ala
1 5

<210> 1353
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1353
Ala Arg Asp Ser Ser Asp Tyr Glu Phe Ala Tyr
1 5 10

<210> 1354
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1354
Gln Asp Ile Lys Ser Tyr
1 5

<210> 1355
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1355
Arg Ala Asn
1

<210> 1356
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1356
Leu Gln Tyr Asp Glu Phe Arg Thr
1 5

<210> 1357
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1357
Glu Phe Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Ser Met Asp Trp Val Lys Gln Ser His Gly Lys Thr Leu Glu Trp Ile
        35   40   45

Gly Tyr Ile Tyr Thr Tyr Ser Gly Gly Ala Gly Tyr Asn Arg Lys Phe
    50   55   60

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80

Leu Glu Leu His Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Asp Ser Ser Asp Tyr Glu Phe Ala Tyr Trp Gly Gln Gly Thr
            100   105   110

Leu Val Thr Val Ser Ala
        115

<210> 1358
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 1358
Asp Ile Lys Met Thr Gln Ser Pro Ser Ser Met Cys Pro Ser Leu Gly
1   5   10   15

Glu Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Lys Ser Tyr
            20   25   30

Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Lys Thr Leu Ile
        35   40   45

Tyr Arg Ala Asn Arg Leu Val Asp Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Gln Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Tyr
65   70   75   80

Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Tyr Asp Glu Phe Arg Thr
85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 1359
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1359
Glu Phe Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Ser Met Asp Trp Val Lys Gln Ser His Gly Lys Thr Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Tyr Thr Tyr Ser Gly Gly Ala Gly Tyr Asn Arg Lys Phe
50 55 60

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Leu Glu Leu His Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Ser Ser Asp Tyr Glu Phe Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

```
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
    210                 215                 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    290                 295                 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
                325                 330                 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350
```

```
Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
        355                 360                 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370                 375                 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385                 390                 395                 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                405                 410                 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            420                 425                 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
```

<210> 1360
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1360

```
Asp Ile Lys Met Thr Gln Ser Pro Ser Ser Met Cys Pro Ser Leu Gly
1               5                   10                  15

Glu Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Lys Ser Tyr
            20                  25                  30

Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Lys Thr Leu Ile
        35                  40                  45

Tyr Arg Ala Asn Arg Leu Val Asp Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Gln Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Tyr
65                  70                  75                  80
```

```
Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Tyr Asp Glu Phe Arg Thr
                85                  90                  95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
            100                 105                 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
        115                 120                 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
    130                 135                 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145                 150                 155                 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165                 170                 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180                 185                 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195                 200                 205

Asn Arg Gly Glu Cys
    210
```

<210> 1361
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1361
```
Thr Ser Gly Met Gly Val Ser
1               5
```

<210> 1362
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1362
His Ile Phe Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 1363
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1363
Arg Asp Gly Tyr Gly Asp Tyr Ala Tyr Phe Asp Val
1 5 10

<210> 1364
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1364
Arg Ala Ser Glu Asn Ile Tyr Ser Asp Leu Ala
1 5 10

<210> 1365
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1365
Ala Ala Thr Ile Leu Thr Asp
1 5

<210> 1366
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1366
Gln His Phe Trp Gly Thr Pro Trp Thr
1 5

<210> 1367
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1367
Gly Phe Ser Leu Asn Thr Ser Gly Met
1 5

<210> 1368
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1368
Phe Trp Asp Asp Asp
1 5

<210> 1369
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1369
Arg Asp Gly Tyr Gly Asp Tyr Ala Tyr Phe Asp
1 5 10

<210> 1370
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1370
Ser Glu Asn Ile Tyr Ser Asp
1 5

<210> 1371
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1371
Ala Ala Thr
1

<210> 1372
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1372
Phe Trp Gly Thr Pro Trp
1 5

<210> 1373
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1373
Gly Phe Ser Leu Asn Thr Ser Gly Met Gly Val Ser
1 5 10

<210> 1374
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1374
His Ile Phe Trp Asp Asp Asp Lys Arg
1 5

<210> 1375
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1375
Arg Asp Gly Tyr Gly Asp Tyr Ala Tyr Phe Asp Val
1 5 10

<210> 1376
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1376
Arg Ala Ser Glu Asn Ile Tyr Ser Asp Leu Ala
1 5 10

<210> 1377
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1377

Ala Ala Thr Ile Leu Thr Asp
1   5

<210> 1378
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1378
Gln His Phe Trp Gly Thr Pro Trp Thr
1   5

<210> 1379
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1379
Asn Thr Ser Gly Met Gly Val Ser
1   5

<210> 1380
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1380
Trp Leu Ala His Ile Phe Trp Asp Asp Asp Lys Arg
1   5   10

<210> 1381
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1381
Ala Arg Arg Asp Gly Tyr Gly Asp Tyr Ala Tyr Phe Asp
1   5   10

<210> 1382
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1382
Tyr Ser Asp Leu Ala Trp Tyr
1   5

<210> 1383
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1383
Leu Leu Val Tyr Ala Ala Thr Ile Leu Thr
1   5   10

<210> 1384
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1384
Gln His Phe Trp Gly Thr Pro Trp
1   5

<210> 1385
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1385
Gly Phe Ser Leu Asn Thr Ser Gly Met Gly
1 5 10

<210> 1386
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1386
Ile Phe Trp Asp Asp Asp Lys
1 5

<210> 1387
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1387
Ala Arg Arg Asp Gly Tyr Gly Asp Tyr Ala Tyr Phe Asp Val
1 5 10

<210> 1388
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1388
Glu Asn Ile Tyr Ser Asp
1 5

<210> 1389
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1389
Ala Ala Thr
1

<210> 1390
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1390
Gln His Phe Trp Gly Thr Pro Trp Thr
1 5

<210> 1391
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1391
Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Asn Thr Ser
20 25 30

Gly Met Gly Val Ser Trp Ile Arg Lys Pro Ser Gly Lys Gly Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Ser Asn Gln Val
65 70 75 80

Phe Leu Met Ile Thr Ser Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Arg Asp Gly Tyr Gly Asp Tyr Ala Tyr Phe Asp Val Trp
100 105 110

Gly Ala Gly Thr Leu Val Thr Val Ser Ala
115 120

<210> 1392
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1392
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Val Ser Val Gly
1 5 10 15

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr Ser Asp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
35 40 45

Tyr Ala Ala Thr Ile Leu Thr Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Gly Asn Tyr Tyr Cys Gln His Phe Trp Gly Thr Pro Trp
85 90 95

Thr Phe Gly Asp Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 1393
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1393
Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Asn Thr Ser
20 25 30

Gly Met Gly Val Ser Trp Ile Arg Lys Pro Ser Gly Lys Gly Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Ser Asn Gln Val
65 70 75 80

Phe Leu Met Ile Thr Ser Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Arg Asp Gly Tyr Gly Asp Tyr Ala Tyr Phe Asp Val Trp
100 105 110

Gly Ala Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro
115 120 125

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
130 135 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145 150 155 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
180 185 190

```
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
        195                 200                 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
    210                 215                 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
225                 230                 235                 240

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                245                 250                 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            260                 265                 270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        275                 280                 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
    290                 295                 300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
305                 310                 315                 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                325                 330                 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            340                 345                 350

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
        355                 360                 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    370                 375                 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385                 390                 395                 400

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                405                 410                 415
```

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
420 425 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
435 440 445

Ser Pro Gly Lys
450

<210> 1394
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1394
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Val Ser Val Gly
1 5 10 15

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr Ser Asp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
35 40 45

Tyr Ala Ala Thr Ile Leu Thr Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Gly Asn Tyr Tyr Cys Gln His Phe Trp Gly Thr Pro Trp
85 90 95

Thr Phe Gly Asp Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

```
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175


Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190


Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205


Phe Asn Arg Gly Glu Cys
    210


<210> 1395
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1395
Ser His Trp Ile His
1               5


<210> 1396
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1396
Asn Ile Tyr Pro Gly Ser Ser Ser Thr Asn Tyr Asn Glu Lys Phe Lys
1               5                   10                  15
```

Arg

<210> 1397
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1397
His Ser Pro Gly His Arg Asp Tyr Ala Met Asp Tyr
1 5 10

<210> 1398
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1398
Lys Ala Ser Gln Asn Val Gly Thr Ala Val Ala
1 5 10

<210> 1399
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1399
Ser Ala Ser Asn Arg Tyr Thr
1 5

<210> 1400
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1400
Gln Gln Tyr Ser Thr Tyr Pro Leu Thr
1 5

<210> 1401
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1401
Gly Tyr Thr Ser Thr Ser His
1 5

<210> 1402
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1402
Tyr Pro Gly Ser Ser Ser
1 5

<210> 1403
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1403
His Ser Pro Gly His Arg Asp Tyr Ala Met Asp
1 5 10

<210> 1404
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1404
Ser Gln Asn Val Gly Thr Ala
1 5

<210> 1405
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1405
Ser Ala Ser
1

<210> 1406
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1406
Tyr Ser Thr Tyr Pro Leu
1 5

<210> 1407
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1407
Gly Tyr Thr Ser Thr Ser His Trp Ile His
1 5 10

<210> 1408
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1408
Asn Ile Tyr Pro Gly Ser Ser Ser Thr Asn
1 5 10

<210> 1409
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1409
His Ser Pro Gly His Arg Asp Tyr Ala Met Asp Tyr
1 5 10

<210> 1410
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1410
Lys Ala Ser Gln Asn Val Gly Thr Ala Val Ala
1 5 10

<210> 1411
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1411
Ser Ala Ser Asn Arg Tyr Thr
1 5

<210> 1412
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1412
Gln Gln Tyr Ser Thr Tyr Pro Leu Thr
1 5

<210> 1413
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1413
Thr Ser His Trp Ile His
1 5

<210> 1414
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1414
Trp Ile Gly Asn Ile Tyr Pro Gly Ser Ser Ser Thr Asn
1 5 10

<210> 1415
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1415
Ala Arg His Ser Pro Gly His Arg Asp Tyr Ala Met Asp
1 5 10

<210> 1416
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1416
Gly Thr Ala Val Ala Trp Tyr
1 5

<210> 1417
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1417
Leu Leu Ile Ala Ser Ala Ser Asn Arg Tyr
1 5 10

<210> 1418
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1418
Gln Gln Tyr Ser Thr Tyr Pro Leu
1 5

<210> 1419
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1419
Gly Tyr Thr Ser Thr Ser His Trp
1 5

<210> 1420
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1420
Ile Tyr Pro Gly Ser Ser Ser Thr
1 5

<210> 1421
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1421
Ala Arg His Ser Pro Gly His Arg Asp Tyr Ala Met Asp Tyr
1 5 10

<210> 1422
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1422
Gln Asn Val Gly Thr Ala
1 5

<210> 1423
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1423

Ser Ala Ser
1

<210> 1424
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1424
Gln Gln Tyr Ser Thr Tyr Pro Leu Thr
1 5

<210> 1425
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1425
Gln Val Gln Leu Gln Gln Pro Gly Ala Asp Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Ser Thr Ser His
20 25 30

Trp Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Asn Ile Tyr Pro Gly Ser Ser Ser Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Arg Met Ala Thr Leu Thr Val Asp Thr Ser Ser Ser Thr Val Tyr
65 70 75 80

Met Val Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg His Ser Pro Gly His Arg Asp Tyr Ala Met Asp Tyr Trp Gly
100 105 110

Leu Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 1426
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1426
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Pro Thr Thr Val Gly
1 5 10 15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45

Ala Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Met Gln Ser
65 70 75 80

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Thr Tyr Pro Leu
85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Met Lys
100 105

<210> 1427
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1427

```
Gln Val Gln Leu Gln Gln Pro Gly Ala Asp Leu Val Lys Pro Gly Ala
1               5                  10                  15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Ser Thr Ser His
            20                  25                  30

Trp Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45

Gly Asn Ile Tyr Pro Gly Ser Ser Ser Thr Asn Tyr Asn Glu Lys Phe
    50                  55                  60

Lys Arg Met Ala Thr Leu Thr Val Asp Thr Ser Ser Ser Thr Val Tyr
65                  70                  75                  80

Met Val Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg His Ser Pro Gly His Arg Asp Tyr Ala Met Asp Tyr Trp Gly
            100                 105                 110

Leu Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220
```

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430
```

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 1428
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1428
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Pro Thr Thr Val Gly
1 5 10 15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45

Ala Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Met Gln Ser
65 70 75 80

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Thr Tyr Pro Leu
85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Met Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 1429
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1429
Thr Ser Gly Met Gly Val Ser
1 5

<210> 1430
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1430
His Ile Phe Trp Asp Asp Asp Arg Arg Tyr Lys Ser Ser Leu Lys Ser
1 5 10 15

<210> 1431
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1431
Arg Val Gly Tyr Gly Asp Tyr Ala Tyr Phe Asp Val
1 5 10

<210> 1432
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1432
Arg Ala Ser Glu Asn Ile Tyr Ser Asp Leu Ala
1 5 10

<210> 1433
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1433
Ala Ala Thr Asn Leu Ala Asp
1 5

<210> 1434
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1434
Gln His Phe Trp Gly Thr Pro Trp Thr
1 5

<210> 1435
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1435
Gly Phe Ser Leu Ser Thr Ser Gly Met
1 5

<210> 1436
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1436
Phe Trp Asp Asp Asp
1 5

<210> 1437
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1437
Arg Val Gly Tyr Gly Asp Tyr Ala Tyr Phe Asp
1 5 10

<210> 1438
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1438
Ser Glu Asn Ile Tyr Ser Asp
1 5

<210> 1439
<211> 3

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1439
Ala Ala Thr
1

<210> 1440
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1440
Phe Trp Gly Thr Pro Trp
1 5

<210> 1441
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1441
Gly Phe Ser Leu Ser Thr Ser Gly Met Gly Val Ser
1 5 10

<210> 1442
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1442
His Ile Phe Trp Asp Asp Asp Arg Arg
1 5

<210> 1443
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1443
Arg Val Gly Tyr Gly Asp Tyr Ala Tyr Phe Asp Val
1 5 10

<210> 1444
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1444
Arg Ala Ser Glu Asn Ile Tyr Ser Asp Leu Ala
1 5 10

<210> 1445
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1445
Ala Ala Thr Asn Leu Ala Asp
1 5

<210> 1446
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1446
Gln His Phe Trp Gly Thr Pro Trp Thr
1 5

<210> 1447
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1447
Ser Thr Ser Gly Met Gly Val Ser
1 5

<210> 1448
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1448
Trp Leu Ala His Ile Phe Trp Asp Asp Asp Arg Arg
1 5 10

<210> 1449
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1449
Ala Arg Arg Val Gly Tyr Gly Asp Tyr Ala Tyr Phe Asp
1 5 10

<210> 1450
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1450

Tyr Ser Asp Leu Ala Trp Tyr
1 5

<210> 1451
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1451
Leu Leu Val Tyr Ala Ala Thr Asn Leu Ala
1 5 10

<210> 1452
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1452
Gln His Phe Trp Gly Thr Pro Trp
1 5

<210> 1453
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1453
Gly Phe Ser Leu Ser Thr Ser Gly Met Gly
1 5 10

<210> 1454
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1454
Ile Phe Trp Asp Asp Asp Arg
1   5

<210> 1455
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1455
Ala Arg Arg Val Gly Tyr Gly Asp Tyr Ala Tyr Phe Asp Val
1   5   10

<210> 1456
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1456
Glu Asn Ile Tyr Ser Asp
1   5

<210> 1457
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1457
Ala Ala Thr
1

<210> 1458
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1458
Gln His Phe Trp Gly Thr Pro Trp Thr
1 5

<210> 1459
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1459
Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Lys Val Gln Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

Gly Met Gly Val Ser Trp Ile Arg Lys Pro Ser Gly Lys Gly Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Trp Asp Asp Asp Arg Arg Tyr Lys Ser Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Ser Asn Gln Val
65 70 75 80

Phe Leu Met Ile Thr Ser Val Asp Thr Ala Asp Ser Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Arg Val Gly Tyr Gly Asp Tyr Ala Tyr Phe Asp Val Trp
100 105 110

Gly Ala Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1460
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1460
Asp Ile Gln Met Thr Gln Tyr Pro Ala Ser Leu Ser Val Ser Val Gly
1 5 10 15

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr Ser Asp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
35 40 45

Tyr Ala Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Gly Asn Tyr Tyr Cys Gln His Phe Trp Gly Thr Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 1461
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1461
Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Lys Val Gln Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

Gly Met Gly Val Ser Trp Ile Arg Lys Pro Ser Gly Lys Gly Leu Glu
35 40 45

```
Trp Leu Ala His Ile Phe Trp Asp Asp Asp Arg Arg Tyr Lys Ser Ser
    50                  55                  60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Ser Asn Gln Val
65                  70                  75                  80

Phe Leu Met Ile Thr Ser Val Asp Thr Ala Asp Ser Ala Thr Tyr Tyr
                85                  90                  95

Cys Ala Arg Arg Val Gly Tyr Gly Asp Tyr Ala Tyr Phe Asp Val Trp
            100                 105                 110

Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
        115                 120                 125

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
    130                 135                 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145                 150                 155                 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
                165                 170                 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
            180                 185                 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
        195                 200                 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
    210                 215                 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
225                 230                 235                 240

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                245                 250                 255
```

```
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            260                 265                 270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        275                 280                 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
    290                 295                 300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
305                 310                 315                 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                325                 330                 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            340                 345                 350

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
        355                 360                 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    370                 375                 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385                 390                 395                 400

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                405                 410                 415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            420                 425                 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        435                 440                 445

