Innovation, Sciences et Développement économique Canada
Office de la Propriété Intellectuelle du Canada

Innovation, Science and Economic Development Canada
Canadian Intellectual Property Office

CA 3089333 C 2023/10/10

(11)(21) **3 089 333**

(12) **BREVET CANADIEN**
CANADIAN PATENT

(13) **C**

(86) **Date de dépôt PCT/PCT Filing Date:** 2019/03/26
(87) **Date publication PCT/PCT Publication Date:** 2019/10/03
(45) **Date de délivrance/Issue Date:** 2023/10/10
(85) **Entrée phase nationale/National Entry:** 2020/07/22
(86) **N° demande PCT/PCT Application No.:** US 2019/024077
(87) **N° publication PCT/PCT Publication No.:** 2019/191100
(30) **Priorités/Priorities:** 2018/03/26 (US62/648,373); 2018/09/21 (US62/734,994)

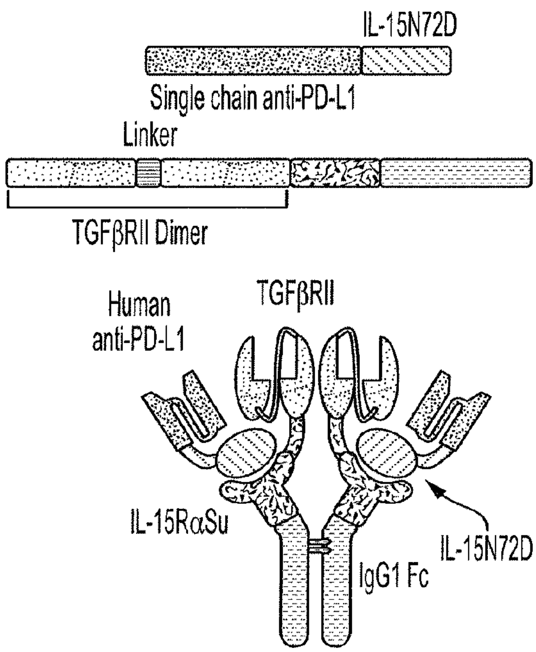
(51) **Cl.Int./Int.Cl.** ***A61K 38/00*** (2006.01), ***A61K 38/20*** (2006.01), ***A61P 35/00*** (2006.01), ***C07K 14/54*** (2006.01), ***C07K 19/00*** (2006.01), ***C12N 15/62*** (2006.01)

(72) **Inventeurs/Inventors:**
LI, QIONGZHEN, US;
ZHU, XIAOYUN, US;
WONG, HING C., US

(73) **Propriétaire/Owner:**
ALTOR BIOSCIENCE LLC, US

(74) **Agent:** SMART & BIGGAR LP

(54) **Titre : MOLECULES D'ASSOCIATION AU RECEPTEUR DU TGF-BETA, IL-15 ET ANTI-PDL1**
(54) **Title: ANTI-PDL1, IL-15 AND TGF-BETA RECEPTOR COMBINATION MOLECULES**



(57) **Abrégé/Abstract:**
The invention features multi- specific protein complexes with one domain comprising IL-15 or a functional variant, a cytokine receptor or cytokine ligand, and a binding domain specific to a disease antigen, immune checkpoint or signaling molecule.

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
03 October 2019 (03.10.2019)

WIPO | PCT

(10) International Publication Number
WO 2019/191100 A1

(51) International Patent Classification:
A61K 38/00 (2006.01) *C07K 14/54* (2006.01)
A61K 38/20 (2006.01) *C07K 19/00* (2006.01)
A61P 35/00 (2006.01) *C12N 15/62* (2006.01)

(21) International Application Number: PCT/US2019/024077

(22) International Filing Date: 26 March 2019 (26.03.2019)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
62/648,373 26 March 2018 (26.03.2018) US
62/734,994 21 September 2018 (21.09.2018) US

(71) Applicant: **ALTOR BIOSCIENCE LLC** [US/US]; 2810 North Commerce Parkway, Miramar, FL 33025 (US).