Ser Pro Gly Lys
    450
```

<210> 1462
<211> 214

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1462
Asp Ile Gln Met Thr Gln Tyr Pro Ala Ser Leu Ser Val Ser Val Gly
1 5 10 15

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr Ser Asp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
35 40 45

Tyr Ala Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Gly Asn Tyr Tyr Cys Gln His Phe Trp Gly Thr Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195   200   205

Phe Asn Arg Gly Glu Cys
    210

<210> 1463
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1463
Asn Tyr Trp Ile Asn
1   5

<210> 1464
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1464
Asn Ile Tyr Pro Gly Ser Asp Ser Ser Asn Tyr Asn Glu Lys Phe Lys
1   5   10   15

Thr

<210> 1465
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1465
Glu Glu Ala Asp Tyr Arg Tyr Thr Trp Phe Val Tyr
1   5   10

<210> 1466
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1466
Lys Ala Ser Gln Asn Val Gly Thr Ala Val Ala
1 5 10

<210> 1467
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1467
Ser Ala Ser Asn Arg Tyr Thr
1 5

<210> 1468
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1468
Gln Gln Tyr Ser Ser Tyr Pro Leu Thr
1 5

<210> 1469
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1469

Gly Tyr Ser Phe Thr Asn Tyr
1 5

<210> 1470
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1470
Tyr Pro Gly Ser Asp Ser
1 5

<210> 1471
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1471
Glu Glu Ala Asp Tyr Arg Tyr Thr Trp Phe Val
1 5 10

<210> 1472
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1472
Ser Gln Asn Val Gly Thr Ala
1 5

<210> 1473
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1473
Ser Ala Ser
1

<210> 1474
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1474
Tyr Ser Ser Tyr Pro Leu
1 5

<210> 1475
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1475
Gly Tyr Ser Phe Thr Asn Tyr Trp Ile Asn
1 5 10

<210> 1476
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1476
Asn Ile Tyr Pro Gly Ser Asp Ser Ser Asn
1 5 10

<210> 1477
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1477
Glu Glu Ala Asp Tyr Arg Tyr Thr Trp Phe Val Tyr
1 5 10

<210> 1478
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1478
Lys Ala Ser Gln Asn Val Gly Thr Ala Val Ala
1 5 10

<210> 1479
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1479
Ser Ala Ser Asn Arg Tyr Thr
1 5

<210> 1480
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1480
Gln Gln Tyr Ser Ser Tyr Pro Leu Thr
1 5

<210> 1481
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1481
Thr Asn Tyr Trp Ile Asn
1 5

<210> 1482
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1482
Trp Ile Gly Asn Ile Tyr Pro Gly Ser Asp Ser Ser Asn
1 5 10

<210> 1483
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1483
Ala Arg Glu Glu Ala Asp Tyr Arg Tyr Thr Trp Phe Val
1 5 10

<210> 1484
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1484
Gly Thr Ala Val Ala Trp Tyr
1 5

<210> 1485
<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1485
Leu Leu Ile Tyr Ser Ala Ser Asn Arg Tyr
1 5 10

<210> 1486
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1486
Gln Gln Tyr Ser Ser Tyr Pro Leu
1 5

<210> 1487
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1487
Gly Tyr Ser Phe Thr Asn Tyr Trp
1 5

<210> 1488
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1488
Ile Tyr Pro Gly Ser Asp Ser Ser
1 5

<210> 1489
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1489
Ala Arg Glu Glu Ala Asp Tyr Arg Tyr Thr Trp Phe Val Tyr
1 5 10

<210> 1490
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1490
Gln Asn Val Gly Thr Ala
1 5

<210> 1491
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1491
Ser Ala Ser
1

<210> 1492
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1492
Gln Gln Tyr Ser Ser Tyr Pro Leu Thr
1 5

<210> 1493
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1493
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asn Tyr
20 25 30

Trp Ile Asn Trp Met Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Asn Ile Tyr Pro Gly Ser Asp Ser Ser Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Thr Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Glu Ala Asp Tyr Arg Tyr Thr Trp Phe Val Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ala
115 120

<210> 1494
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1494

```
Asp Ile Lys Met Thr Gln Ser Gln Lys Phe Met Ser Thr Thr Val Gly
1               5                   10                  15


Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala
            20                  25                  30


Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Phe Ser Asn Met Gln Ser
65                  70                  75                  80


Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Ser Tyr Pro Leu
                85                  90                  95


Thr Phe Gly Ala Gly Thr Lys Leu Glu Met Lys
            100                 105


<210> 1495
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 1495
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asn Tyr
            20                  25                  30


Trp Ile Asn Trp Met Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Asn Ile Tyr Pro Gly Ser Asp Ser Ser Asn Tyr Asn Glu Lys Phe
    50                  55                  60
```

```
Lys Thr Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Glu Ala Asp Tyr Arg Tyr Thr Trp Phe Val Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285
```

```
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445

Pro Gly Lys
    450
```

<210> 1496
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1496
Asp Ile Lys Met Thr Gln Ser Gln Lys Phe Met Ser Thr Thr Val Gly
1   5   10   15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala
            20   25   30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
        35   40   45

Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
    50   55   60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Phe Ser Asn Met Gln Ser
65   70   75   80

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Ser Tyr Pro Leu
                85   90   95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Met Lys Arg Thr Val Ala Ala
            100   105   110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115   120   125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130   135   140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145   150   155   160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165   170   175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180   185   190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195   200   205

Phe Asn Arg Gly Glu Cys
    210

<210> 1497
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1497
Ser Tyr Trp Ile Asn
1   5

<210> 1498
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1498
Asn Ile Tyr Pro Gly Ser Ser Ser Thr Asn Tyr Asn Glu Lys Phe Lys
1   5   10   15

Asn

<210> 1499
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1499
Glu Glu Tyr Ser Tyr Lys Ser Ser Trp Phe Ala Tyr
1   5   10

<210> 1500
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1500
Lys Ala Ser Gln Asn Val Gly Thr Ala Val Ala
1 5 10

<210> 1501
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1501
Ser Ala Ser Asn Arg Tyr Asn
1 5

<210> 1502
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1502
Gln Gln Tyr Ser Thr Tyr Pro Tyr Thr
1 5

<210> 1503
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1503
Gly Tyr Ser Phe Thr Ser Tyr
1 5

<210> 1504
<211> 6

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1504
Tyr Pro Gly Ser Ser Ser
1 5

<210> 1505
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1505
Glu Glu Tyr Ser Tyr Lys Ser Ser Trp Phe Ala
1 5 10

<210> 1506
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1506
Ser Gln Asn Val Gly Thr Ala
1 5

<210> 1507
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1507
Ser Ala Ser
1

<210> 1508
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1508
Tyr Ser Thr Tyr Pro Tyr
1 5

<210> 1509
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1509
Gly Tyr Ser Phe Thr Ser Tyr Trp Ile Asn
1 5 10

<210> 1510
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1510
Asn Ile Tyr Pro Gly Ser Ser Ser Thr Asn
1 5 10

<210> 1511
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1511
Glu Glu Tyr Ser Tyr Lys Ser Ser Trp Phe Ala Tyr
1 5 10

<210> 1512
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1512
Lys Ala Ser Gln Asn Val Gly Thr Ala Val Ala
1 5 10

<210> 1513
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1513
Ser Ala Ser Asn Arg Tyr Asn
1 5

<210> 1514
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1514
Gln Gln Tyr Ser Thr Tyr Pro Tyr Thr
1 5

<210> 1515
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1515

Thr Ser Tyr Trp Ile Asn
1 5

<210> 1516
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1516
Trp Ile Gly Asn Ile Tyr Pro Gly Ser Ser Ser Thr Asn
1 5 10

<210> 1517
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1517
Ala Arg Glu Glu Tyr Ser Tyr Lys Ser Ser Trp Phe Ala
1 5 10

<210> 1518
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1518
Gly Thr Ala Val Ala Trp Tyr
1 5

<210> 1519
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1519
Leu Leu Ile Tyr Ser Ala Ser Asn Arg Tyr
1   5   10

<210> 1520
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1520
Gln Gln Tyr Ser Thr Tyr Pro Tyr
1   5

<210> 1521
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1521
Gly Tyr Ser Phe Thr Ser Tyr Trp
1   5

<210> 1522
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1522
Ile Tyr Pro Gly Ser Ser Ser Thr
1   5

<210> 1523
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1523
Ala Arg Glu Glu Tyr Ser Tyr Lys Ser Ser Trp Phe Ala Tyr
1 5 10

<210> 1524
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1524
Gln Asn Val Gly Thr Ala
1 5

<210> 1525
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1525
Ser Ala Ser
1

<210> 1526
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1526
Gln Gln Tyr Ser Thr Tyr Pro Tyr Thr
1 5

<210> 1527
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1527
Glu Val Gln Leu Gln Gln Ser Gly Thr Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Pro Glu Trp Ile
35 40 45

Gly Asn Ile Tyr Pro Gly Ser Ser Ser Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Asn Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Glu Tyr Ser Tyr Lys Ser Ser Trp Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ala
115 120

<210> 1528
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1528
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Thr Val Gly
1 5 10 15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Asn Arg Tyr Asn Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Met Gln Ser
65 70 75 80

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Thr Tyr Pro Tyr
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 1529
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1529
Glu Val Gln Leu Gln Gln Ser Gly Thr Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Pro Glu Trp Ile
35 40 45

Gly Asn Ile Tyr Pro Gly Ser Ser Ser Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Asn Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Tyr Cys
85 90 95

```
Ala Arg Glu Glu Tyr Ser Tyr Lys Ser Ser Trp Phe Ala Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300
```

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Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320


Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335


Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350


Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
        355                 360                 365


Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380


Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400


Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415


Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430


His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445


Pro Gly Lys
    450


<210> 1530
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 1530
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Thr Val Gly
1               5                   10                  15
```

```
Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala
            20                  25                  30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Ser Ala Ser Asn Arg Tyr Asn Gly Val Pro Asp Arg Phe Thr Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Met Gln Ser
65                  70                  75                  80

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Thr Tyr Pro Tyr
                85                  90                  95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 1531
<211> 5

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1531
Ser Tyr Trp Ile Ser
1 5

<210> 1532
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1532
Asn Ile Tyr Pro Gly Ser Ser Ser Ser Asn Tyr Asn Glu Asn Phe Lys
1 5 10 15

Ser

<210> 1533
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1533
Glu Glu Tyr Ser Tyr Phe Pro Ser Trp Phe Ala Tyr
1 5 10

<210> 1534
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1534

Lys Ala Ser Gln Asn Val Gly Thr Ala Val Ala
1 5 10

<210> 1535
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1535
Ser Ala Ser Asn Arg Tyr Thr
1 5

<210> 1536
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1536
Gln Gln Tyr Ser Thr Tyr Pro Phe Thr
1 5

<210> 1537
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1537
Gly Tyr Thr Phe Thr Ser Tyr
1 5

<210> 1538
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1538
Tyr Pro Gly Ser Ser Ser
1 5

<210> 1539
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1539
Glu Glu Tyr Ser Tyr Phe Pro Ser Trp Phe Ala
1 5 10

<210> 1540
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1540
Ser Gln Asn Val Gly Thr Ala
1 5

<210> 1541
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1541
Ser Ala Ser
1

<210> 1542
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1542
Tyr Ser Thr Tyr Pro Phe
1 5

<210> 1543
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1543
Gly Tyr Thr Phe Thr Ser Tyr Trp Ile Ser
1 5 10

<210> 1544
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1544
Asn Ile Tyr Pro Gly Ser Ser Ser Ser Asn
1 5 10

<210> 1545
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1545
Glu Glu Tyr Ser Tyr Phe Pro Ser Trp Phe Ala Tyr
1 5 10

<210> 1546
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1546
Lys Ala Ser Gln Asn Val Gly Thr Ala Val Ala
1 5 10

<210> 1547
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1547
Ser Ala Ser Asn Arg Tyr Thr
1 5

<210> 1548
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1548
Gln Gln Tyr Ser Thr Tyr Pro Phe Thr
1 5

<210> 1549
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1549
Thr Ser Tyr Trp Ile Ser
1 5

<210> 1550
<211> 13

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1550
Trp Ile Gly Asn Ile Tyr Pro Gly Ser Ser Ser Ser Asn
1 5 10

<210> 1551
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1551
Ala Arg Glu Glu Tyr Ser Tyr Phe Pro Ser Trp Phe Ala
1 5 10

<210> 1552
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1552
Gly Thr Ala Val Ala Trp Phe
1 5

<210> 1553
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1553
Leu Leu Ile Tyr Ser Ala Ser Asn Arg Tyr
1 5 10

<210> 1554
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1554
Gln Gln Tyr Ser Thr Tyr Pro Phe
1 5

<210> 1555
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1555
Gly Tyr Thr Phe Thr Ser Tyr Trp
1 5

<210> 1556
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1556
Ile Tyr Pro Gly Ser Ser Ser Ser
1 5

<210> 1557
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1557
Ala Arg Glu Glu Tyr Ser Tyr Phe Pro Ser Trp Phe Ala Tyr
1 5 10

<210> 1558
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1558
Gln Asn Val Gly Thr Ala
1 5

<210> 1559
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1559
Ser Ala Ser
1

<210> 1560
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1560
Gln Gln Tyr Ser Thr Tyr Pro Phe Thr
1 5

<210> 1561
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1561

```
Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30


Trp Ile Ser Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Asn Ile Tyr Pro Gly Ser Ser Ser Ser Asn Tyr Asn Glu Asn Phe
    50                  55                  60


Lys Ser Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser Thr Ala His
65                  70                  75                  80


Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Phe Tyr Cys
                85                  90                  95


Ala Arg Glu Glu Tyr Ser Tyr Phe Pro Ser Trp Phe Ala Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Ser Val Thr Val Ser Ser
        115                 120


<210> 1562
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 1562
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Thr Ile Gly
1               5                   10                  15


Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala
            20                  25                  30


Val Ala Trp Phe Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
        35                  40                  45
```

Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
    50   55   60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Met Gln Ser
65   70   75   80

Glu Asp Leu Ala Asn Tyr Phe Cys Gln Gln Tyr Ser Thr Tyr Pro Phe
                85   90   95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 1563
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 1563
Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20   25   30

Trp Ile Ser Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Asn Ile Tyr Pro Gly Ser Ser Ser Ser Asn Tyr Asn Glu Asn Phe
    50   55   60

Lys Ser Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser Thr Ala His
65   70   75   80

Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Phe Tyr Cys
                85   90   95

Ala Arg Glu Glu Tyr Ser Tyr Phe Pro Ser Trp Phe Ala Tyr Trp Gly
            100   105   110

```
Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335
```

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 1564
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1564
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Thr Ile Gly
1 5 10 15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala
20 25 30

Val Ala Trp Phe Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45

```
Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Met Gln Ser
65                  70                  75                  80

Glu Asp Leu Ala Asn Tyr Phe Cys Gln Gln Tyr Ser Thr Tyr Pro Phe
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 1565
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1565
Ser Phe Trp Ile Asn
1 5

<210> 1566
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1566
Asn Ile Tyr Pro Gly Ser Ser Ser Thr Asn Tyr Ser Glu Lys Phe Lys
1 5 10 15

Asn

<210> 1567
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1567
Glu Glu Tyr Ser Tyr Lys Ser Ser Trp Phe Ala Tyr
1 5 10

<210> 1568
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1568
Lys Ala Ser Gln Asn Val Gly Thr Ala Val Ala
1 5 10

<210> 1569
<211> 7

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1569
Ser Ala Ser Asn Arg Tyr Asn
1 5

<210> 1570
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1570
Gln Gln Tyr Ser Thr Tyr Pro Tyr Thr
1 5

<210> 1571
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1571
Gly Tyr Ser Phe Ala Ser Phe
1 5

<210> 1572
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1572
Tyr Pro Gly Ser Ser Ser
1 5

<210> 1573
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1573
Glu Glu Tyr Ser Tyr Lys Ser Ser Trp Phe Ala
1 5 10

<210> 1574
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1574
Ser Gln Asn Val Gly Thr Ala
1 5

<210> 1575
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1575
Ser Ala Ser
1

<210> 1576
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1576
Tyr Ser Thr Tyr Pro Tyr
1 5

<210> 1577
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1577
Gly Tyr Ser Phe Ala Ser Phe Trp Ile Asn
1 5 10

<210> 1578
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1578
Asn Ile Tyr Pro Gly Ser Ser Ser Thr Asn
1 5 10

<210> 1579
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1579
Glu Glu Tyr Ser Tyr Lys Ser Ser Trp Phe Ala Tyr
1 5 10

<210> 1580
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1580

Lys Ala Ser Gln Asn Val Gly Thr Ala Val Ala
1 5 10

<210> 1581
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1581
Ser Ala Ser Asn Arg Tyr Asn
1 5

<210> 1582
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1582
Gln Gln Tyr Ser Thr Tyr Pro Tyr Thr
1 5

<210> 1583
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1583
Ala Ser Phe Trp Ile Asn
1 5

<210> 1584
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1584
Trp Ile Gly Asn Ile Tyr Pro Gly Ser Ser Ser Thr Asn
1   5   10

<210> 1585
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1585
Ala Arg Glu Glu Tyr Ser Tyr Lys Ser Ser Trp Phe Ala
1   5   10

<210> 1586
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1586
Gly Thr Ala Val Ala Trp Tyr
1   5

<210> 1587
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1587
Leu Leu Ile Tyr Ser Ala Ser Asn Arg Tyr
1   5   10

<210> 1588
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1588
Gln Gln Tyr Ser Thr Tyr Pro Tyr
1 5

<210> 1589
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1589
Gly Tyr Ser Phe Ala Ser Phe Trp
1 5

<210> 1590
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1590
Ile Tyr Pro Gly Ser Ser Ser Thr
1 5

<210> 1591
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1591
Ala Arg Glu Glu Tyr Ser Tyr Lys Ser Ser Trp Phe Ala Tyr
1 5 10

<210> 1592
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1592
Gln Asn Val Gly Thr Ala
1 5

<210> 1593
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1593
Ser Ala Ser
1

<210> 1594
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1594
Gln Gln Tyr Ser Thr Tyr Pro Tyr Thr
1 5

<210> 1595
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1595
Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Ser Phe Ala Ser Phe
20 25 30

```
Trp Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Pro Glu Trp Ile
        35                  40                  45


Gly Asn Ile Tyr Pro Gly Ser Ser Ser Thr Asn Tyr Ser Glu Lys Phe
    50                  55                  60


Lys Asn Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80


Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Glu Glu Tyr Ser Tyr Lys Ser Ser Trp Phe Ala Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 1596
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 1596
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Thr Val Gly
1               5                   10                  15


Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala
            20                  25                  30


Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Ser Ala Ser Asn Arg Tyr Asn Gly Val Pro Asp Arg Phe Thr Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Met Gln Ser
65                  70                  75                  80
```

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Thr Tyr Pro Tyr
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 1597
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1597
Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Ser Phe Ala Ser Phe
20 25 30

Trp Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Pro Glu Trp Ile
35 40 45

Gly Asn Ile Tyr Pro Gly Ser Ser Ser Thr Asn Tyr Ser Glu Lys Phe
50 55 60

Lys Asn Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Glu Tyr Ser Tyr Lys Ser Ser Trp Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

```
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350
```

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 1598
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1598
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Thr Val Gly
1 5 10 15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Asn Arg Tyr Asn Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

```
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Met Gln Ser
65                  70                  75                  80


Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Thr Tyr Pro Tyr
                85                  90                  95


Thr Phe Gly Ser Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala
            100                 105                 110


Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175


Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190


Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205


Phe Asn Arg Gly Glu Cys
    210


<210> 1599
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1599
Asp Asp Tyr Ile His
1               5
```

<210> 1600
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1600
Arg Ile Asp Pro Ala Asn Gly Asn Pro Arg Tyr Ala Pro Lys Phe Gln
1 5 10 15

Asp

<210> 1601
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1601
Asp Asp Glu Gly Tyr Tyr Tyr Phe Asp Val
1 5 10

<210> 1602
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1602
Arg Ala Ser Lys Ser Ile Ser Lys Tyr Leu Ala
1 5 10

<210> 1603
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1603
Ser Gly Ser Thr Leu Gln Ser
1 5

<210> 1604
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1604
Gln Gln His Asn Glu Tyr Pro Leu Thr
1 5

<210> 1605
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1605
Gly Phe Asn Ile Lys Asp Asp
1 5

<210> 1606
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1606
Asp Pro Ala Asn Gly Asn
1 5

<210> 1607
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1607
Asp Asp Glu Gly Tyr Tyr Tyr Phe Asp
1 5

<210> 1608
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1608
Ser Lys Ser Ile Ser Lys Tyr
1 5

<210> 1609
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1609
Ser Gly Ser
1

<210> 1610
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1610
His Asn Glu Tyr Pro Leu
1 5

<210> 1611
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1611
Gly Phe Asn Ile Lys Asp Asp Tyr Ile His
1 5 10

<210> 1612
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1612
Arg Ile Asp Pro Ala Asn Gly Asn Pro Arg
1 5 10

<210> 1613
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1613
Asp Asp Glu Gly Tyr Tyr Tyr Phe Asp Val
1 5 10

<210> 1614
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1614
Arg Ala Ser Lys Ser Ile Ser Lys Tyr Leu Ala
1 5 10

<210> 1615
<211> 7

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1615
Ser Gly Ser Thr Leu Gln Ser
1 5

<210> 1616
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1616
Gln Gln His Asn Glu Tyr Pro Leu Thr
1 5

<210> 1617
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1617
Lys Asp Asp Tyr Ile His
1 5

<210> 1618
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1618
Trp Ile Gly Arg Ile Asp Pro Ala Asn Gly Asn Pro Arg
1 5 10

<210> 1619
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1619
Ala Arg Asp Asp Glu Gly Tyr Tyr Tyr Phe Asp
1 5 10

<210> 1620
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1620
Ser Lys Tyr Leu Ala Trp Tyr
1 5

<210> 1621
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1621
Val Leu Ile Tyr Ser Gly Ser Thr Leu Gln
1 5 10

<210> 1622
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1622
Gln Gln His Asn Glu Tyr Pro Leu
1 5

<210> 1623
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1623
Gly Phe Asn Ile Lys Asp Asp Tyr
1 5

<210> 1624
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1624
Ile Asp Pro Ala Asn Gly Asn Pro
1 5

<210> 1625
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1625
Ala Arg Asp Asp Glu Gly Tyr Tyr Tyr Phe Asp Val
1 5 10

<210> 1626
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1626

Lys Ser Ile Ser Lys Tyr
1 5

<210> 1627
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1627
Ser Gly Ser
1

<210> 1628
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1628
Gln Gln His Asn Glu Tyr Pro Leu Thr
1 5

<210> 1629
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1629
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asp
20 25 30

Tyr Ile His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

```
Gly Arg Ile Asp Pro Ala Asn Gly Asn Pro Arg Tyr Ala Pro Lys Phe
    50                  55                  60

Gln Asp Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
65                  70                  75                  80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Asp Glu Gly Tyr Tyr Tyr Phe Asp Val Trp Gly Ala Gly
            100                 105                 110

Thr Ser Val Thr Val Ser Ser
        115
```

<210> 1630
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1630

```
Asp Ile Lys Met Thr Gln Ser Pro Ser Tyr Leu Ala Ala Ser Pro Gly
1               5                   10                  15

Glu Thr Ile Thr Ile Asn Cys Arg Ala Ser Lys Ser Ile Ser Lys Tyr
            20                  25                  30

Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Thr Asn Lys Val Leu Ile
        35                  40                  45

Tyr Ser Gly Ser Thr Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65                  70                  75                  80

Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Gln His Asn Glu Tyr Pro Leu
                85                  90                  95
```

Thr Phe Gly Asp Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 1631
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1631
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asp
20 25 30

Tyr Ile His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Arg Ile Asp Pro Ala Asn Gly Asn Pro Arg Tyr Ala Pro Lys Phe
50 55 60

Gln Asp Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Asp Glu Gly Tyr Tyr Tyr Phe Asp Val Trp Gly Ala Gly
100 105 110

Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

```
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
```

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys

<210> 1632
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1632
Asp Ile Lys Met Thr Gln Ser Pro Ser Tyr Leu Ala Ala Ser Pro Gly
1 5 10 15

Glu Thr Ile Thr Ile Asn Cys Arg Ala Ser Lys Ser Ile Ser Lys Tyr
20 25 30

Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Thr Asn Lys Val Leu Ile
35 40 45

Tyr Ser Gly Ser Thr Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Gln His Asn Glu Tyr Pro Leu
85 90 95

```
Thr Phe Gly Asp Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110


Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175


Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190


Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205


Phe Asn Arg Gly Glu Cys
    210


<210> 1633
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1633
Ser Tyr Trp Ile Asn
1               5


<210> 1634
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
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<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1634
Asn Ile Tyr Pro Phe Ser Ser Ser Thr Asn Tyr Asn Glu Lys Phe Lys
1 5 10 15

Lys

<210> 1635
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1635
Glu Glu Phe Ser His Tyr Pro Ser Trp Phe Ala Tyr
1 5 10

<210> 1636
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1636
Lys Ala Ser Gln Asn Val Gly Ile Ala Val Ala
1 5 10

<210> 1637
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1637
Ser Ala Ser Asn Arg Tyr Thr
1 5

<210> 1638
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1638
Gln Gln Tyr Ser Thr Asp Pro Tyr Thr
1 5

<210> 1639
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1639
Gly Tyr Thr Phe Thr Ser Tyr
1 5

<210> 1640
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1640
Tyr Pro Phe Ser Ser Ser
1 5

<210> 1641
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1641
Glu Glu Phe Ser His Tyr Pro Ser Trp Phe Ala
1 5 10

<210> 1642
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1642
Ser Gln Asn Val Gly Ile Ala
1 5

<210> 1643
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1643
Ser Ala Ser
1

<210> 1644
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1644
Tyr Ser Thr Asp Pro Tyr
1 5

<210> 1645
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1645

Gly Tyr Thr Phe Thr Ser Tyr Trp Ile Asn
1 5 10

<210> 1646
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1646
Asn Ile Tyr Pro Phe Ser Ser Ser Thr Asn
1 5 10

<210> 1647
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1647
Glu Glu Phe Ser His Tyr Pro Ser Trp Phe Ala Tyr
1 5 10

<210> 1648
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1648
Lys Ala Ser Gln Asn Val Gly Ile Ala Val Ala
1 5 10

<210> 1649
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1649
Ser Ala Ser Asn Arg Tyr Thr
1 5

<210> 1650
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1650
Gln Gln Tyr Ser Thr Asp Pro Tyr Thr
1 5

<210> 1651
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1651
Thr Ser Tyr Trp Ile Asn
1 5

<210> 1652
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1652
Trp Ile Gly Asn Ile Tyr Pro Phe Ser Ser Ser Thr Asn
1 5 10

<210> 1653
<211> 13
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1653
Ala Arg Glu Glu Phe Ser His Tyr Pro Ser Trp Phe Ala
1 5 10

<210> 1654
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1654
Gly Ile Ala Val Ala Trp Phe
1 5

<210> 1655
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1655
Leu Leu Ile Tyr Ser Ala Ser Asn Arg Tyr
1 5 10

<210> 1656
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1656
Gln Gln Tyr Ser Thr Asp Pro Tyr
1 5

<210> 1657
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1657
Gly Tyr Thr Phe Thr Ser Tyr Trp
1 5

<210> 1658
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1658
Ile Tyr Pro Phe Ser Ser Ser Thr
1 5

<210> 1659
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1659
Ala Arg Glu Glu Phe Ser His Tyr Pro Ser Trp Phe Ala Tyr
1 5 10

<210> 1660
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1660
Gln Asn Val Gly Ile Ala
1 5

<210> 1661
<211> 3

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1661
Ser Ala Ser
1

<210> 1662
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1662
Gln Gln Tyr Ser Thr Asp Pro Tyr Thr
1 5

<210> 1663
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1663
Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Ile Asn Trp Met Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Asn Ile Tyr Pro Phe Ser Ser Ser Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Lys Lys Ala Thr Leu Thr Val Asp Ala Ser Ser Ser Thr Ala Ser
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Glu Glu Phe Ser His Tyr Pro Ser Trp Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Leu Thr Val Ser Ser
115 120

<210> 1664
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1664
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Thr Val Gly
1 5 10 15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Ile Ala
20 25 30

Val Ala Trp Phe Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Gly Asn Met Gln Ser
65 70 75 80

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Thr Asp Pro Tyr
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 1665
<211> 451

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1665
Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Ile Asn Trp Met Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Asn Ile Tyr Pro Phe Ser Ser Ser Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Lys Lys Ala Thr Leu Thr Val Asp Ala Ser Ser Ser Thr Ala Ser
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Glu Glu Phe Ser His Tyr Pro Ser Trp Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

```
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400
```

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 1666
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1666
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Thr Val Gly
1 5 10 15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Ile Ala
20 25 30

Val Ala Trp Phe Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Gly Asn Met Gln Ser
65 70 75 80

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Thr Asp Pro Tyr
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 1667
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1667
Ser Tyr Trp Ile Asn
1 5

<210> 1668
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1668
Asn Ile Tyr Pro Gly Ser Ser Ser Thr Asn Tyr Asn Glu Lys Phe Lys
1 5 10 15

Asn

<210> 1669
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1669
Glu Leu Gly Ala Tyr Tyr His Tyr Ser Ala Met Asp Tyr
1 5 10

<210> 1670
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1670
Lys Ala Ser Gln Asn Val Gly Thr Ala Val Ala
1 5 10

<210> 1671
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1671
Ser Ala Ser Asn Arg Tyr Thr
1 5

<210> 1672
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1672
Gln Gln Tyr Ser Ile Tyr Pro Phe Thr
1 5

<210> 1673
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1673
Gly Tyr Thr Phe Thr Ser Tyr
1 5

<210> 1674
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1674
Tyr Pro Gly Ser Ser Ser
1 5

<210> 1675
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1675
Glu Leu Gly Ala Tyr Tyr His Tyr Ser Ala Met Asp
1 5 10

<210> 1676
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1676
Ser Gln Asn Val Gly Thr Ala
1 5

<210> 1677
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1677
Ser Ala Ser
1

<210> 1678
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1678
Tyr Ser Ile Tyr Pro Phe
1 5

<210> 1679
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1679
Gly Tyr Thr Phe Thr Ser Tyr Trp Ile Asn
1 5 10

<210> 1680
<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1680
Asn Ile Tyr Pro Gly Ser Ser Ser Thr Asn
1 5 10

<210> 1681
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1681
Glu Leu Gly Ala Tyr Tyr His Tyr Ser Ala Met Asp Tyr
1 5 10

<210> 1682
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1682
Lys Ala Ser Gln Asn Val Gly Thr Ala Val Ala
1 5 10

<210> 1683
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1683
Ser Ala Ser Asn Arg Tyr Thr
1 5

<210> 1684
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1684
Gln Gln Tyr Ser Ile Tyr Pro Phe Thr
1 5

<210> 1685
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1685
Thr Ser Tyr Trp Ile Asn
1 5

<210> 1686
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1686
Trp Ile Gly Asn Ile Tyr Pro Gly Ser Ser Ser Thr Asn
1 5 10

<210> 1687
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1687
Thr Arg Glu Leu Gly Ala Tyr Tyr His Tyr Ser Ala Met Asp
1 5 10

<210> 1688
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1688
Gly Thr Ala Val Ala Trp Tyr
1 5

<210> 1689
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1689
Leu Leu Ile Tyr Ser Ala Ser Asn Arg Tyr
1 5 10

<210> 1690
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1690
Gln Gln Tyr Ser Ile Tyr Pro Phe
1 5

<210> 1691
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1691

Gly Tyr Thr Phe Thr Ser Tyr Trp
1 5

<210> 1692
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1692
Ile Tyr Pro Gly Ser Ser Ser Thr
1 5

<210> 1693
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1693
Thr Arg Glu Leu Gly Ala Tyr Tyr His Tyr Ser Ala Met Asp Tyr
1 5 10 15

<210> 1694
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1694
Gln Asn Val Gly Thr Ala
1 5

<210> 1695
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1695
Ser Ala Ser
1

<210> 1696
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1696
Gln Gln Tyr Ser Ile Tyr Pro Phe Thr
1 5

<210> 1697
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1697
Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Asn Ile Tyr Pro Gly Ser Ser Ser Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Asn Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser Thr Val Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Glu Leu Gly Ala Tyr Tyr His Tyr Ser Ala Met Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 1698
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1698
Asp Ile Val Leu Thr Gln Ser Gln Lys Ile Met Ser Thr Thr Val Gly
1 5 10 15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Met Gln Ser
65 70 75 80

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Ile Tyr Pro Phe
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 1699
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1699
Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20   25   30

Trp Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Asn Ile Tyr Pro Gly Ser Ser Ser Thr Asn Tyr Asn Glu Lys Phe
    50   55   60

Lys Asn Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser Thr Val Tyr
65   70   75   80

Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Tyr Cys
                85   90   95

Thr Arg Glu Leu Gly Ala Tyr Tyr His Tyr Ser Ala Met Asp Tyr Trp
            100   105   110

Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
        115   120   125

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
    130   135   140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145   150   155   160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
                165   170   175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
            180   185   190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
        195   200   205

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His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
    210                 215                 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
225                 230                 235                 240

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                245                 250                 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            260                 265                 270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        275                 280                 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
    290                 295                 300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
305                 310                 315                 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                325                 330                 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            340                 345                 350

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
        355                 360                 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    370                 375                 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385                 390                 395                 400

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                405                 410                 415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            420                 425                 430
```

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
435 440 445

Ser Pro Gly Lys
450

<210> 1700
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1700
Asp Ile Val Leu Thr Gln Ser Gln Lys Ile Met Ser Thr Thr Val Gly
1 5 10 15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Met Gln Ser
65 70 75 80

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Ile Tyr Pro Phe
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 1701
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1701
Ser Tyr Trp Met His
1 5

<210> 1702
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1702
Asn Ile Asn Pro Ser Ser Gly Tyr Ala Val Tyr Asn Gln Lys Phe Lys
1 5 10 15

Asp

<210> 1703
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1703
Arg Val Phe Tyr Gly Asp Ser Trp Phe Ala Tyr
1 5 10

<210> 1704
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1704
Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala
1 5 10

<210> 1705
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1705
Asn Ala Lys Thr Leu Ala Asp
1 5

<210> 1706
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1706
Gln His Phe Trp Ser Thr Thr Trp Thr
1 5

<210> 1707
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1707
Gly Tyr Ile Phe Thr Ser Tyr
1 5

<210> 1708
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1708
Asn Pro Ser Ser Gly Tyr
1 5

<210> 1709
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1709
Arg Val Phe Tyr Gly Asp Ser Trp Phe Ala
1 5 10

<210> 1710
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1710

Ser Gly Asn Ile His Asn Tyr
1   5

<210> 1711
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1711
Asn Ala Lys
1

<210> 1712
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1712
Phe Trp Ser Thr Thr Trp
1   5

<210> 1713
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1713
Gly Tyr Ile Phe Thr Ser Tyr Trp Met His
1   5   10

<210> 1714
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1714
Asn Ile Asn Pro Ser Ser Gly Tyr Ala Val
1 5 10

<210> 1715
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1715
Arg Val Phe Tyr Gly Asp Ser Trp Phe Ala Tyr
1 5 10

<210> 1716
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1716
Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala
1 5 10

<210> 1717
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1717
Asn Ala Lys Thr Leu Ala Asp
1 5

<210> 1718
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1718
Gln His Phe Trp Ser Thr Thr Trp Thr
1 5

<210> 1719
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1719
Thr Ser Tyr Trp Met His
1 5

<210> 1720
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1720
Trp Ile Gly Asn Ile Asn Pro Ser Ser Gly Tyr Ala Val
1 5 10

<210> 1721
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1721
Ala Arg Arg Val Phe Tyr Gly Asp Ser Trp Phe Ala
1 5 10

<210> 1722
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1722
His Asn Tyr Leu Ala Trp Tyr
1 5

<210> 1723
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1723
Leu Leu Val Tyr Asn Ala Lys Thr Leu Ala
1 5 10

<210> 1724
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1724
Gln His Phe Trp Ser Thr Thr Trp
1 5

<210> 1725
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1725
Gly Tyr Ile Phe Thr Ser Tyr Trp
1 5

<210> 1726
<211> 8

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1726
Ile Asn Pro Ser Ser Gly Tyr Ala
1 5

<210> 1727
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1727
Ala Arg Arg Val Phe Tyr Gly Asp Ser Trp Phe Ala Tyr
1 5 10

<210> 1728
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1728
Gly Asn Ile His Asn Tyr
1 5

<210> 1729
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1729
Asn Ala Lys
1

<210> 1730
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1730
Gln His Phe Trp Ser Thr Thr Trp Thr
1 5

<210> 1731
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1731
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Ser Tyr
20 25 30

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Asn Ile Asn Pro Ser Ser Gly Tyr Ala Val Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Lys Ala Thr Leu Thr Ala Asp Gln Ser Ser Ser Thr Ala Tyr
65 70 75 80

Ile Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Arg Val Phe Tyr Gly Asp Ser Trp Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 1732
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1732
Asp Val Gln Met Ile Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
35 40 45