(72) Inventors: **LI, Qiongzhen**; 1435 NW 208th Terrace, Pembroke Pines, FL 33029 (US). **ZHU, Xiaoyun**; 2966 Wentworth Street, Weston, FL 33332 (US). **WONG, Hing, C.**; 2966 Wentworth Street, Weston, FL 33332 (US).

(74) Agent: **CORLESS, Peter, F.** et al.; Mintz Levin Cohn Ferris Glovsky and Popeo, P.C., One Financial Center, Boston, MA 02111 (US).

(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JO, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Published:
— *with international search report (Art. 21(3))*

(54) **Title:** ANTI-PDL1, IL-15 AND TGF-BETA RECEPTOR COMBINATION MOLECULES

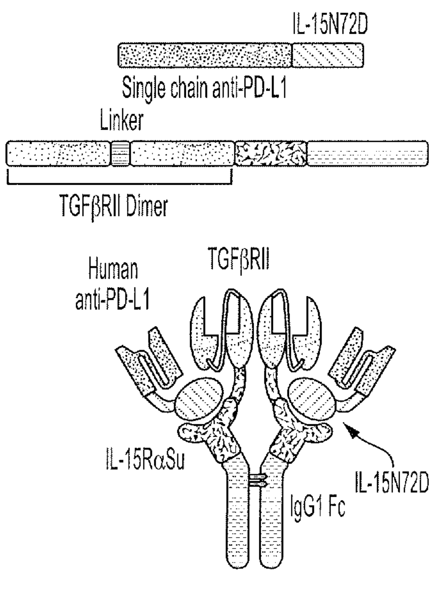


FIG. 1

(57) **Abstract:** The invention features multi- specific protein complexes with one domain comprising IL-15 or a functional variant, a cytokine receptor or cytokine ligand, and a binding domain specific to a disease antigen, immune checkpoint or signaling molecule.

WO 2019/191100 A1

ANTI-PDL1, IL-15 AND TGF-BETA RECEPTOR COMBINATION MOLECULES

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of priority to U.S. Provisional Application No. 62/648,373 filed March 26, 2018, and U.S. Provisional Application No. 62/734,994 filed September 21, 2018.

FIELD OF THE INVENTION

This invention relates generally to the field of multimeric fusion molecules.

BACKGROUND OF THE INVENTION

Cancer immunotherapy studies have now demonstrated promising clinical response rates in patients with melanoma and subsets of patients with other solid tumors. Those studies have involved monoclonal antibody (MAb) checkpoint inhibitors such as anti-CTLA4, anti–programmed cell death-1 (PD-1), and anti–programmed cell death protein-1 ligand (PD-L1), as well as cytokines such as IL-2 and IL-15.[1-5]

Most antibodies directed against PD-1/PD-L1 are of the IgG4 isotype, or of the IgG1 isotype engineered with an Fc domain mutation to impair antibody dependent cellular cytotoxicity (ADCC) activity. Multiple anti-cancer MAbs, such as anti-CTLA4 (ipilimumab), anti-CD20 (rituximab), anti-HER2 (trastuzumab, pertuzumab), and anti-EGFR (cetuximab), however, are of the IgG1 isotype, and thus have the potential to mediate ADCC. The ADCC mechanism has been implicated to contribute to clinical efficacy,[9-11] although other studies have not supported this finding. Atezolizumab (TECENTRIQ®, Genentech) and avelumab (BAVENCIO®, EMD Serono) are fully human anti-PD-L1 therapies of the IgG1 isotype that have been FDA approved for the treatment of non-small cell lung cancer (NSCLC), bladder cancer, urothelial cancer, and metastatic Merkel cell carcinoma.[12-15]

Since PD-L1 is expressed on some immune cells, studies were conducted to evaluate avelumab-mediated ADCC using whole peripheral blood mononuclear cells (PBMC) as targets. Using natural killer (NK) cells from healthy donors and cancer patients, substantial lysis of a range of human tumor cell types was observed, with little or no lysis when human PBMC subsets were used as targets. Similar results were also seen in the analysis of 123 immune cell subsets from PBMC of patients treated with up to nine doses of avelumab.[13,16]

Date Reçue/Date Received 2021-09-16

Moreover, while clinical benefit of using avelumab has been observed in a range of human tumors, adverse events beyond those seen with other anti-PD1/PD-L1 MAbs have not been observed.[3,14,17,18]

Despite the promising results described above, only 10-30% of patients with most carcinomas achieve objective responses when treated with anti-PD-1/PD-L1 monotherapies, even in trials that enrolled only those patients whose pre-treatment tumor specimens expressed PD-L1.[19]

Prior to the invention described herein, there was a pressing need to develop new strategies to target various effector molecules to a disease site to provide therapeutic benefit without the side effects associated with non-specific immune activity.

SUMMARY

The invention is based, at least in part, on the surprising discovery that multi-specific IL-15-based protein complexes enhance the stimulation of immune cells and promote their activity against disease cells, thereby resulting in reduction or prevention of disease. These IL-15-based protein complexes also show increased binding to disease and target antigens. Provided herein are multi-specific protein complexes with at least one domain comprising IL-15 or a functional variant, a transforming growth factor-beta receptor type 2 (TGFβRII) domain, and a binding domain specific to a disease antigen, immune checkpoint or signaling molecule. In particular, the complexes comprise an IL-15N72D:IL-15RαSu/Fc scaffold fused to an antibody or antibody binding fragment and a TGFβRII domain which binds transforming growth factor-beta (TGFβ). Specifically, described herein are protein complexes comprising binding domains that specifically bind to programmed death ligand 1 (PD-L1), programmed death 1 (PD-1), cytotoxic T-lymphocyte associated protein 4 (CTLA-4), cluster of differentiation 47 (CD47), T-cell immunoglobulin and mucin-domain containing-3 (TIM-3, TIM3) or glucocorticoid-induced tumor necrosis factor receptor (TNFR) family related gene (GITR). These complexes augment immune activity by providing immunostimulatory cytokines to the immune cells. Such cytokines are known in the art and can be used alone or in combination with other cytokines or agents. These complexes further augment immune responses through immune checkpoint blockade via the anti-PD-L1, PD-1, CTLA-4, CD47, TIM3 or GITR binding domains. Finally, the complexes can bind TGFβ and block its immunosuppressive activities that in turn promote tumor growth and metastasis and other diseases.

In some cases, these complexes also recognize antigens, such as PD-L1, single stranded deoxyribonucleic acid (ssDNA), CD20, human epidermal growth factor receptor 2 (HER2), epidermal growth factor receptor (EGFR), CD19, CD38, CD52, disialoganglioside (GD2), CD33, Notch1, intercellular adhesion molecule 1 (ICAM-1), tissue factor or HIV envelope, expressed on disease cells and stimulate antibody-dependent cell-mediated cytotoxicity (ADCC) and complement-dependent cytotoxicity (CDC) against the disease cell via the Fc binding domain.

Provided is an isolated soluble fusion protein complex comprising at least two soluble proteins. For example, the first protein comprises an interleukin-15 (IL-15) polypeptide, e.g., a variant IL-15 polypeptide comprising an N72D mutation (IL-15N72D). The second protein comprises a soluble IL-15 receptor alpha sushi-binding domain (IL-15RαSu) fused to an immunoglobulin Fc domain (IL-15RαSu/Fc). A third component of the isolated soluble fusion protein complex comprises a binding domain that recognizes a disease antigen, immune checkpoint molecule or a signaling molecule, e.g., PD-L1, PD-1, CTLA-4, CD47, TIM3 or GITR, wherein the binding domain is fused to the either the IL-15N72D or the IL-15RαSu/Fc protein. A fourth component of the soluble fusion immune complex comprises a cytokine receptor, e.g. TGFβRII, or cytokine. In some aspects, these binding domains are fused to both the IL-15N72D and IL-15RαSu/Fc proteins. In other aspects, one of these binding domains is fused to the IL-15N72D or the IL-15RαSu/Fc proteins and a second binding domain, i.e. specific to an immune checkpoint or signaling molecule or a disease antigen, is fused to the same or other protein. In some aspects, the cytokine receptor, e.g. TGFβRII, is fused to the IL-15N72D and/or IL-15RαSu/Fc proteins. In some aspects the cytokine receptor, e.g. TGFβRII, is fused or linked to the IgG1 Fc via a linker molecule. In another aspect, the cytokine receptor, e.g. TGFβRII, is a dimer fused to IL-15N72D and IL-15RαSu/Fc proteins. In one aspect, the disease antigen is associated with neoplasia, infectious disease, or autoimmune disease. In some cases, the first and/or second soluble protein further comprises a binding domain that recognizes a disease antigen, e.g., PD-L1, ssDNA, CD20, HER2, EGFR, CD19, CD38, CD52, GD2, CD33, Notch1, intercellular adhesion molecule 1 (ICAM-1), tissue factor or HIV envelope or other known antigens, expressed on disease cells. Alternatively, either the IL-15N72D or the IL-15RαSu/Fc protein comprise the binding domain specific to a disease antigen, immune checkpoint or signaling molecule and the other protein (IL-15RαSu/Fc or IL-15N72D protein, respectively) do not comprise an additional fused binding domain. The IL-15N72D domain of the first protein binds to the soluble IL-