Tyr Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp Ser Thr Thr Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 1733
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1733
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Lys Pro Gly Ala
1 5 10 15

```
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Ser Tyr
            20                  25                  30

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45

Gly Asn Ile Asn Pro Ser Ser Gly Tyr Ala Val Tyr Asn Gln Lys Phe
    50                  55                  60

Lys Asp Lys Ala Thr Leu Thr Ala Asp Gln Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

Ile Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Arg Val Phe Tyr Gly Asp Ser Trp Phe Ala Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240
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Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445
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Gly Lys
450

<210> 1734
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1734
Asp Val Gln Met Ile Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
35 40 45

Tyr Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp Ser Thr Thr Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 1735
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1735
Ser Tyr Tyr Met His
1 5

<210> 1736
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1736
Tyr Ile Asp Pro Phe Asn Gly Asn Thr Asn Tyr Lys Gln Lys Phe Lys
1 5 10 15

Gly

<210> 1737
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1737
Pro Asn Ser Asn Tyr Val Gly Thr Trp Phe Ala Tyr
1 5 10

<210> 1738
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1738
His Ala Ser Gln Asn Ile Asn Val Trp Leu Ser
1 5 10

<210> 1739
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1739
Lys Ala Ser Asn Leu His Thr
1 5

<210> 1740
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1740
Gln Gln Gly Gln Ser Phe Pro Phe Thr
1 5

<210> 1741
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1741
Gly Tyr Ser Phe Thr Ser Tyr
1 5

<210> 1742
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1742
Asp Pro Phe Asn Gly Asn
1 5

<210> 1743
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1743
Pro Asn Ser Asn Tyr Val Gly Thr Trp Phe Ala
1 5 10

<210> 1744
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1744
Ser Gln Asn Ile Asn Val Trp
1 5

<210> 1745
<211> 3

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1745
Lys Ala Ser
1

<210> 1746
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1746
Gly Gln Ser Phe Pro Phe
1 5

<210> 1747
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1747
Gly Tyr Ser Phe Thr Ser Tyr Tyr Met His
1 5 10

<210> 1748
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1748
Tyr Ile Asp Pro Phe Asn Gly Asn Thr Asn
1 5 10

<210> 1749
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1749
Pro Asn Ser Asn Tyr Val Gly Thr Trp Phe Ala Tyr
1 5 10

<210> 1750
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1750
His Ala Ser Gln Asn Ile Asn Val Trp Leu Ser
1 5 10

<210> 1751
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1751
Lys Ala Ser Asn Leu His Thr
1 5

<210> 1752
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1752
Gln Gln Gly Gln Ser Phe Pro Phe Thr
1 5

<210> 1753
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1753
Thr Ser Tyr Tyr Met His
1 5

<210> 1754
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1754
Trp Ile Gly Tyr Ile Asp Pro Phe Asn Gly Asn Thr Asn
1 5 10

<210> 1755
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1755
Ala Ser Pro Asn Ser Asn Tyr Val Gly Thr Trp Phe Ala
1 5 10

<210> 1756
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1756

Asn Val Trp Leu Ser Trp Tyr
1 5

<210> 1757
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1757
Leu Leu Ile Tyr Lys Ala Ser Asn Leu His
1 5 10

<210> 1758
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1758
Gln Gln Gly Gln Ser Phe Pro Phe
1 5

<210> 1759
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1759
Gly Tyr Ser Phe Thr Ser Tyr Tyr
1 5

<210> 1760
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1760
Ile Asp Pro Phe Asn Gly Asn Thr
1 5

<210> 1761
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1761
Ala Ser Pro Asn Ser Asn Tyr Val Gly Thr Trp Phe Ala Tyr
1 5 10

<210> 1762
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1762
Gln Asn Ile Asn Val Trp
1 5

<210> 1763
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1763
Lys Ala Ser
1

<210> 1764
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1764
Gln Gln Gly Gln Ser Phe Pro Phe Thr
1 5

<210> 1765
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1765
Glu Phe Gln Leu Gln Gln Ser Gly Pro Glu Leu Met Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Tyr Met His Trp Met Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asp Pro Phe Asn Gly Asn Thr Asn Tyr Lys Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Ser Pro Asn Ser Asn Tyr Val Gly Thr Trp Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1766
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1766
Asn Thr Gln Met Asn Gln Thr Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Thr Val Thr Ile Thr Cys His Ala Ser Gln Asn Ile Asn Val Trp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Asn Ile Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Asn Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Gly Gln Ser Phe Pro Phe
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 1767
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1767
Glu Phe Gln Leu Gln Gln Ser Gly Pro Glu Leu Met Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Tyr Met His Trp Met Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

```
Gly Tyr Ile Asp Pro Phe Asn Gly Asn Thr Asn Tyr Lys Gln Lys Phe
    50                  55                  60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

Met His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Ser Pro Asn Ser Asn Tyr Val Gly Thr Trp Phe Ala Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255
```

```
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445

Pro Gly Lys
    450
```

<210> 1768
<211> 214

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1768
Asn Thr Gln Met Asn Gln Thr Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Thr Val Thr Ile Thr Cys His Ala Ser Gln Asn Ile Asn Val Trp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Asn Ile Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Asn Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Gly Gln Ser Phe Pro Phe
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195   200   205

Phe Asn Arg Gly Glu Cys
    210

<210> 1769
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1769
Asp Tyr Tyr Met Asn
1   5

<210> 1770
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1770
Val Ile Asn Pro Tyr Asn Gly Gly Thr Thr Tyr Asn Gln Arg Phe Thr
1   5   10   15

Gly

<210> 1771
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1771
Asn Tyr Gly Ala Met Asp Ser
1   5

<210> 1772
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1772
Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala
1 5 10

<210> 1773
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1773
Asn Ala Lys Thr Leu Ala Asp
1 5

<210> 1774
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1774
Gln His Phe Trp Ile Thr Pro Pro Thr
1 5

<210> 1775
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1775

Gly Tyr Thr Phe Thr Asp Tyr
1 5

<210> 1776
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1776
Asn Pro Tyr Asn Gly Gly
1 5

<210> 1777
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1777
Asn Tyr Gly Ala Met Asp
1 5

<210> 1778
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1778
Ser Gly Asn Ile His Asn Tyr
1 5

<210> 1779
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1779
Asn Ala Lys
1

<210> 1780
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1780
Phe Trp Ile Thr Pro Pro
1 5

<210> 1781
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1781
Gly Tyr Thr Phe Thr Asp Tyr Tyr Met Asn
1 5 10

<210> 1782
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1782
Val Ile Asn Pro Tyr Asn Gly Gly Thr Thr
1 5 10

<210> 1783
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1783
Asn Tyr Gly Ala Met Asp Ser
1 5

<210> 1784
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1784
Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala
1 5 10

<210> 1785
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1785
Asn Ala Lys Thr Leu Ala Asp
1 5

<210> 1786
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1786
Gln His Phe Trp Ile Thr Pro Pro Thr
1 5

<210> 1787
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1787
Thr Asp Tyr Tyr Met Asn
1 5

<210> 1788
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1788
Trp Ile Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Thr
1 5 10

<210> 1789
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1789
Ala Arg Asn Tyr Gly Ala Met Asp
1 5

<210> 1790
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1790
His Asn Tyr Leu Ala Trp Tyr
1 5

<210> 1791
<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1791
Leu Leu Val Ser Asn Ala Lys Thr Leu Ala
1 5 10

<210> 1792
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1792
Gln His Phe Trp Ile Thr Pro Pro
1 5

<210> 1793
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1793
Gly Tyr Thr Phe Thr Asp Tyr Tyr
1 5

<210> 1794
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1794
Ile Asn Pro Tyr Asn Gly Gly Thr
1 5

<210> 1795
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1795
Ala Arg Asn Tyr Gly Ala Met Asp Ser
1 5

<210> 1796
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1796
Gly Asn Ile His Asn Tyr
1 5

<210> 1797
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1797
Asn Ala Lys
1

<210> 1798
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1798
Gln His Phe Trp Ile Thr Pro Pro Thr
1 5

<210> 1799
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1799
Gln Val Gln Leu Gln Gln Ser Gly Pro Val Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met Asn Trp Val Met Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Thr Tyr Asn Gln Arg Phe
50 55 60

Thr Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asn Tyr Gly Ala Met Asp Ser Trp Gly Gln Gly Thr Ser Val
100 105 110

Thr Val Ser Ser
115

<210> 1800
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1800

```
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr
            20                  25                  30


Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
        35                  40                  45


Ser Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Gly Gly
    50                  55                  60


Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp Ile Thr Pro Pro
                85                  90                  95


Thr Phe Gly Ala Gly Thr Arg Leu Glu Ile Lys
            100                 105


<210> 1801
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 1801
Gln Val Gln Leu Gln Gln Ser Gly Pro Val Leu Val Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30


Tyr Met Asn Trp Val Met Gln Ser His Gly Lys Ser Leu Glu Trp Ile
        35                  40                  45


Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Thr Tyr Asn Gln Arg Phe
    50                  55                  60
```

```
Thr Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asn Tyr Gly Ala Met Asp Ser Trp Gly Gln Gly Thr Ser Val
            100                 105                 110

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        115                 120                 125

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    130                 135                 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145                 150                 155                 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                165                 170                 175

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            180                 185                 190

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        195                 200                 205

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    210                 215                 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
225                 230                 235                 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            260                 265                 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285
```

```
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    290                 295                 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305                 310                 315                 320

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
                325                 330                 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            340                 345                 350

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
        355                 360                 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    370                 375                 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385                 390                 395                 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            420                 425                 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
```

<210> 1802
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1802

```
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15
```

```
Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
        35                  40                  45

Ser Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Gly Gly
    50                  55                  60

Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp Ile Thr Pro Pro
                85                  90                  95

Thr Phe Gly Ala Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 1803
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1803
Asp Tyr Tyr Met Asn
1 5

<210> 1804
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1804
Asp Ile Asn Pro Asn Gly Gly Gly Thr Ser Asp Asn Pro Lys Phe Lys
1 5 10 15

Gly

<210> 1805
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1805
Thr Ser Gly Thr Asp Trp Tyr Phe Asp Val
1 5 10

<210> 1806
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1806
Lys Ala Ser Gln Asn Val Gly Thr Ala Val Ala
1 5 10

<210> 1807
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1807
Ser Ala Ser Asn Arg Tyr Thr
1 5

<210> 1808
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1808
Gln Gln Tyr Ser Ser Tyr Pro Phe Thr
1 5

<210> 1809
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1809
Gly Tyr Lys Phe Thr Asp Tyr
1 5

<210> 1810
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1810
Asn Pro Asn Gly Gly Gly
1 5

<210> 1811
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1811
Thr Ser Gly Thr Asp Trp Tyr Phe Asp
1 5

<210> 1812
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1812
Ser Gln Asn Val Gly Thr Ala
1 5

<210> 1813
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1813
Ser Ala Ser
1

<210> 1814
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1814
Tyr Ser Ser Tyr Pro Phe
1 5

<210> 1815
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1815
Gly Tyr Lys Phe Thr Asp Tyr Tyr Met Asn
1 5 10

<210> 1816
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1816
Asp Ile Asn Pro Asn Gly Gly Gly Thr Ser
1 5 10

<210> 1817
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1817
Thr Ser Gly Thr Asp Trp Tyr Phe Asp Val
1 5 10

<210> 1818
<211> 11

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1818
Lys Ala Ser Gln Asn Val Gly Thr Ala Val Ala
1 5 10

<210> 1819
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1819
Ser Ala Ser Asn Arg Tyr Thr
1 5

<210> 1820
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1820
Gln Gln Tyr Ser Ser Tyr Pro Phe Thr
1 5

<210> 1821
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1821
Thr Asp Tyr Tyr Met Asn
1 5

<210> 1822
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1822
Trp Ile Gly Asp Ile Asn Pro Asn Gly Gly Gly Thr Ser
1 5 10

<210> 1823
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1823
Ala Arg Thr Ser Gly Thr Asp Trp Tyr Phe Asp
1 5 10

<210> 1824
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1824
Gly Thr Ala Val Ala Trp Tyr
1 5

<210> 1825
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1825
Leu Leu Ile Tyr Ser Ala Ser Asn Arg Tyr
1 5 10

<210> 1826
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1826
Gln Gln Tyr Ser Ser Tyr Pro Phe
1 5

<210> 1827
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1827
Gly Tyr Lys Phe Thr Asp Tyr Tyr
1 5

<210> 1828
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1828
Ile Asn Pro Asn Gly Gly Gly Thr
1 5

<210> 1829
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1829

Ala Arg Thr Ser Gly Thr Asp Trp Tyr Phe Asp Val
1 5 10

<210> 1830
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1830
Gln Asn Val Gly Thr Ala
1 5

<210> 1831
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1831
Ser Ala Ser
1

<210> 1832
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1832
Gln Gln Tyr Ser Ser Tyr Pro Phe Thr
1 5

<210> 1833
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1833
Asp Val Gln Leu Gln Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Ile Ala Cys Lys Thr Ser Gly Tyr Lys Phe Thr Asp Tyr
            20   25   30

Tyr Met Asn Trp Val Lys Gln Ser Leu Gly Lys Ser Leu Asp Trp Ile
        35   40   45

Gly Asp Ile Asn Pro Asn Gly Gly Gly Thr Ser Asp Asn Pro Lys Phe
    50   55   60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Gly Val Tyr Tyr Cys
                85   90   95

Ala Arg Thr Ser Gly Thr Asp Trp Tyr Phe Asp Val Trp Gly Thr Gly
            100   105   110

Thr Thr Val Thr Val Ser Ser
        115

<210> 1834
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 1834
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Thr Val Gly
1   5   10   15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala
            20   25   30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
        35   40   45

Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
    50   55   60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Met Gln Ser
65   70   75   80

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Ser Tyr Pro Phe
                85   90   95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Met Lys
            100   105

<210> 1835
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 1835
Asp Val Gln Leu Gln Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Ile Ala Cys Lys Thr Ser Gly Tyr Lys Phe Thr Asp Tyr
            20   25   30

Tyr Met Asn Trp Val Lys Gln Ser Leu Gly Lys Ser Leu Asp Trp Ile
        35   40   45

Gly Asp Ile Asn Pro Asn Gly Gly Gly Thr Ser Asp Asn Pro Lys Phe
    50   55   60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Gly Val Tyr Tyr Cys
                85   90   95

Ala Arg Thr Ser Gly Thr Asp Trp Tyr Phe Asp Val Trp Gly Thr Gly
            100   105   110

```
Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
```

```
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445

Lys
```

<210> 1836
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1836

```
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Thr Val Gly
1               5                   10                  15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala
            20                  25                  30
```

```
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Met Gln Ser
65                  70                  75                  80

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Ser Tyr Pro Phe
                85                  90                  95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Met Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 1837
<211> 5
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1837
Thr Ala Gly Ile Gln
1 5

<210> 1838
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1838
Trp Ile Asn Thr His Ala Gly Glu Ser Lys Tyr Ala Asp Asp Phe Lys
1 5 10 15

Gly

<210> 1839
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1839
Ser Gly Asp Tyr Asp Gly Ser His Pro Phe Ala Tyr
1 5 10

<210> 1840
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1840
Arg Ala Ser Gln Asp Ile Arg Pro Tyr Leu Asn
1 5 10

<210> 1841
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1841
Tyr Thr Ser Arg Leu His Ser
1 5

<210> 1842
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1842
Gln Gln Asp Asn Thr Leu Pro Tyr Thr
1 5

<210> 1843
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1843
Gly Tyr Thr Phe Thr Thr Ala
1 5

<210> 1844
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1844
Asn Thr His Ala Gly Glu
1 5

<210> 1845
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1845
Ser Gly Asp Tyr Asp Gly Ser His Pro Phe Ala
1 5 10

<210> 1846
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1846
Ser Gln Asp Ile Arg Pro Tyr
1 5

<210> 1847
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1847
Tyr Thr Ser
1

<210> 1848
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1848

Asp Asn Thr Leu Pro Tyr
1 5

<210> 1849
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1849
Gly Tyr Thr Phe Thr Thr Ala Gly Ile Gln
1 5 10

<210> 1850
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1850
Trp Ile Asn Thr His Ala Gly Glu Ser Lys
1 5 10

<210> 1851
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1851
Ser Gly Asp Tyr Asp Gly Ser His Pro Phe Ala Tyr
1 5 10

<210> 1852
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1852
Arg Ala Ser Gln Asp Ile Arg Pro Tyr Leu Asn
1 5 10

<210> 1853
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1853
Tyr Thr Ser Arg Leu His Ser
1 5

<210> 1854
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1854
Gln Gln Asp Asn Thr Leu Pro Tyr Thr
1 5

<210> 1855
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1855
Thr Thr Ala Gly Ile Gln
1 5

<210> 1856
<211> 13
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1856
Trp Ile Gly Trp Ile Asn Thr His Ala Gly Glu Ser Lys
1 5 10

<210> 1857
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1857
Ala Arg Ser Gly Asp Tyr Asp Gly Ser His Pro Phe Ala
1 5 10

<210> 1858
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1858
Arg Pro Tyr Leu Asn Trp Tyr
1 5

<210> 1859
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1859
Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His
1 5 10

<210> 1860
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1860
Gln Gln Asp Asn Thr Leu Pro Tyr
1 5

<210> 1861
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1861
Gly Tyr Thr Phe Thr Thr Ala Gly
1 5

<210> 1862
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1862
Ile Asn Thr His Ala Gly Glu Ser
1 5

<210> 1863
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1863
Ala Arg Ser Gly Asp Tyr Asp Gly Ser His Pro Phe Ala Tyr
1 5 10

<210> 1864
<211> 6

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1864
Gln Asp Ile Arg Pro Tyr
1 5

<210> 1865
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1865
Tyr Thr Ser
1

<210> 1866
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1866
Gln Gln Asp Asn Thr Leu Pro Tyr Thr
1 5

<210> 1867
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1867
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
1 5 10 15

```
Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Ala
            20                  25                  30


Gly Ile Gln Trp Val Gln Lys Met Pro Gly Lys Gly Phe Lys Trp Ile
        35                  40                  45


Gly Trp Ile Asn Thr His Ala Gly Glu Ser Lys Tyr Ala Asp Asp Phe
    50                  55                  60


Lys Gly Arg Phe Ala Val Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr
65                  70                  75                  80


Leu Gln Ile Ser Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys
                85                  90                  95


Ala Arg Ser Gly Asp Tyr Asp Gly Ser His Pro Phe Ala Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Ser Val Thr Val Ser Ser
        115                 120


<210> 1868
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 1868
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Pro Tyr
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Glu Gly Thr Ile Lys Leu Leu Ile
        35                  40                  45


Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
```

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Asp Asn Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 1869
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1869
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
1 5 10 15

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Ala
20 25 30

Gly Ile Gln Trp Val Gln Lys Met Pro Gly Lys Gly Phe Lys Trp Ile
35 40 45

Gly Trp Ile Asn Thr His Ala Gly Glu Ser Lys Tyr Ala Asp Asp Phe
50 55 60

Lys Gly Arg Phe Ala Val Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Leu Gln Ile Ser Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys
85 90 95

Ala Arg Ser Gly Asp Tyr Asp Gly Ser His Pro Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

```
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350
```

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 1870
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1870
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Pro Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Glu Gly Thr Ile Lys Leu Leu Ile
35 40 45

Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

```
Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65                  70                  75                  80


Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Asp Asn Thr Leu Pro Tyr
                85                  90                  95


Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110


Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175


Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190


Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205


Phe Asn Arg Gly Glu Cys
    210


<210> 1871
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1871
Asp Tyr Tyr Met Asn
1               5
```

<210> 1872
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1872
Asp Ile Asn Pro Asn Gly Gly Gly Thr Ser Asp Asn Pro Lys Phe Lys
1 5 10 15

Gly

<210> 1873
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1873
Thr Ser Gly Thr Asp Trp Tyr Phe Asp Val
1 5 10

<210> 1874
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1874
Lys Ala Ser Gln Asn Val Gly Thr Ala Val Ala
1 5 10

<210> 1875
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1875
Ser Thr Ser Asn Arg Tyr Thr
1 5

<210> 1876
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1876
Gln Gln Tyr Ser Ile Tyr Pro Phe Thr
1 5

<210> 1877
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1877
Gly Tyr Thr Phe Thr Asp Tyr
1 5

<210> 1878
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1878
Asn Pro Asn Gly Gly Gly
1 5

<210> 1879
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1879
Thr Ser Gly Thr Asp Trp Tyr Phe Asp
1 5

<210> 1880
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1880
Ser Gln Asn Val Gly Thr Ala
1 5

<210> 1881
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1881
Ser Thr Ser
1

<210> 1882
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1882
Tyr Ser Ile Tyr Pro Phe
1 5

<210> 1883
<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1883
Gly Tyr Thr Phe Thr Asp Tyr Tyr Met Asn
1 5 10

<210> 1884
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1884
Asp Ile Asn Pro Asn Gly Gly Gly Thr Ser
1 5 10

<210> 1885
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1885
Thr Ser Gly Thr Asp Trp Tyr Phe Asp Val
1 5 10

<210> 1886
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1886
Lys Ala Ser Gln Asn Val Gly Thr Ala Val Ala
1 5 10

<210> 1887
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1887
Ser Thr Ser Asn Arg Tyr Thr
1 5

<210> 1888
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1888
Gln Gln Tyr Ser Ile Tyr Pro Phe Thr
1 5

<210> 1889
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1889
Thr Asp Tyr Tyr Met Asn
1 5

<210> 1890
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1890
Trp Ile Gly Asp Ile Asn Pro Asn Gly Gly Gly Thr Ser
1 5 10

<210> 1891
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1891
Ala Arg Thr Ser Gly Thr Asp Trp Tyr Phe Asp
1 5 10

<210> 1892
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1892
Gly Thr Ala Val Ala Trp Tyr
1 5

<210> 1893
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1893
Leu Leu Ile Tyr Ser Thr Ser Asn Arg Tyr
1 5 10

<210> 1894
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1894

Gln Gln Tyr Ser Ile Tyr Pro Phe
1 5

<210> 1895
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1895
Gly Tyr Thr Phe Thr Asp Tyr Tyr
1 5

<210> 1896
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1896
Ile Asn Pro Asn Gly Gly Gly Thr
1 5

<210> 1897
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1897
Ala Arg Thr Ser Gly Thr Asp Trp Tyr Phe Asp Val
1 5 10

<210> 1898
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1898
Gln Asn Val Gly Thr Ala
1 5

<210> 1899
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1899
Ser Thr Ser
1

<210> 1900
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1900
Gln Gln Tyr Ser Ile Tyr Pro Phe Thr
1 5

<210> 1901
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1901
Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Asp Trp Ile
35 40 45