15RαSu domain of the second protein to form a soluble fusion protein complex. An exemplary fusion protein complex comprises an anti-PD-L1 antibody covalently linked to an IL-15N72D and/or an IL-15RαSu/Fc fusion protein. In other aspects, a cytokine receptor, e.g. TGFβRII, and/or the binding domain are covalently linked to a soluble IL-15 receptor alpha sushi-binding domain (IL-15RαSu) fused to an immunoglobulin Fc domain whereas the second protein comprises a binding domain that recognizes disease antigens covalently linked and a variant interleukin-15 (IL-15) polypeptide comprising an N72D mutation (IL-15N72D). In another aspect, the second protein comprises a cytokine receptor, e.g. TGFβRII.

In certain embodiments, an isolated soluble fusion protein complex comprises at least two soluble proteins, wherein a first soluble protein comprises an interleukin-15 (IL-15) polypeptide domain and a second soluble protein comprises a soluble IL-15 receptor alpha sushi-binding domain (IL-15RαSu) fused to an immunoglobulin Fc domain, wherein the immunoglobulin Fc (IgG Fc) domain is fused or linked to a glycosylate or an aglycosylated transforming growth factor-beta receptor type 2 (TGFβRII) domain; the first and/or second soluble protein further comprises a binding domain that specifically binds to a disease antigen, immune checkpoint molecule or immune signaling molecule, and the IL-15 domain of the first soluble protein binds to the IL-15RαSu domain of the second soluble protein to form a soluble fusion protein complex. An example of an aglycosylated TGFβRII amino acid sequence is as follows:

IPPHVQKSVNNDMIVTDNNGAVKFPQLCKFCDVRFSTCDNQKSCMQNCPITSICEKP
QEVCVAVWRKQDENITLETVCHDPKLPYHDFILEDAASPKCIMKEKKKPGETFFMCS
CSSDECNDNIIFSEEYQTSNPD (SEQ ID NO: 35).

In this and other embodiments, the immunoglobulin Fc domain is linked to a transforming growth factor-beta receptor type 2 (TGFβRII) domain via a linker molecule. In these and other embodiments, the immunoglobulin Fc domain is an IgG Fc variant comprising a hinge region lacking a free cysteine at residue position 70. In certain embodiments, the cysteine is substituted with a serine at residue position 70 (IgGFcC70S). An example of Δfree cysteine IL15RαSuFc amino acid sequence is as follows:

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWT
TPSLKCIREPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA

VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK (SEQ ID NO: 36).