```
Gly Asp Ile Asn Pro Asn Gly Gly Gly Thr Ser Asp Asn Pro Lys Phe
    50                  55                  60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Asn Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Thr Ser Gly Thr Asp Trp Tyr Phe Asp Val Trp Gly Thr Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ala
        115
```

<210> 1902
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1902

```
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Thr Val Gly
1               5                   10                  15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala
            20                  25                  30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Ser Thr Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Met Gln Ser
65                  70                  75                  80

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Ile Tyr Pro Phe
                85                  90                  95
```

Thr Phe Gly Ser Gly Thr Lys Leu Glu Met Lys
100 105

<210> 1903
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1903
Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Asp Trp Ile
35 40 45

Gly Asp Ile Asn Pro Asn Gly Gly Gly Thr Ser Asp Asn Pro Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Thr Ser Gly Thr Asp Trp Tyr Phe Asp Val Trp Gly Thr Gly
100 105 110

Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

```
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
```

```
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445

Lys
```

<210> 1904
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1904

```
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Thr Val Gly
1               5                   10                  15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala
            20                  25                  30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Ser Thr Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Met Gln Ser
65                  70                  75                  80
```

```
Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Ile Tyr Pro Phe
                85                  90                  95


Thr Phe Gly Ser Gly Thr Lys Leu Glu Met Lys Arg Thr Val Ala Ala
            100                 105                 110


Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175


Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190


Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205


Phe Asn Arg Gly Glu Cys
    210


<210> 1905
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1905
Asp Tyr Tyr Met Ser
1               5


<210> 1906
<211> 19
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1906
Leu Ser Arg Asn Lys Gly Asn Gly Tyr Thr Thr Glu Tyr Ser Ala Ser
1 5 10 15

Val Lys Gly

<210> 1907
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1907
Thr Val Thr Gly Thr Leu Phe Tyr Tyr Ala Leu Asp Tyr
1 5 10

<210> 1908
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1908
Arg Ala Ser Glu Asn Ile Tyr Ser Tyr Leu Ala
1 5 10

<210> 1909
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1909
Asn Ala Lys Thr Leu Ala Ala
1 5

<210> 1910
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1910
Gln His His Tyr Gly Thr Pro Leu Thr
1 5

<210> 1911
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1911
Gly Phe Thr Phe Thr Asp Tyr
1 5

<210> 1912
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1912
Arg Asn Lys Gly Asn Gly Tyr Thr
1 5

<210> 1913
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1913

Thr Val Thr Gly Thr Leu Phe Tyr Tyr Ala Leu Asp
1 5 10

<210> 1914
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1914
Ser Glu Asn Ile Tyr Ser Tyr
1 5

<210> 1915
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1915
Asn Ala Lys
1

<210> 1916
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1916
His Tyr Gly Thr Pro Leu
1 5

<210> 1917
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1917
Gly Phe Thr Phe Thr Asp Tyr Tyr Met Ser
1 5 10

<210> 1918
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1918
Leu Ser Arg Asn Lys Gly Asn Gly Tyr Thr Thr Glu
1 5 10

<210> 1919
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1919
Thr Val Thr Gly Thr Leu Phe Tyr Tyr Ala Leu Asp Tyr
1 5 10

<210> 1920
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1920
Arg Ala Ser Glu Asn Ile Tyr Ser Tyr Leu Ala
1 5 10

<210> 1921
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1921
Asn Ala Lys Thr Leu Ala Ala
1 5

<210> 1922
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1922
Gln His His Tyr Gly Thr Pro Leu Thr
1 5

<210> 1923
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1923
Thr Asp Tyr Tyr Met Ser
1 5

<210> 1924
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1924
Trp Leu Ala Leu Ser Arg Asn Lys Gly Asn Gly Tyr Thr Thr Glu
1 5 10 15

<210> 1925
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1925
Ala Arg Thr Val Thr Gly Thr Leu Phe Tyr Tyr Ala Leu Asp
1 5 10

<210> 1926
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1926
Tyr Ser Tyr Leu Ala Trp Tyr
1 5

<210> 1927
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1927
Phe Leu Val Tyr Asn Ala Lys Thr Leu Ala
1 5 10

<210> 1928
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1928
Gln His His Tyr Gly Thr Pro Leu
1 5

<210> 1929
<211> 8

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1929
Gly Phe Thr Phe Thr Asp Tyr Tyr
1 5

<210> 1930
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1930
Ser Arg Asn Lys Gly Asn Gly Tyr Thr Thr
1 5 10

<210> 1931
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1931
Ala Arg Thr Val Thr Gly Thr Leu Phe Tyr Tyr Ala Leu Asp Tyr
1 5 10 15

<210> 1932
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1932
Glu Asn Ile Tyr Ser Tyr
1 5

<210> 1933
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1933
Asn Ala Lys
1

<210> 1934
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1934
Gln His His Tyr Gly Thr Pro Leu Thr
1 5

<210> 1935
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1935
Glu Phe Gln Leu Gln Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Ser Leu Ser Cys Ala Ala Pro Gly Phe Thr Phe Thr Asp Tyr
20 25 30

Tyr Met Ser Trp Val Arg Gln Ser Pro Gly Lys Ala Leu Glu Trp Leu
35 40 45

Ala Leu Ser Arg Asn Lys Gly Asn Gly Tyr Thr Thr Glu Tyr Ser Ala
50 55 60

```
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Gln Ser Ile
65                  70                  75                  80


Leu Tyr Leu Gln Met Asn Val Leu Arg Ala Glu Asp Ser Ala Thr Tyr
                85                  90                  95


Tyr Cys Ala Arg Thr Val Thr Gly Thr Leu Phe Tyr Tyr Ala Leu Asp
            100                 105                 110


Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 1936
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 1936
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr Ser Tyr
            20                  25                  30


Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Phe Leu Val
        35                  40                  45


Tyr Asn Ala Lys Thr Leu Ala Ala Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn Arg Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Gly Thr Tyr Tyr Cys Gln His His Tyr Gly Thr Pro Leu
                85                  90                  95


Thr Phe Gly Asp Gly Thr Arg Leu Glu Ile Lys
            100                 105
```

<210> 1937
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1937
Glu Phe Gln Leu Gln Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Ser Leu Ser Cys Ala Ala Pro Gly Phe Thr Phe Thr Asp Tyr
20 25 30

Tyr Met Ser Trp Val Arg Gln Ser Pro Gly Lys Ala Leu Glu Trp Leu
35 40 45

Ala Leu Ser Arg Asn Lys Gly Asn Gly Tyr Thr Thr Glu Tyr Ser Ala
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Gln Ser Ile
65 70 75 80

Leu Tyr Leu Gln Met Asn Val Leu Arg Ala Glu Asp Ser Ala Thr Tyr
85 90 95

Tyr Cys Ala Arg Thr Val Thr Gly Thr Leu Phe Tyr Tyr Ala Leu Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys
115 120 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
130 135 140

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
145 150 155 160

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
165 170 175

```
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
            180                 185                 190

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
        195                 200                 205

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
    210                 215                 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
225                 230                 235                 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
                245                 250                 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
            260                 265                 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
        275                 280                 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
    290                 295                 300

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
305                 310                 315                 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
                325                 330                 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
            340                 345                 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
        355                 360                 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
    370                 375                 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
385                 390                 395                 400
```

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
435 440 445

Ser Leu Ser Pro Gly Lys
450

<210> 1938
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1938
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Phe Leu Val
35 40 45

Tyr Asn Ala Lys Thr Leu Ala Ala Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn Arg Leu Gln Pro
65 70 75 80

Glu Asp Phe Gly Thr Tyr Tyr Cys Gln His His Tyr Gly Thr Pro Leu
85 90 95

Thr Phe Gly Asp Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

```
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175


Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190


Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205


Phe Asn Arg Gly Glu Cys
    210


<210> 1939
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1939
Thr Tyr Thr Met His
1               5


<210> 1940
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1940
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Tyr Ile Asn Pro Ser Ser Gly Tyr Thr Lys Tyr Asn Gln Lys Phe Thr
1   5   10   15

Asp

<210> 1941
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1941
Leu Trp Ala Tyr
1

<210> 1942
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1942
Arg Ser Ser Gln Ser Leu Val His Ser Ser Gly Asn Thr Tyr Leu His
1   5   10   15

<210> 1943
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1943
Lys Gly Ser Asn Arg Phe Ser
1   5

<210> 1944
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1944
Ser Gln Ser Thr His Val Pro Phe Thr
1 5

<210> 1945
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1945
Gly Tyr Thr Phe Thr Thr Tyr
1 5

<210> 1946
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1946
Asn Pro Ser Ser Gly Tyr
1 5

<210> 1947
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1947
Leu Trp Ala
1

<210> 1948
<211> 12

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1948
Ser Gln Ser Leu Val His Ser Ser Gly Asn Thr Tyr
1 5 10

<210> 1949
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1949
Lys Gly Ser
1

<210> 1950
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1950
Ser Thr His Val Pro Phe
1 5

<210> 1951
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1951
Gly Tyr Thr Phe Thr Thr Tyr Thr Met His
1 5 10

<210> 1952
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1952
Tyr Ile Asn Pro Ser Ser Gly Tyr Thr Lys
1 5 10

<210> 1953
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1953
Leu Trp Ala Tyr
1

<210> 1954
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1954
Arg Ser Ser Gln Ser Leu Val His Ser Ser Gly Asn Thr Tyr Leu His
1 5 10 15

<210> 1955
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1955
Lys Gly Ser Asn Arg Phe Ser
1 5

<210> 1956
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1956
Ser Gln Ser Thr His Val Pro Phe Thr
1 5

<210> 1957
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1957
Thr Thr Tyr Thr Met His
1 5

<210> 1958
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1958
Trp Ile Gly Tyr Ile Asn Pro Ser Ser Gly Tyr Thr Lys
1 5 10

<210> 1959
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1959

Ala Arg Leu Trp Ala
1 5

<210> 1960
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1960
Val His Ser Ser Gly Asn Thr Tyr Leu His Trp Tyr
1 5 10

<210> 1961
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1961
Leu Leu Ile Tyr Lys Gly Ser Asn Arg Phe
1 5 10

<210> 1962
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1962
Ser Gln Ser Thr His Val Pro Phe
1 5

<210> 1963
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1963
Gly Tyr Thr Phe Thr Thr Tyr Thr
1   5

<210> 1964
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1964
Ile Asn Pro Ser Ser Gly Tyr Thr
1   5

<210> 1965
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1965
Ala Arg Leu Trp Ala Tyr
1   5

<210> 1966
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 1966
Gln Ser Leu Val His Ser Ser Gly Asn Thr Tyr
1   5   10

<210> 1967
<211> 3
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1967
Lys Gly Ser
1

<210> 1968
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1968
Ser Gln Ser Thr His Val Pro Phe Thr
1 5

<210> 1969
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1969
Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr
20 25 30

Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Ser Gly Tyr Thr Lys Tyr Asn Gln Lys Phe
50 55 60

Thr Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Leu Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
100 105 110

Ala

<210> 1970
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1970
Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

Ser Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Gly Ser Asn Arg Phe Ser Gly Val Ser
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
85 90 95

Thr His Val Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Met Lys
100 105 110

<210> 1971
<211> 443
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 1971

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Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
1               5                  10                  15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr
            20                  25                  30

Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45

Gly Tyr Ile Asn Pro Ser Ser Gly Tyr Thr Lys Tyr Asn Gln Lys Phe
    50                  55                  60

Thr Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Leu Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
            100                 105                 110

Ala Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
        115                 120                 125

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
    130                 135                 140

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
145                 150                 155                 160

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
                165                 170                 175

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
            180                 185                 190

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
        195                 200                 205
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Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
    210                 215                 220

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
225                 230                 235                 240

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
                245                 250                 255

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
            260                 265                 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
        275                 280                 285

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
    290                 295                 300

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
305                 310                 315                 320

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
                325                 330                 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
            340                 345                 350

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
        355                 360                 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
    370                 375                 380

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
385                 390                 395                 400

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
                405                 410                 415
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Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
420 425 430

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 1972
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1972
Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

Ser Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Gly Ser Asn Arg Phe Ser Gly Val Ser
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
85 90 95

Thr His Val Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Met Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 1973
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1973
Asn Tyr Val Val His
1 5

<210> 1974
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1974
Val Ile Trp Thr Asp Gly Ser Thr Asp Tyr Asn Ala Ala Phe Ile Ser
1 5 10 15

<210> 1975
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1975
Asn Asn Gly Tyr Phe Pro Ala Phe Phe Ala Tyr
1 5 10

<210> 1976
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1976
Lys Ala Ser Gln Asn Val Asp Thr Asp Ile Thr
1 5 10

<210> 1977
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1977
Ser Ala Ser Tyr Arg Tyr Ser
1 5

<210> 1978
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1978
Gln Gln Tyr Asn Ser Tyr Pro Leu Thr
1 5

<210> 1979
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1979
Gly Phe Ser Leu Ser Asn Tyr
1 5

<210> 1980
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1980
Trp Thr Asp Gly Ser
1 5

<210> 1981
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1981
Asn Asn Gly Tyr Phe Pro Ala Phe Phe Ala
1 5 10

<210> 1982
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1982
Ser Gln Asn Val Asp Thr Asp
1 5

<210> 1983
<211> 3

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1983
Ser Ala Ser
1

<210> 1984
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1984
Tyr Asn Ser Tyr Pro Leu
1 5

<210> 1985
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1985
Gly Phe Ser Leu Ser Asn Tyr Val Val His
1 5 10

<210> 1986
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1986
Val Ile Trp Thr Asp Gly Ser Thr Asp
1 5

<210> 1987
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1987
Asn Asn Gly Tyr Phe Pro Ala Phe Phe Ala Tyr
1 5 10

<210> 1988
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1988
Lys Ala Ser Gln Asn Val Asp Thr Asp Ile Thr
1 5 10

<210> 1989
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1989
Ser Ala Ser Tyr Arg Tyr Ser
1 5

<210> 1990
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1990
Gln Gln Tyr Asn Ser Tyr Pro Leu Thr
1 5

<210> 1991
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1991
Ser Asn Tyr Val Val His
1 5

<210> 1992
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1992
Trp Leu Gly Val Ile Trp Thr Asp Gly Ser Thr Asp
1 5 10

<210> 1993
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1993
Ala Arg Asn Asn Gly Tyr Phe Pro Ala Phe Phe Ala
1 5 10

<210> 1994
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 1994

Asp Thr Asp Ile Thr Trp Tyr
1 5

<210> 1995
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1995
Ala Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr
1 5 10

<210> 1996
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1996
Gln Gln Tyr Asn Ser Tyr Pro Leu
1 5

<210> 1997
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1997
Gly Phe Ser Leu Ser Asn Tyr Val
1 5

<210> 1998
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1998
Ile Trp Thr Asp Gly Ser Thr
1 5

<210> 1999
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 1999
Ala Arg Asn Asn Gly Tyr Phe Pro Ala Phe Phe Ala Tyr
1 5 10

<210> 2000
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2000
Gln Asn Val Asp Thr Asp
1 5

<210> 2001
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2001
Ser Ala Ser
1

<210> 2002
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2002
Gln Gln Tyr Asn Ser Tyr Pro Leu Thr
1 5

<210> 2003
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 2003
Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln
1 5 10 15

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asn Tyr
20 25 30

Val Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Thr Asp Gly Ser Thr Asp Tyr Asn Ala Ala Phe Ile
50 55 60

Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65 70 75 80

Lys Met Asn Ser Leu Gln Ala Asp Asp Thr Ala Ile Tyr Tyr Cys Ala
85 90 95

Arg Asn Asn Gly Tyr Phe Pro Ala Phe Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ala
115

<210> 2004
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 2004
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15

Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Asp Thr Asp
20 25 30

Ile Thr Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile
35 40 45

Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Asn Val Gln Ser
65 70 75 80

Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Met Lys
100 105

<210> 2005
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 2005
Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln
1 5 10 15

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asn Tyr
20 25 30

Val Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

```
Gly Val Ile Trp Thr Asp Gly Ser Thr Asp Tyr Asn Ala Ala Phe Ile
    50                  55                  60

Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65                  70                  75                  80

Lys Met Asn Ser Leu Gln Ala Asp Asp Thr Ala Ile Tyr Tyr Cys Ala
                85                  90                  95

Arg Asn Asn Gly Tyr Phe Pro Ala Phe Phe Ala Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
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```
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445

Lys
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<210> 2006
<211> 214

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 2006
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15

Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Asp Thr Asp
20 25 30

Ile Thr Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile
35 40 45

Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Asn Val Gln Ser
65 70 75 80

Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Met Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 2007
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2007
Ser Tyr Trp Ile Thr
1 5

<210> 2008
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2008
Asp Ile Tyr Pro Gly Ser Gly Ser Thr Asn Tyr Asn Glu Lys Phe Lys
1 5 10 15

Ser

<210> 2009
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2009
Glu Ser Ile Thr Thr Arg Ile Thr Pro Phe Asp His
1 5 10

<210> 2010
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2010
Arg Ser Ser Gln Ser Leu Val His Ser Ser Gly Asn Thr Tyr Leu His
1 5 10 15

<210> 2011
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2011
Lys Gly Ser Asn Arg Phe Ser
1 5

<210> 2012
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2012
Ser Gln Ser Thr His Val Pro Phe Thr
1 5

<210> 2013
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2013

Gly Tyr Thr Phe Ser Ser Tyr
1 5

<210> 2014
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2014
Tyr Pro Gly Ser Gly Ser
1 5

<210> 2015
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2015
Glu Ser Ile Thr Thr Arg Ile Thr Pro Phe Asp
1 5 10

<210> 2016
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2016
Ser Gln Ser Leu Val His Ser Ser Gly Asn Thr Tyr
1 5 10

<210> 2017
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2017
Lys Gly Ser
1

<210> 2018
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2018
Ser Thr His Val Pro Phe
1 5

<210> 2019
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2019
Gly Tyr Thr Phe Ser Ser Tyr Trp Ile Thr
1 5 10

<210> 2020
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2020
Asp Ile Tyr Pro Gly Ser Gly Ser Thr Asn
1 5 10

<210> 2021
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2021
Glu Ser Ile Thr Thr Arg Ile Thr Pro Phe Asp His
1 5 10

<210> 2022
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2022
Arg Ser Ser Gln Ser Leu Val His Ser Ser Gly Asn Thr Tyr Leu His
1 5 10 15

<210> 2023
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2023
Lys Gly Ser Asn Arg Phe Ser
1 5

<210> 2024
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2024
Ser Gln Ser Thr His Val Pro Phe Thr
1 5

<210> 2025
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2025
Ser Ser Tyr Trp Ile Thr
1 5

<210> 2026
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2026
Trp Val Gly Asp Ile Tyr Pro Gly Ser Gly Ser Thr Asn
1 5 10

<210> 2027
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2027
Ala Arg Glu Ser Ile Thr Thr Arg Ile Thr Pro Phe Asp
1 5 10

<210> 2028
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2028
Val His Ser Ser Gly Asn Thr Tyr Leu His Trp Tyr
1 5 10

<210> 2029
<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2029
Leu Leu Ile Tyr Lys Gly Ser Asn Arg Phe
1 5 10

<210> 2030
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2030
Ser Gln Ser Thr His Val Pro Phe
1 5

<210> 2031
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2031
Gly Tyr Thr Phe Ser Ser Tyr Trp
1 5

<210> 2032
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2032
Ile Tyr Pro Gly Ser Gly Ser Thr
1 5

<210> 2033
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2033
Ala Arg Glu Ser Ile Thr Thr Arg Ile Thr Pro Phe Asp His
1 5 10

<210> 2034
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2034
Gln Ser Leu Val His Ser Ser Gly Asn Thr Tyr
1 5 10

<210> 2035
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2035
Lys Gly Ser
1

<210> 2036
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2036
Ser Gln Ser Thr His Val Pro Phe Thr
1 5

<210> 2037
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 2037
Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Ser Ser Tyr
20 25 30

Trp Ile Thr Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Asp Ile Tyr Pro Gly Ser Gly Ser Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Ser Lys Ala Ala Leu Thr Val Asp Thr Ser Ser Ser Thr Ala Phe
65 70 75 80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Ser Ile Thr Thr Arg Ile Thr Pro Phe Asp His Trp Gly
100 105 110

Gln Gly Thr Thr Leu Thr Val Ser Ser
115 120

<210> 2038
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 2038

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Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1               5                   10                  15


Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
            20                  25                  30


Ser Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35                  40                  45


Pro Lys Leu Leu Ile Tyr Lys Gly Ser Asn Arg Phe Ser Gly Val Ser
    50                  55                  60


Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80


Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
                85                  90                  95


Thr His Val Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110


<210> 2039
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 2039
Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Ser Ser Tyr
            20                  25                  30


Trp Ile Thr Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Val
        35                  40                  45


Gly Asp Ile Tyr Pro Gly Ser Gly Ser Thr Asn Tyr Asn Glu Lys Phe
    50                  55                  60
```

```
Lys Ser Lys Ala Ala Leu Thr Val Asp Thr Ser Ser Ser Thr Ala Phe
65                  70                  75                  80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Ser Ile Thr Thr Arg Ile Thr Pro Phe Asp His Trp Gly
            100                 105                 110

Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285
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```
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445

Pro Gly Lys
    450
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<210> 2040
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2040
Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1   5   10   15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
            20   25   30

Ser Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35   40   45

Pro Lys Leu Leu Ile Tyr Lys Gly Ser Asn Arg Phe Ser Gly Val Ser
    50   55   60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65   70   75   80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
                85   90   95

Thr His Val Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
            100   105   110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
        115   120   125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
    130   135   140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145   150   155   160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
                165   170   175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
            180   185   190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
        195   200   205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 2041
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2041
Ser Tyr Trp Ile Asn
1 5

<210> 2042
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2042
Asn Ile Tyr Pro Gly Ser Ser Ser Thr Asn Tyr Asn Glu Lys Phe Lys
1 5 10 15

Ser

<210> 2043
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2043
Glu Leu Gly Gly Tyr Tyr Arg Tyr Asn Ala Met Asp Tyr
1 5 10

<210> 2044
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2044
Lys Ala Ser Gln Asp Ile Asn Arg Tyr Leu Ser
1 5 10

<210> 2045
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2045
Arg Ala Asn Thr Leu Val Asp
1 5

<210> 2046
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2046
Leu Gln Tyr Asp Glu Phe Pro Tyr Thr
1 5

<210> 2047
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2047
Gly Tyr Thr Phe Asn Ser Tyr
1 5

<210> 2048
<211> 6

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2048
Tyr Pro Gly Ser Ser Ser
1 5

<210> 2049
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2049
Glu Leu Gly Gly Tyr Tyr Arg Tyr Asn Ala Met Asp
1 5 10

<210> 2050
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2050
Ser Gln Asp Ile Asn Arg Tyr
1 5

<210> 2051
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2051
Arg Ala Asn
1

<210> 2052
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2052
Tyr Asp Glu Phe Pro Tyr
1 5

<210> 2053
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2053
Gly Tyr Thr Phe Asn Ser Tyr Trp Ile Asn
1 5 10

<210> 2054
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2054
Asn Ile Tyr Pro Gly Ser Ser Ser Thr Asn
1 5 10

<210> 2055
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2055
Glu Leu Gly Gly Tyr Tyr Arg Tyr Asn Ala Met Asp Tyr
1 5 10

<210> 2056
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2056
Lys Ala Ser Gln Asp Ile Asn Arg Tyr Leu Ser
1 5 10

<210> 2057
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2057
Arg Ala Asn Thr Leu Val Asp
1 5

<210> 2058
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2058
Leu Gln Tyr Asp Glu Phe Pro Tyr Thr
1 5

<210> 2059
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2059

Asn Ser Tyr Trp Ile Asn
1 5

<210> 2060
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2060
Trp Ile Gly Asn Ile Tyr Pro Gly Ser Ser Ser Thr Asn
1 5 10

<210> 2061
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2061
Ala Arg Glu Leu Gly Gly Tyr Tyr Arg Tyr Asn Ala Met Asp
1 5 10

<210> 2062
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2062
Asn Arg Tyr Leu Ser Trp Phe
1 5

<210> 2063
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2063
Thr Leu Ile Tyr Arg Ala Asn Thr Leu Val
1 5 10

<210> 2064
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2064
Leu Gln Tyr Asp Glu Phe Pro Tyr
1 5

<210> 2065
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2065
Gly Tyr Thr Phe Asn Ser Tyr Trp
1 5

<210> 2066
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2066
Ile Tyr Pro Gly Ser Ser Ser Thr
1 5

<210> 2067
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2067
Ala Arg Glu Leu Gly Gly Tyr Tyr Arg Tyr Asn Ala Met Asp Tyr
1 5 10 15

<210> 2068
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2068
Gln Asp Ile Asn Arg Tyr
1 5

<210> 2069
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2069
Arg Ala Asn
1

<210> 2070
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2070
Leu Gln Tyr Asp Glu Phe Pro Tyr Thr
1 5

<210> 2071
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 2071
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Asn Ser Tyr
20 25 30

Trp Ile Asn Trp Met Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Asn Ile Tyr Pro Gly Ser Ser Ser Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Ser Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Leu Gly Gly Tyr Tyr Arg Tyr Asn Ala Met Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 2072
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 2072
Asp Ile Val Leu Thr Gln Ser Pro Ser Ser Met Tyr Ala Ser Leu Gly
1 5 10 15

Glu Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Arg Tyr
20 25 30

Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Lys Thr Leu Ile
35 40 45

Tyr Arg Ala Asn Thr Leu Val Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Gln Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Tyr
65 70 75 80

Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Tyr Asp Glu Phe Pro Tyr
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Met Lys
100 105

<210> 2073
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 2073
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Asn Ser Tyr
20 25 30

Trp Ile Asn Trp Met Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Asn Ile Tyr Pro Gly Ser Ser Ser Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Ser Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Tyr Cys
85 90 95

```
Ala Arg Glu Leu Gly Gly Tyr Tyr Arg Tyr Asn Ala Met Asp Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
        115                 120                 125

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
    130                 135                 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145                 150                 155                 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
                165                 170                 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
            180                 185                 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
        195                 200                 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
    210                 215                 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
225                 230                 235                 240

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                245                 250                 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            260                 265                 270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        275                 280                 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
    290                 295                 300
```

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
305 310 315 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
325 330 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
340 345 350

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
355 360 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
370 375 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385 390 395 400

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
405 410 415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
420 425 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
435 440 445

Ser Pro Gly Lys
450

<210> 2074
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 2074
Asp Ile Val Leu Thr Gln Ser Pro Ser Ser Met Tyr Ala Ser Leu Gly
1 5 10 15

```
Glu Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Arg Tyr
            20                  25                  30

Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Lys Thr Leu Ile
        35                  40                  45

Tyr Arg Ala Asn Thr Leu Val Asp Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Gln Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Tyr
65                  70                  75                  80

Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Tyr Asp Glu Phe Pro Tyr
                85                  90                  95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Met Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
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<210> 2075
<211> 5

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2075
Ser Tyr Trp Met His
1 5

<210> 2076
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2076
Met Ile His Pro Asn Ser Gly Ser Thr Asn Tyr Asn Glu Lys Phe Lys
1 5 10 15

Ser

<210> 2077
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2077
Cys Gly Tyr Asp Gly Ala Trp Phe Ala Tyr
1 5 10

<210> 2078
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2078

Ser Ala Ser Gln Gly Ile Ser Asn Cys Leu Asn
1 5 10

<210> 2079
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2079
Tyr Thr Ser Ser Leu His Ser
1 5

<210> 2080
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2080
Gln Gln Tyr Ser Lys Val Pro Tyr Thr
1 5

<210> 2081
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2081
Gly Tyr Thr Phe Thr Ser Tyr
1 5

<210> 2082
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2082
His Pro Asn Ser Gly Ser
1 5

<210> 2083
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2083
Cys Gly Tyr Asp Gly Ala Trp Phe Ala
1 5

<210> 2084
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2084
Ser Gln Gly Ile Ser Asn Cys
1 5

<210> 2085
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2085
Tyr Thr Ser
1

<210> 2086
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2086
Tyr Ser Lys Val Pro Tyr
1 5

<210> 2087
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2087
Gly Tyr Thr Phe Thr Ser Tyr Trp Met His
1 5 10

<210> 2088
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2088
Met Ile His Pro Asn Ser Gly Ser Thr Asn
1 5 10

<210> 2089
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2089
Cys Gly Tyr Asp Gly Ala Trp Phe Ala Tyr
1 5 10

<210> 2090
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2090
Ser Ala Ser Gln Gly Ile Ser Asn Cys Leu Asn
1 5 10

<210> 2091
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2091
Tyr Thr Ser Ser Leu His Ser
1 5

<210> 2092
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2092
Gln Gln Tyr Ser Lys Val Pro Tyr Thr
1 5

<210> 2093
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2093
Thr Ser Tyr Trp Met His
1 5

<210> 2094
<211> 13

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2094
Trp Ile Gly Met Ile His Pro Asn Ser Gly Ser Thr Asn
1 5 10

<210> 2095
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2095
Ala Arg Cys Gly Tyr Asp Gly Ala Trp Phe Ala
1 5 10

<210> 2096
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2096
Ser Asn Cys Leu Asn Trp Tyr
1 5

<210> 2097
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2097
Leu Leu Ile His Tyr Thr Ser Ser Leu His
1 5 10

<210> 2098
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2098
Gln Gln Tyr Ser Lys Val Pro Tyr
1 5

<210> 2099
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2099
Gly Tyr Thr Phe Thr Ser Tyr Trp
1 5

<210> 2100
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2100
Ile His Pro Asn Ser Gly Ser Thr
1 5

<210> 2101
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2101
Ala Arg Cys Gly Tyr Asp Gly Ala Trp Phe Ala Tyr
1 5 10

<210> 2102
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2102
Gln Gly Ile Ser Asn Cys
1 5

<210> 2103
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2103
Tyr Thr Ser
1

<210> 2104
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2104
Gln Gln Tyr Ser Lys Val Pro Tyr Thr
1 5

<210> 2105
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 2105

Gln Val Gln Leu Lys Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Met Ile His Pro Asn Ser Gly Ser Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Cys Gly Tyr Asp Gly Ala Trp Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Ser Val Thr Val Ser Ser
115

<210> 2106
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 2106
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Ser Ala Ser Gln Gly Ile Ser Asn Cys
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

```
His Tyr Thr Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Gly Gly Ser Gly Thr His Tyr Ser Leu Thr Ile Ser Asn Leu Glu Pro
65                  70                  75                  80


Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Lys Val Pro Tyr
                85                  90                  95


Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
            100                 105


<210> 2107
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 2107
Gln Val Gln Leu Lys Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30


Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Met Ile His Pro Asn Ser Gly Ser Thr Asn Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80


Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Cys Gly Tyr Asp Gly Ala Trp Phe Ala Tyr Trp Gly Gln Gly
            100                 105                 110
```

```
Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
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```
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445

Lys
```

<210> 2108
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 2108

```
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1               5                   10                  15

Asp Arg Val Thr Ile Ser Cys Ser Ala Ser Gln Gly Ile Ser Asn Cys
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
        35                  40                  45
```

```
His Tyr Thr Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Gly Gly Ser Gly Thr His Tyr Ser Leu Thr Ile Ser Asn Leu Glu Pro
65                  70                  75                  80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Lys Val Pro Tyr
                85                  90                  95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
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<210> 2109
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2109
Asn Tyr Trp Met Gln
1 5

<210> 2110
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2110
Glu Ile Asp Pro Ser Asp Thr Phe Thr Asn Tyr Asn Gln Asn Phe Lys
1 5 10 15

Asp

<210> 2111
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2111
Gly Asp Trp Asp Arg Asp Trp Tyr Phe Asp Val
1 5 10

<210> 2112
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2112
Lys Ser Ser Gln Ser Leu Leu Tyr Ser Asp Gly Lys Thr Tyr Leu Asn
1 5 10 15

<210> 2113
<211> 7

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2113
Leu Val Ser Lys Leu Asp Ser
1 5

<210> 2114
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2114
Leu Gln Ala Thr His Phe Pro His Thr
1 5

<210> 2115
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2115
Gly Tyr Thr Phe Thr Asn Tyr
1 5

<210> 2116
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2116
Asp Pro Ser Asp Thr Phe
1 5

<210> 2117
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2117
Gly Asp Trp Asp Arg Asp Trp Tyr Phe Asp
1 5 10

<210> 2118
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2118
Ser Gln Ser Leu Leu Tyr Ser Asp Gly Lys Thr Tyr
1 5 10

<210> 2119
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2119
Leu Val Ser
1

<210> 2120
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2120
Ala Thr His Phe Pro His
1 5

<210> 2121
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2121
Gly Tyr Thr Phe Thr Asn Tyr Trp Met Gln
1 5 10

<210> 2122
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2122
Glu Ile Asp Pro Ser Asp Thr Phe Thr Asn
1 5 10

<210> 2123
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2123
Gly Asp Trp Asp Arg Asp Trp Tyr Phe Asp Val
1 5 10

<210> 2124
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2124

Lys Ser Ser Gln Ser Leu Leu Tyr Ser Asp Gly Lys Thr Tyr Leu Asn
1 5 10 15

<210> 2125
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2125
Leu Val Ser Lys Leu Asp Ser
1 5

<210> 2126
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2126
Leu Gln Ala Thr His Phe Pro His Thr
1 5

<210> 2127
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2127
Thr Asn Tyr Trp Met Gln
1 5

<210> 2128
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2128
Trp Ile Gly Glu Ile Asp Pro Ser Asp Thr Phe Thr Asn
1   5   10

<210> 2129
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 2129
Ala Arg Gly Asp Trp Asp Arg Asp Trp Tyr Phe Asp
1   5   10

<210> 2130
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 2130
Leu Tyr Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu
1   5   10

<210> 2131
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 2131
Leu Leu Ile Tyr Leu Val Ser Lys Leu Asp
1   5   10

<210> 2132
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2132
Leu Gln Ala Thr His Phe Pro His
1 5

<210> 2133
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2133
Gly Tyr Thr Phe Thr Asn Tyr Trp
1 5

<210> 2134
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2134
Ile Asp Pro Ser Asp Thr Phe Thr
1 5

<210> 2135
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2135
Ala Arg Gly Asp Trp Asp Arg Asp Trp Tyr Phe Asp Val
1 5 10

<210> 2136
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2136
Gln Ser Leu Leu Tyr Ser Asp Gly Lys Thr Tyr
1 5 10

<210> 2137
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2137
Leu Val Ser
1

<210> 2138
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2138
Leu Gln Ala Thr His Phe Pro His Thr
1 5

<210> 2139
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 2139
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Trp Met Gln Trp Val Gln Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asp Pro Ser Asp Thr Phe Thr Asn Tyr Asn Gln Asn Phe
50 55 60

Lys Asp Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Asp Trp Asp Arg Asp Trp Tyr Phe Asp Val Trp Gly Thr
100 105 110

Gly Thr Leu Val Thr Val Ser Ala
115 120

<210> 2140
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2140
Asp Ile Val Met Thr Gln Thr Pro Leu Thr Leu Ser Val Thr Ile Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Glu Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Thr Glu Asp Leu Gly Ile Tyr Tyr Cys Leu Gln Ala
85 90 95

Thr His Phe Pro His Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105 110

<210> 2141
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2141
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Trp Met Gln Trp Val Gln Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asp Pro Ser Asp Thr Phe Thr Asn Tyr Asn Gln Asn Phe
50 55 60

Lys Asp Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Asp Trp Asp Arg Asp Trp Tyr Phe Asp Val Trp Gly Thr
100 105 110

Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

```
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350
```

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 2142
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2142
Asp Ile Val Met Thr Gln Thr Pro Leu Thr Leu Ser Val Thr Ile Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Glu Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

```
Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80

Ser Arg Val Glu Thr Glu Asp Leu Gly Ile Tyr Tyr Cys Leu Gln Ala
                85                  90                  95

Thr His Phe Pro His Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
            100                 105                 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
        115                 120                 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
    130                 135                 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145                 150                 155                 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
                165                 170                 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
            180                 185                 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
        195                 200                 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215
```

<210> 2143
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2143

```
Asp Thr Tyr Met His
1               5
```

<210> 2144
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2144
Arg Ile Asp Pro Ala Asn Gly His Thr Lys Phe Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 2145
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2145
Arg Phe Ala Tyr
1

<210> 2146
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2146
Arg Ala Ser His Glu Ile Ser Gly Tyr Leu Ser
1 5 10

<210> 2147
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2147
Ala Ala Ser Thr Leu Asp Ser
1 5