In certain embodiments, the immunoglobulin Fc domain is an IgG-Fc variant lacking a hinge region. For example, the IL15RαSuFc lacks the amino acid residues EPKSC at positions 66 to 70. An example of Δhinge IL15RαSuFc amino acid sequence is as follows:

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWT TPSLKCIR~~EPKSC~~DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK (SEQ ID NO: 37)

In these and other embodiments, one of the first or second soluble protein further comprises a second binding domain that specifically binds to a disease antigen, immune checkpoint molecule, or immune signaling molecule. In these and other embodiments, the IL-15 polypeptide is an IL-15 variant comprising an N72D mutation (IL-15N72D), an IL-15K41Q mutation, an IL-15L45S mutation, an IL-15I67T mutation, an IL-15N79Ymutation, an IL-15E93A mutation or combinations thereof. An example of IL-15-K41Q, L45S, I67T, N79Y, E93A amino acid sequence is as follows:

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMQCFLSELQVISLESGDAS IHDTVENLTILANDSLSSNGYVTESGCKECEELEAKNIKEFLQSFVHIVQMFINTS (SEQ ID NO: 38).

In certain embodiments, the IL-15 polypeptide is an IL-15 variant comprising an L45S mutation. An example of IL15-L45S amino acid sequence is as follows:

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLSELQVISLESGDAS IHDTVENLIILANDSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS (SEQ ID NO: 39).

In certain embodiments, the binding domain comprises an immunoglobulin light chain variable domain covalently linked to an immunoglobulin heavy chain variable domain by a polypeptide linker sequence. In these and other embodiments, the binding domain specifically binds to one or more molecules comprising: programmed death ligand 1 (PD-L1), programmed death 1 (PD-1), cytotoxic T-lymphocyte associated protein 4 (CTLA-4), cluster of differentiation 33 (CD33), cluster of differentiation 47 (CD47), glucocorticoid-induced tumor necrosis factor receptor (TNFR) family related gene (GITR), lymphocyte function-associated antigen 1 (LFA-1), tissue factor (TF), delta-like protein 4 (DLL4), single strand DNA or T-cell immunoglobulin and mucin-domain containing-3 (Tim-3). In certain embodiments, the binding domain specifically binds to one or more molecules comprising: programmed death ligand 1 (PD-L1). In these and other embodiments, the TGFβRII domain binds to transforming factor beta (TGFβ). In these and other embodiments, the first fusion protein complex is covalently linked to a second fusion protein complex by a disulfide bond linking the Fc domain of the first soluble fusion protein complex to the Fc domain of the second soluble fusion protein complex.

In certain embodiments, an isolated soluble fusion protein complex comprises at least two soluble proteins, wherein a first soluble protein comprises an interleukin-15 (IL-15) polypeptide domain and a second soluble protein comprises a soluble IL-15 receptor alpha sushi-binding domain (IL-15RαSu) fused to an immunoglobulin Fc domain, the first and/or second soluble protein further comprises a binding domain that specifically binds to a disease antigen, immune checkpoint molecule or immune signaling molecule, and the IL-15 domain of the first soluble protein binds to the IL-15RαSu domain of the second soluble protein to form a soluble fusion protein complex. In certain embodiments, the immunoglobulin Fc (IgG Fc) domain further comprises a glycosylate or an aglycosylated transforming growth factor-beta receptor type 2 (TGFβRII) domain which is fused or linked to the IgG Fc domain via a linker molecule. In certain embodiments, the immunoglobulin Fc (IgG Fc) domain lacks the TGFβRII domain. In these and other embodiments, the immunoglobulin Fc domain is an IgG Fc variant comprising a hinge region lacking a free cysteine at residue position 70. In these and other embodiments, the cysteine is substituted with a serine at residue position 70 (IgG-FcC70S). In these and other embodiments, the immunoglobulin Fc domain is an IgG-Fc variant lacking a hinge region.In these and other embodiments, one of the first or second soluble protein further comprises a second binding domain that specifically binds to a disease antigen, immune checkpoint molecule, or immune signaling molecule. In these and other embodiments, the IL-15 polypeptide is an IL-15 variant comprising an N72D mutation (IL-15N72D), an IL-15K41Q mutation, an IL-15L45S mutation, an IL-15I67T mutation, an IL-15N79Ymutation, an IL-15E93A mutation or combinations thereof. In these and other embodiments, the binding domain comprises an immunoglobulin light chain variable domain covalently linked to an immunoglobulin heavy chain variable domain by a polypeptide linker sequence. In these and other embodiments, the binding domain specifically binds to one or more molecules comprising: programmed death ligand 1 (PD-L1), programmed death 1 (PD-1), cytotoxic T-lymphocyte associated protein 4 (CTLA-4), cluster of differentiation 33 (CD33), cluster of differentiation 47 (CD47), glucocorticoid-induced tumor necrosis factor receptor (TNFR) family related gene (GITR), lymphocyte function-associated antigen 1 (LFA-1), tissue factor (TF), delta-like protein 4 (DLL4), single strand DNA or T-cell immunoglobulin and mucin-domain containing-3 (Tim-3). In certain embodiments, the binding domain specifically binds to one or more molecules comprising: programmed death ligand 1 (PD-L1). In certain embodiments, the first fusion protein complex is covalently linked to a second fusion protein complex by a disulfide bond linking the Fc domain of the first soluble fusion protein complex to the Fc domain of the second soluble fusion protein complex.