<210> 2148
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2148
Leu Gln Tyr Ser Ser Tyr Pro Tyr Thr
1 5

<210> 2149
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2149
Gly Phe Asn Ile Lys Asp Thr
1 5

<210> 2150
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2150
Asp Pro Ala Asn Gly His
1 5

<210> 2151
<211> 3
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2151
Arg Phe Ala
1

<210> 2152
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2152
Ser His Glu Ile Ser Gly Tyr
1 5

<210> 2153
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2153
Ala Ala Ser
1

<210> 2154
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2154
Tyr Ser Ser Tyr Pro Tyr
1 5

<210> 2155
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2155
Gly Phe Asn Ile Lys Asp Thr Tyr Met His
1 5 10

<210> 2156
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2156
Arg Ile Asp Pro Ala Asn Gly His Thr Lys
1 5 10

<210> 2157
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2157
Arg Phe Ala Tyr
1

<210> 2158
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2158
Arg Ala Ser His Glu Ile Ser Gly Tyr Leu Ser
1 5 10

<210> 2159
<211> 7

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2159
Ala Ala Ser Thr Leu Asp Ser
1 5

<210> 2160
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2160
Leu Gln Tyr Ser Ser Tyr Pro Tyr Thr
1 5

<210> 2161
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2161
Lys Asp Thr Tyr Met His
1 5

<210> 2162
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2162
Trp Ile Gly Arg Ile Asp Pro Ala Asn Gly His Thr Lys
1 5 10

<210> 2163
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2163
Ala Ile Arg Phe Ala
1 5

<210> 2164
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2164
Ser Gly Tyr Leu Ser Trp Leu
1 5

<210> 2165
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2165
Arg Leu Ile Tyr Ala Ala Ser Thr Leu Asp
1 5 10

<210> 2166
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2166
Leu Gln Tyr Ser Ser Tyr Pro Tyr
1 5

<210> 2167
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2167
Gly Phe Asn Ile Lys Asp Thr Tyr
1 5

<210> 2168
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2168
Ile Asp Pro Ala Asn Gly His Thr
1 5

<210> 2169
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2169
Ala Ile Arg Phe Ala Tyr
1 5

<210> 2170
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2170

His Glu Ile Ser Gly Tyr
1 5

<210> 2171
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2171
Ala Ala Ser
1

<210> 2172
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2172
Leu Gln Tyr Ser Ser Tyr Pro Tyr Thr
1 5

<210> 2173
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2173
Glu Val Lys Leu Val Glu Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Arg Ile Asp Pro Ala Asn Gly His Thr Lys Phe Asp Pro Lys Phe
    50   55   60

Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
65   70   75   80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Ile Arg Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
            100   105   110

Ala

<210> 2174
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 2174
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1   5   10   15

Asp Arg Val Ser Leu Thr Cys Arg Ala Ser His Glu Ile Ser Gly Tyr
            20   25   30

Leu Ser Trp Leu Gln Gln Lys Pro Asp Gly Thr Phe Lys Arg Leu Ile
        35   40   45

Tyr Ala Ala Ser Thr Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly
    50   55   60

Ser Arg Ser Gly Ser Asp Tyr Ser Leu Ser Ile Ser Ser Leu Glu Ser
65   70   75   80

Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Tyr Ser Ser Tyr Pro Tyr
                85   90   95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Met Lys
100 105

<210> 2175
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2175
Glu Val Lys Leu Val Glu Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Arg Ile Asp Pro Ala Asn Gly His Thr Lys Phe Asp Pro Lys Phe
50 55 60

Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ile Arg Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
100 105 110

Ala Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
115 120 125

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
130 135 140

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
145 150 155 160

```
Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
                165                 170                 175

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
            180                 185                 190

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
        195                 200                 205

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
    210                 215                 220

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
225                 230                 235                 240

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
                245                 250                 255

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
            260                 265                 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
        275                 280                 285

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
    290                 295                 300

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
305                 310                 315                 320

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
                325                 330                 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
            340                 345                 350

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
        355                 360                 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
    370                 375                 380
```

```
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
385                 390                 395                 400


Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
                405                 410                 415


Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
            420                 425                 430


Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440
```

<210> 2176
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 2176

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1               5                   10                  15


Asp Arg Val Ser Leu Thr Cys Arg Ala Ser His Glu Ile Ser Gly Tyr
            20                  25                  30


Leu Ser Trp Leu Gln Gln Lys Pro Asp Gly Thr Phe Lys Arg Leu Ile
        35                  40                  45


Tyr Ala Ala Ser Thr Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly
    50                  55                  60


Ser Arg Ser Gly Ser Asp Tyr Ser Leu Ser Ile Ser Ser Leu Glu Ser
65                  70                  75                  80


Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Tyr Ser Ser Tyr Pro Tyr
                85                  90                  95


Thr Phe Gly Ser Gly Thr Lys Leu Glu Met Lys Arg Thr Val Ala Ala
            100                 105                 110
```

```
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175


Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190


Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205


Phe Asn Arg Gly Glu Cys
    210


<210> 2177
<211> 161
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 2177
Ser Gln Phe Arg Val Ser Pro Leu Asp Arg Thr Trp Asn Leu Gly Glu
1               5                   10                  15


Thr Val Glu Leu Lys Cys Gln Val Leu Leu Ser Asn Pro Thr Ser Gly
            20                  25                  30


Cys Ser Trp Leu Phe Gln Pro Arg Gly Ala Ala Ala Ser Pro Thr Phe
        35                  40                  45


Leu Leu Tyr Leu Ser Gln Asn Lys Pro Lys Ala Ala Glu Gly Leu Asp
    50                  55                  60
```

```
Thr Gln Arg Phe Ser Gly Lys Arg Leu Gly Asp Thr Phe Val Leu Thr
65                  70                  75                  80

Leu Ser Asp Phe Arg Arg Glu Asn Glu Gly Tyr Tyr Phe Cys Ser Ala
                85                  90                  95

Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val Pro Val Phe Leu
            100                 105                 110

Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
        115                 120                 125

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
    130                 135                 140

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
145                 150                 155                 160

Asp
```

<210> 2178
<211> 152
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 2178

```
Asn Ser Val Leu Gln Gln Thr Pro Ala Tyr Ile Lys Val Gln Thr Asn
1               5                   10                  15

Lys Met Val Met Leu Ser Cys Glu Ala Lys Ile Ser Leu Ser Asn Met
            20                  25                  30

Arg Ile Tyr Trp Leu Arg Gln Arg Gln Ala Pro Ser Ser Asp Ser His
        35                  40                  45

His Glu Phe Leu Ala Leu Trp Asp Ser Ala Lys Gly Thr Ile His Gly
    50                  55                  60
```

Glu Glu Val Glu Gln Glu Lys Ile Ala Val Phe Arg Asp Ala Ser Arg
65 70 75 80

Phe Ile Leu Asn Leu Thr Ser Val Lys Pro Glu Asp Ser Gly Ile Tyr
85 90 95

Phe Cys Met Ile Val Gly Ser Pro Glu Leu Thr Phe Gly Lys Gly Thr
100 105 110

Gln Leu Ser Val Val Asp Phe Leu Pro Thr Thr Ala Gln Pro Thr Lys
115 120 125

Lys Ser Thr Leu Lys Lys Arg Val Cys Arg Leu Pro Arg Pro Glu Thr
130 135 140

Gln Lys Gly Pro Leu Cys Ser Pro
145 150

<210> 2179
<211> 412
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 2179
Met Ala Trp Val Trp Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
1 5 10 15

Ile Gln Ala Ser Gln Phe Arg Val Ser Pro Leu Asp Arg Thr Trp Asn
20 25 30

Leu Gly Glu Thr Val Glu Leu Lys Cys Gln Val Leu Leu Ser Asn Pro
35 40 45

Thr Ser Gly Cys Ser Trp Leu Phe Gln Pro Arg Gly Ala Ala Ala Ser
50 55 60

Pro Thr Phe Leu Leu Tyr Leu Ser Gln Asn Lys Pro Lys Ala Ala Glu
65 70 75 80

```
Gly Leu Asp Thr Gln Arg Phe Ser Gly Lys Arg Leu Gly Asp Thr Phe
                85                  90                  95

Val Leu Thr Leu Ser Asp Phe Arg Arg Glu Asn Glu Gly Tyr Tyr Phe
            100                 105                 110

Cys Ser Ala Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val Pro
        115                 120                 125

Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro
    130                 135                 140

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
145                 150                 155                 160

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
                165                 170                 175

Phe Ala Cys Asp Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
            180                 185                 190

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        195                 200                 205

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    210                 215                 220

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
225                 230                 235                 240

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                245                 250                 255

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            260                 265                 270

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        275                 280                 285
```

```
Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    290                 295                 300

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
305                 310                 315                 320

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                325                 330                 335

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            340                 345                 350

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        355                 360                 365

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
    370                 375                 380

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
385                 390                 395                 400

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                405                 410
```

<210> 2180
<211> 185
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2180

```
Asp Gly Asn Glu Glu Met Gly Gly Ile Thr Gln Thr Pro Tyr Lys Val
1               5                   10                  15

Ser Ile Ser Gly Thr Thr Val Ile Leu Thr Cys Pro Gln Tyr Pro Gly
            20                  25                  30

Ser Glu Ile Leu Trp Gln His Asn Asp Lys Asn Ile Gly Gly Asp Glu
        35                  40                  45
```

Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp His Leu Ser Leu Lys Glu
    50   55   60

Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr Val Cys Tyr Pro Arg Gly
65   70   75   80

Ser Lys Pro Glu Asp Ala Asn Phe Tyr Leu Tyr Leu Arg Ala Arg Val
                85   90   95

Cys Glu Asn Cys Met Glu Met Asp Val Met Ser Val Ala Thr Ile Val
            100   105   110

Ile Val Asp Ile Cys Ile Thr Gly Gly Leu Leu Leu Leu Val Tyr Tyr
        115   120   125

Trp Ser Lys Asn Arg Lys Ala Lys Ala Lys Pro Val Thr Arg Gly Ala
    130   135   140

Gly Ala Gly Gly Arg Gln Arg Gly Gln Asn Lys Glu Arg Pro Pro Pro
145   150   155   160

Val Pro Asn Pro Asp Tyr Glu Pro Ile Arg Lys Gly Gln Arg Asp Leu
                165   170   175

Tyr Ser Gly Leu Asn Gln Arg Arg Ile
            180   185

<210> 2181
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 2181
Ser Gln Phe Arg Val Ser Pro Leu Asp Arg Thr Trp Asn Leu Gly Glu
1   5   10   15

Thr Val Glu Leu Lys Cys Gln Val Leu Leu Ser Asn Pro Thr Ser Gly
            20   25   30

```
Cys Ser Trp Leu Phe Gln Pro Arg Gly Ala Ala Ala Ser Pro Thr Phe
        35                  40                  45

Leu Leu Tyr Leu Ser Gln Asn Lys Pro Lys Ala Ala Glu Gly Leu Asp
    50                  55                  60

Thr Gln Arg Phe Ser Gly Lys Arg Leu Gly Asp Thr Phe Val Leu Thr
65                  70                  75                  80

Leu Ser Asp Phe Arg Arg Glu Asn Glu Gly Tyr Tyr Phe Cys Ser Ala
                85                  90                  95

Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val Pro Val Phe Leu
            100                 105                 110

Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
        115                 120                 125

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
    130                 135                 140

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
145                 150                 155                 160

Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu
                165                 170                 175

Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn Arg Arg Arg
            180                 185                 190

Val Cys Lys Cys Pro Arg Pro Val Val Lys Ser Gly Asp Lys Pro Ser
        195                 200                 205

Leu Ser Ala Arg Tyr Val
    210
```

<210> 2182
<211> 189
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 2182

```
Leu Gln Gln Thr Pro Ala Tyr Ile Lys Val Gln Thr Asn Lys Met Val
1               5                  10                  15

Met Leu Ser Cys Glu Ala Lys Ile Ser Leu Ser Asn Met Arg Ile Tyr
            20                  25                  30

Trp Leu Arg Gln Arg Gln Ala Pro Ser Ser Asp Ser His His Glu Phe
        35                  40                  45

Leu Ala Leu Trp Asp Ser Ala Lys Gly Thr Ile His Gly Glu Glu Val
    50                  55                  60

Glu Gln Glu Lys Ile Ala Val Phe Arg Asp Ala Ser Arg Phe Ile Leu
65                  70                  75                  80

Asn Leu Thr Ser Val Lys Pro Glu Asp Ser Gly Ile Tyr Phe Cys Met
                85                  90                  95

Ile Val Gly Ser Pro Glu Leu Thr Phe Gly Lys Gly Thr Gln Leu Ser
            100                 105                 110

Val Val Asp Phe Leu Pro Thr Thr Ala Gln Pro Thr Lys Lys Ser Thr
        115                 120                 125

Leu Lys Lys Arg Val Cys Arg Leu Pro Arg Pro Glu Thr Gln Lys Gly
    130                 135                 140

Pro Leu Cys Ser Pro Ile Thr Leu Gly Leu Leu Val Ala Gly Val Leu
145                 150                 155                 160

Val Leu Leu Val Ser Leu Gly Val Ala Ile His Leu Cys Cys Arg Arg
                165                 170                 175

Arg Arg Ala Arg Leu Arg Phe Met Lys Gln Phe Tyr Lys
            180                 185
```

<210> 2183
<211> 19

<212> PRT
<213> Homo sapiens

<400> 2183
Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro
1   5   10   15

Ser Pro Ser

<210> 2184
<211> 6
<212> PRT
<213> Homo sapiens

<400> 2184
Val Pro Pro Pro Pro Pro
1   5

<210> 2185
<211> 58
<212> PRT
<213> Homo sapiens

<400> 2185
Glu Ser Pro Lys Ala Gln Ala Ser Ser Val Pro Thr Ala Gln Pro Gln
1   5   10   15

Ala Glu Gly Ser Leu Ala Lys Ala Thr Thr Ala Pro Ala Thr Thr Arg
            20   25   30

Asn Thr Gly Arg Gly Gly Glu Glu Lys Lys Lys Glu Lys Glu Lys Glu
        35   40   45

Glu Gln Glu Glu Arg Glu Thr Lys Thr Pro
    50   55

<210> 2186
<211> 15
<212> PRT
<213> Homo sapiens

<400> 2186
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1   5   10   15

<210> 2187
<211> 12
<212> PRT
<213> Homo sapiens

<400> 2187
Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro
1   5   10

<210> 2188
<211> 62
<212> PRT
<213> Homo sapiens

<400> 2188
Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro Arg Cys
1   5   10   15

Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
            20   25   30

Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu
        35   40   45

Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
    50   55   60

<210> 2189
<211> 12
<212> PRT
<213> Homo sapiens

<400> 2189
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro
1   5   10

<210> 2190
<211> 12
<212> PRT
<213> Homo sapiens

<400> 2190
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
1   5   10

<210> 2191
<211> 4

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2191
Cys Pro Pro Cys
1

<210> 2192
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2192
Cys Pro Ser Cys
1

<210> 2193
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2193
Cys Pro Arg Cys
1

<210> 2194
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2194
Ser Pro Pro Cys
1

<210> 2195
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2195
Cys Pro Pro Ser
1

<210> 2196
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2196
Ser Pro Pro Ser
1

<210> 2197
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2197
Asp Lys Thr His Thr Cys Ala Ala
1 5

<210> 2198
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2198
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10

<210> 2199
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2199
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Thr Cys Pro Pro Cys
1 5 10 15

Pro Ala

<210> 2200
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2200
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Thr Cys Pro Pro Cys
1 5 10 15

Pro Ala Thr Cys Pro Pro Cys Pro Ala
20 25

<210> 2201
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 2201
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Gly Lys Pro Thr Leu
1 5 10 15

Tyr Asn Ser Leu Val Met Ser Asp Thr Ala Gly Thr Cys Tyr
20 25 30

<210> 2202
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 2202
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Gly Lys Pro Thr His
1 5 10 15

Val Asn Val Ser Val Val Met Ala Glu Val Asp Gly Thr Cys Tyr
20 25 30

<210> 2203
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2203
Asp Lys Thr His Thr Cys Cys Val Glu Cys Pro Pro Cys Pro Ala
1 5 10 15

<210> 2204
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2204
Asp Lys Thr His Thr Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys Asp
1 5 10 15

Thr Pro Pro Pro Cys Pro Arg Cys Pro Ala
20 25

<210> 2205
<211> 11

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2205
Asp Lys Thr His Thr Cys Pro Ser Cys Pro Ala
1 5 10

<210> 2206
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2206
Ala Asp Ala Ala Pro
1 5

<210> 2207
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2207
Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro
1 5 10

<210> 2208
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2208
Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro
1 5 10

<210> 2209
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2209
Ala Lys Thr Thr Ala Pro
1 5

<210> 2210
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2210
Ala Lys Thr Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro
1 5 10

<210> 2211
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2211
Ala Lys Thr Thr Pro Lys Leu Glu Glu Gly Glu Phe Ser Glu Ala Arg
1 5 10 15

Val

<210> 2212
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2212
Ala Lys Thr Thr Pro Lys Leu Gly Gly
1   5

<210> 2213
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 2213
Ala Lys Thr Thr Pro Pro
1   5

<210> 2214
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 2214
Ala Lys Thr Thr Pro Pro Ser Val Thr Pro Leu Ala Pro
1   5   10

<210> 2215
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 2215
Ala Ser Thr Lys Gly Pro
1   5

<210> 2216
<211> 13
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2216
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
1 5 10

<210> 2217
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2217
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ala Ser Thr
1 5 10 15

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
20 25

<210> 2218
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2218
Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr
1 5 10

<210> 2219
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2219
Gly Glu Gly Glu Ser Gly Glu Gly Glu Ser Gly Glu Gly Glu Ser
1 5 10 15

<210> 2220
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2220
Gly Glu Gly Glu Ser Gly Glu Gly Glu Ser Gly Glu Gly Glu Ser Gly
1 5 10 15

Glu Gly Glu Ser
20

<210> 2221
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2221
Gly Glu Gly Gly Ser Gly Glu Gly Gly Ser Gly Glu Gly Gly Ser
1 5 10 15

<210> 2222
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2222
Gly Glu Asn Lys Val Glu Tyr Ala Pro Ala Leu Met Ala Leu Ser
1 5 10 15

<210> 2223
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2223
Gly Gly Glu Gly Ser Gly Gly Glu Gly Ser Gly Gly Glu Gly Ser
1 5 10 15

<210> 2224
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2224
Gly Gly Gly Glu Ser Gly Gly Glu Gly Ser Gly Glu Gly Gly Ser
1 5 10 15

<210> 2225
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2225
Gly Gly Gly Glu Ser Gly Gly Gly Glu Ser Gly Gly Gly Glu Ser
1 5 10 15

<210> 2226
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2226
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 2227
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2227
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 2228
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2228
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser
20

<210> 2229
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2229
Gly Gly Gly Lys Ser Gly Gly Gly Lys Ser Gly Gly Gly Lys Ser
1 5 10 15

<210> 2230
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2230
Gly Gly Gly Lys Ser Gly Gly Lys Gly Ser Gly Lys Gly Gly Ser
1 5 10 15

<210> 2231
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2231
Gly Gly Lys Gly Ser Gly Gly Lys Gly Ser Gly Gly Lys Gly Ser
1 5 10 15

<210> 2232
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2232
Gly Gly Ser Gly Gly
1 5

<210> 2233
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2233
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 2234
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2234
Gly His Glu Ala Ala Ala Val Met Gln Val Gln Tyr Pro Ala Ser
1 5 10 15

<210> 2235
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2235
Gly Lys Gly Gly Ser Gly Lys Gly Gly Ser Gly Lys Gly Gly Ser
1 5 10 15

<210> 2236
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2236
Gly Lys Gly Lys Ser Gly Lys Gly Lys Ser Gly Lys Gly Lys Ser
1 5 10 15

<210> 2237
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2237
Gly Lys Gly Lys Ser Gly Lys Gly Lys Ser Gly Lys Gly Lys Ser Gly
1 5 10 15

Lys Gly Lys Ser
20

<210> 2238
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2238
Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser
1 5 10 15

<210> 2239
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2239
Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly
1 5 10 15

Lys Pro Gly Ser
20

<210> 2240
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2240
Gly Pro Ala Lys Glu Leu Thr Pro Leu Lys Glu Ala Lys Val Ser
1 5 10 15

<210> 2241
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2241
Gly Ser Ala Gly Ser Ala Ala Gly Ser Gly Glu Phe
1 5 10

<210> 2242
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2242
Ile Arg Pro Arg Ala Ile Gly Gly Ser Lys Pro Arg Val Ala
1 5 10

<210> 2243
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2243
Lys Glu Ser Gly Ser Val Ser Ser Glu Gln Leu Ala Gln Phe Arg Ser
1 5 10 15

Leu Asp

<210> 2244
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2244
Lys Thr Thr Pro Lys Leu Glu Glu Gly Glu Phe Ser Glu Ala Arg
1 5 10 15

<210> 2245
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2245
Gln Pro Lys Ala Ala Pro
1 5

<210> 2246
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2246
Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro
1 5 10

<210> 2247
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2247
Arg Ala Asp Ala Ala Ala Ala Gly Gly Pro Gly Ser
1 5 10

<210> 2248
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2248
Arg Ala Asp Ala Ala Pro
1 5

<210> 2249
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2249
Arg Ala Asp Ala Ala Pro Thr Val Ser
1 5

<210> 2250
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2250
Ser Ala Lys Thr Thr Pro
1 5

<210> 2251
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2251
Ser Ala Lys Thr Thr Pro Lys Leu Glu Glu Gly Glu Phe Ser Glu Ala
1 5 10 15

Arg Val

<210> 2252
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2252
Ser Ala Lys Thr Thr Pro Lys Leu Gly Gly
1 5 10

<210> 2253
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2253
Ser Thr Ala Gly Asp Thr His Leu Gly Gly Glu Asp Phe Asp
1 5 10

<210> 2254
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2254
Thr Val Ala Ala Pro
1 5

<210> 2255
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2255
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
1 5 10

<210> 2256
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2256
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Thr Val Ala Ala
1 5 10 15

Pro Ser Val Phe Ile Phe Pro Pro
            20

<210> 2257
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 2257
Arg Ala Asp Ala Ala Ala Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly
1   5   10   15

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            20   25

<210> 2258
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 2258
Gly Gly Ser Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser
1   5   10   15

Thr Gly Gly Ser
            20

<210> 2259
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 2259
Gly Gly Gly Ser Gly Gly Gly Ser
1   5

<210> 2260
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2260
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10

<210> 2261
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2261
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10 15

<210> 2262
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2262
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10 15

Gly Gly Gly Ser
20

<210> 2263
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2263
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 2264
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2264
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser
20

<210> 2265
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2265
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25

<210> 2266
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2266

Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
1   5   10   15

Lys Gly

<210> 2267
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2267
Ile Arg Pro Arg Ala Ile Gly Gly Ser Lys Pro Arg Val Ala
1   5   10

<210> 2268
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2268
Gly Lys Gly Gly Ser Gly Lys Gly Gly Ser Gly Lys Gly Gly Ser
1   5   10   15

<210> 2269
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2269
Gly Gly Lys Gly Ser Gly Gly Lys Gly Ser Gly Gly Lys Gly Ser
1   5   10   15

<210> 2270
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2270
Gly Gly Gly Lys Ser Gly Gly Gly Lys Ser Gly Gly Gly Lys Ser
1 5 10 15

<210> 2271
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2271
Gly Lys Gly Lys Ser Gly Lys Gly Lys Ser Gly Lys Gly Lys Ser
1 5 10 15

<210> 2272
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2272
Gly Gly Gly Lys Ser Gly Gly Lys Gly Ser Gly Lys Gly Gly Ser
1 5 10 15

<210> 2273
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2273
Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser
1 5 10 15

<210> 2274
<211> 20

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2274
Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly
1 5 10 15

Lys Pro Gly Ser
20

<210> 2275
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2275
Gly Lys Gly Lys Ser Gly Lys Gly Lys Ser Gly Lys Gly Lys Ser Gly
1 5 10 15

Lys Gly Lys Ser
20

<210> 2276
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2276
Ser Thr Ala Gly Asp Thr His Leu Gly Gly Glu Asp Phe Asp
1 5 10

<210> 2277
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2277
Gly Glu Gly Gly Ser Gly Glu Gly Gly Ser Gly Glu Gly Gly Ser
1 5 10 15

<210> 2278
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2278
Gly Gly Glu Gly Ser Gly Gly Glu Gly Ser Gly Gly Glu Gly Ser
1 5 10 15

<210> 2279
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2279
Gly Glu Gly Glu Ser Gly Glu Gly Glu Ser Gly Glu Gly Glu Ser
1 5 10 15

<210> 2280
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2280
Gly Gly Gly Glu Ser Gly Gly Glu Gly Ser Gly Glu Gly Gly Ser
1 5 10 15

<210> 2281
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2281
Gly Glu Gly Glu Ser Gly Glu Gly Glu Ser Gly Glu Gly Glu Ser Gly
1 5 10 15

Glu Gly Glu Ser
20

<210> 2282
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2282
Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
1 5 10 15

Lys Gly

<210> 2283
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2283
Pro Arg Gly Ala Ser Lys Ser Gly Ser Ala Ser Gln Thr Gly Ser Ala
1 5 10 15

Pro Gly Ser

<210> 2284
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2284
Gly Thr Ala Ala Ala Gly Ala Gly Ala Ala Gly Gly Ala Ala Ala Gly
1 5 10 15

Ala Ala Gly

<210> 2285
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2285
Gly Thr Ser Gly Ser Ser Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly
1 5 10 15

Gly Gly Gly

<210> 2286
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2286
Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly
1 5 10 15

Lys Pro Gly Ser
20

<210> 2287
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2287
Gly Ser Gly Ser
1

<210> 2288
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2288
Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro
1 5 10

<210> 2289
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2289
Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro
1 5 10 15

Ala Pro Ala Pro
20

<210> 2290
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 2290
Ala Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Ala
1 5 10 15

Lys Glu Ala Ala Ala Ala Lys Glu Ala Ala Ala Ala Lys Ala Ala Ala
            20   25   30

<210> 2291
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 2291
Asn Asn Asn Ala Ala Trp Ser
1   5

<210> 2292
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 2292
Arg Thr Tyr Tyr Arg Ser Lys Trp Leu Tyr Asp Tyr Ala Val Ser Val
1   5   10   15

Lys Ser

<210> 2293
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 2293
Gly Tyr Ser Ser Ser Phe Asp Tyr
1   5

<210> 2294
<211> 14

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2294
Thr Gly Thr Ser Ser Asn Ile Gly Thr Tyr Lys Phe Val Ser
1 5 10

<210> 2295
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2295
Glu Val Ser Lys Arg Pro Ser
1 5

<210> 2296
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2296
Val Ser Tyr Ala Gly Ser Gly Thr Leu Leu
1 5 10

<210> 2297
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 2297
Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Phe Asn Asn
20 25 30

Asn Ala Ala Trp Ser Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
35 40 45

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Leu Tyr Asp Tyr Ala
50 55 60

Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65 70 75 80

Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95

Tyr Tyr Cys Ala Arg Gly Tyr Ser Ser Ser Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 2298
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 2298
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asn Ile Gly Thr Tyr
20 25 30

Lys Phe Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Val
35 40 45

Met Ile Tyr Glu Val Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Val Ser Tyr Ala Gly Ser
85 90 95

Gly Thr Leu Leu Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 2299
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2299
Thr Tyr Ala Met Asn
1 5

<210> 2300
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2300
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Ala Ser
1 5 10 15

Val Lys Gly

<210> 2301
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2301

His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr
1 5 10

<210> 2302
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2302
Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2303
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2303
Gly Thr Asn Lys Arg Ala Pro
1 5

<210> 2304
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2304
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 2305
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2305
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr
            20   25   30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Ala
    50   55   60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser
65   70   75   80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85   90   95

Tyr Cys Ala Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
            100   105   110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 2306
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 2306
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
1   5   10   15

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
            20   25   30

Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
        35   40   45

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Thr Pro Ala Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val
65 70 75 80

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2307
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2307
Asp Thr Tyr Ile His
1 5

<210> 2308
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 2308
Arg Ile Asp Pro Ala Asn Asp Asn Thr Leu Tyr Ala Ser Lys Phe Gln
1 5 10 15

Gly

<210> 2309
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2309
Gly Tyr Gly Tyr Tyr Val Phe Asp His
1 5

<210> 2310
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2310
Arg Thr Ser Arg Ser Ile Ser Gln Tyr Leu Ala
1 5 10

<210> 2311
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2311
Ser Gly Ser Gly Ser
1 5

<210> 2312
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2312
Gln Gln His Asn Glu Asn Pro Leu Thr
1 5

<210> 2313
<211> 118

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 2313
Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

Tyr Ile His Phe Val Arg Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Arg Ile Asp Pro Ala Asn Asp Asn Thr Leu Tyr Ala Ser Lys Phe
50 55 60

Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

Met His Leu Cys Ser Leu Thr Ser Gly Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Gly Arg Gly Tyr Gly Tyr Tyr Val Phe Asp His Trp Gly Gln Gly Thr
100 105 110

Thr Leu Thr Val Ser Ser
115

<210> 2314
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 2314
Asp Val Gln Ile Asn Gln Ser Pro Ser Phe Leu Ala Ala Ser Pro Gly
1 5 10 15

```
Glu Thr Ile Thr Ile Asn Cys Arg Thr Ser Arg Ser Ile Ser Gln Tyr
            20                  25                  30

Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Thr Asn Lys Leu Leu Ile
        35                  40                  45

Tyr Ser Gly Ser Thr Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Gly Leu Glu Pro
65                  70                  75                  80

Glu Asp Phe Ala Met Tyr Tyr Cys Gln Gln His Asn Glu Asn Pro Leu
                85                  90                  95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Arg
            100                 105
```

<210> 2315
<211> 330
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
wild-type IgG1 sequence

<400> 2315

```
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1               5                   10                  15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                  70                  75                  80
```

```
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
            100                 105                 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
        115                 120                 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
    130                 135                 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145                 150                 155                 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
                165                 170                 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
            180                 185                 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195                 200                 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    210                 215                 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225                 230                 235                 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
                245                 250                 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
            260                 265                 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
        275                 280                 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
    290                 295                 300
```

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 2316
<211> 326
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
wild-type IgG2 sequence

<400> 2316
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1 5 10 15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
100 105 110

Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
115 120 125

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
130 135 140

```
Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
145                 150                 155                 160

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
                165                 170                 175

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
            180                 185                 190

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
        195                 200                 205

Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
    210                 215                 220

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
225                 230                 235                 240

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
                245                 250                 255

Ser Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
            260                 265                 270

Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
        275                 280                 285

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
    290                 295                 300

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
305                 310                 315                 320

Ser Leu Ser Pro Gly Lys
                325
```

<210> 2317
<211> 327
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
wild-type IgG4 sequence

<400> 2317
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1 5 10 15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro
100 105 110

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
115 120 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
130 135 140

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145 150 155 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
165 170 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
180 185 190

```
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
        195                 200                 205


Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
    210                 215                 220


Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225                 230                 235                 240


Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
                245                 250                 255


Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
            260                 265                 270


Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
        275                 280                 285


Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
    290                 295                 300


Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305                 310                 315                 320


Leu Ser Leu Ser Leu Gly Lys
                325


<210> 2318
<211> 110
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
      wild-type IgG1 CH2 sequence

<400> 2318
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
1               5                   10                  15


Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            20                  25                  30
```

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        35   40   45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    50   55   60

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65   70   75   80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                85   90   95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
            100   105   110

<210> 2319
<211> 107
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
      wild-type IgG1 CH3 sequence

<400> 2319
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
1   5   10   15

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
            20   25   30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
        35   40   45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
    50   55   60

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65   70   75   80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
                85   90   95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 2320
<211> 184
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2320
Met Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser
1 5 10 15

Leu Leu His Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr
20 25 30

Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser
35 40 45

Val Lys Gly Thr Asn Ala Ile Leu Trp Thr Cys Leu Gly Leu Ser Leu
50 55 60

Ile Ile Ser Leu Ala Val Phe Val Leu Met Phe Leu Leu Arg Lys Ile
65 70 75 80

Asn Ser Glu Pro Leu Lys Asp Glu Phe Lys Asn Thr Gly Ser Gly Leu
85 90 95

Leu Gly Met Ala Asn Ile Asp Leu Glu Lys Ser Arg Thr Gly Asp Glu
100 105 110

Ile Ile Leu Pro Arg Gly Leu Glu Tyr Thr Val Glu Glu Cys Thr Cys
115 120 125

Glu Asp Cys Ile Lys Ser Lys Pro Lys Val Asp Ser Asp His Cys Phe
130 135 140

Pro Leu Pro Ala Met Glu Glu Gly Ala Thr Ile Leu Val Thr Thr Lys
145 150 155 160

Thr Asn Asp Tyr Cys Lys Ser Leu Pro Ala Ala Leu Ser Ala Thr Glu
165 170 175

Ile Glu Lys Ser Ile Ser Ala Arg
180

<210> 2321
<211> 750
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2321
Met Trp Asn Leu Leu His Glu Thr Asp Ser Ala Val Ala Thr Ala Arg
1 5 10 15

Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly Gly Phe
20 25 30

Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser Ser Asn Glu
35 40 45

Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala Phe Leu Asp Glu
50 55 60

Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu Tyr Asn Phe Thr Gln Ile
65 70 75 80

Pro His Leu Ala Gly Thr Glu Gln Asn Phe Gln Leu Ala Lys Gln Ile
85 90 95

Gln Ser Gln Trp Lys Glu Phe Gly Leu Asp Ser Val Glu Leu Ala His
100 105 110

Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys Thr His Pro Asn Tyr Ile
115 120 125

Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile Phe Asn Thr Ser Leu Phe
130 135 140

```
Glu Pro Pro Pro Pro Gly Tyr Glu Asn Val Ser Asp Ile Val Pro Pro
145                 150                 155                 160

Phe Ser Ala Phe Ser Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr
                165                 170                 175

Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met
            180                 185                 190

Lys Ile Asn Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val
        195                 200                 205

Phe Arg Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly
    210                 215                 220

Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys
225                 230                 235                 240

Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Gly Val Gln Arg Gly
                245                 250                 255

Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro Gly Tyr
            260                 265                 270

Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Glu Ala Val Gly
        275                 280                 285

Leu Pro Ser Ile Pro Val His Pro Ile Gly Tyr Tyr Asp Ala Gln Lys
    290                 295                 300

Leu Leu Glu Lys Met Gly Gly Ser Ala Pro Pro Asp Ser Ser Trp Arg
305                 310                 315                 320

Gly Ser Leu Lys Val Pro Tyr Asn Val Gly Pro Gly Phe Thr Gly Asn
                325                 330                 335

Phe Ser Thr Gln Lys Val Lys Met His Ile His Ser Thr Asn Glu Val
            340                 345                 350

Thr Arg Ile Tyr Asn Val Ile Gly Thr Leu Arg Gly Ala Val Glu Pro
        355                 360                 365
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Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ser Trp Val Phe Gly
    370                 375                 380

Gly Ile Asp Pro Gln Ser Gly Ala Ala Val Val His Glu Ile Val Arg
385                 390                 395                 400

Ser Phe Gly Thr Leu Lys Lys Glu Gly Trp Arg Pro Arg Arg Thr Ile
                405                 410                 415

Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Leu Leu Gly Ser Thr
            420                 425                 430

Glu Trp Ala Glu Glu Asn Ser Arg Leu Leu Gln Glu Arg Gly Val Ala
        435                 440                 445

Tyr Ile Asn Ala Asp Ser Ser Ile Glu Gly Asn Tyr Thr Leu Arg Val
    450                 455                 460

Asp Cys Thr Pro Leu Met Tyr Ser Leu Val His Asn Leu Thr Lys Glu
465                 470                 475                 480

Leu Lys Ser Pro Asp Glu Gly Phe Glu Gly Lys Ser Leu Tyr Glu Ser
                485                 490                 495

Trp Thr Lys Lys Ser Pro Ser Pro Glu Phe Ser Gly Met Pro Arg Ile
            500                 505                 510

Ser Lys Leu Gly Ser Gly Asn Asp Phe Glu Val Phe Phe Gln Arg Leu
        515                 520                 525

Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr Lys Asn Trp Glu Thr Asn
    530                 535                 540

Lys Phe Ser Gly Tyr Pro Leu Tyr His Ser Val Tyr Glu Thr Tyr Glu
545                 550                 555                 560

Leu Val Glu Lys Phe Tyr Asp Pro Met Phe Lys Tyr His Leu Thr Val
                565                 570                 575
```

Ala Gln Val Arg Gly Gly Met Val Phe Glu Leu Ala Asn Ser Ile Val
580 585 590

Leu Pro Phe Asp Cys Arg Asp Tyr Ala Val Val Leu Arg Lys Tyr Ala
595 600 605

Asp Lys Ile Tyr Ser Ile Ser Met Lys His Pro Gln Glu Met Lys Thr
610 615 620

Tyr Ser Val Ser Phe Asp Ser Leu Phe Ser Ala Val Lys Asn Phe Thr
625 630 635 640

Glu Ile Ala Ser Lys Phe Ser Glu Arg Leu Gln Asp Phe Asp Lys Ser
645 650 655

Asn Pro Ile Val Leu Arg Met Met Asn Asp Gln Leu Met Phe Leu Glu
660 665 670

Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg
675 680 685

His Val Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser
690 695 700

Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Glu Ser Lys Val Asp
705 710 715 720

Pro Ser Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Tyr Val Ala Ala
725 730 735

Phe Thr Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala
740 745 750

<210> 2322
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
6xHis tag

<400> 2322

His His His His His His
1   5

<210> 2323
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 2323
Asp Tyr Lys Asp Asp Asp Asp Lys
1   5