In certain embodiments, the binding domain comprises a single chain antibody (scAb or scFv) wherein an immunoglobulin light chain variable domain is covalently linked to an immunoglobulin heavy chain variable domain by a polypeptide linker sequence. Alternatively, the binding domain comprises a soluble or extracellular ligand or receptor domain capable of acting as an immune checkpoint inhibitor or immune agonist.

Exemplary polynucleotide molecules comprise nucleic acid sequences comprising SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 16, 17, 18, 19 or combinations thereof. In one aspect, the nucleic acid sequence(s) further comprises a promoter, translation initiation signal, and leader sequence operably linked to the sequence encoding the fusion protein. In certain embodiments, an expression vector compres a nucleic acid sequence comprising SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 16, 17, 18, 19 or combinations thereof.

Exemplary polypeptide molecules comprise amino acid sequences comprising SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34 or combinations thereof.

In some embodiments, the isolated soluble fusion protein complexes are encoded by a nucleic acid sequence that has at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to SEQ ID NO: 1.

In some embodiments, the isolated soluble fusion protein complexes are encoded by a nucleic acid sequence that has at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to SEQ ID NO: 3.

In some embodiments, the isolated soluble fusion protein complexes are encoded by a nucleic acid sequence that has at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to SEQ ID NO: 5.

In some embodiments, the isolated soluble fusion protein complexes are encoded by a nucleic acid sequence that has at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to SEQ ID NO: 7.

In some embodiments, the isolated soluble fusion protein complexes are encoded by a nucleic acid sequence that has at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to SEQ ID NO: 9.

In some embodiments, the isolated soluble fusion protein complexes are encoded by a nucleic acid sequence that has at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to SEQ ID NO: 11.

In some embodiments, the isolated soluble fusion protein complexes are encoded by a nucleic acid sequence that has at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to SEQ ID NO: 13.

In some embodiments, the isolated soluble fusion protein complexes are encoded by a nucleic acid sequence that has at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to SEQ ID NO: 15.

In some embodiments, the isolated soluble fusion protein complexes are encoded by a nucleic acid sequence that has at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to SEQ ID NO: 16.

In some embodiments, the isolated soluble fusion protein complexes are encoded by a nucleic acid sequence that has at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to SEQ ID NO: 17.

In some embodiments, the isolated soluble fusion protein complexes are encoded by a nucleic acid sequence that has at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to SEQ ID NO: 18.

In some embodiments, the isolated soluble fusion protein complexes are encoded by a nucleic acid sequence that has at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to SEQ ID NO: 19.

Also provided are expression vector(s) comprising the nucleic acid sequences described herein. For example, the nucleic acid sequence is in a vector for replication, expression, or both.

In some embodiments, the isolated soluble fusion protein complexes comprise an amino acid sequence having at least about 70% (such as at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater) sequence identity to SEQ ID NO: 2.

In some embodiments, the isolated soluble fusion protein complexes comprise an amino acid sequence having at least about 70% (such as at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater) sequence identity to SEQ ID NO: 4.

In some embodiments, the isolated soluble fusion protein complexes comprise an amino acid sequence having at least about 70% (such as at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater) sequence identity to SEQ ID NO: 6.

In some embodiments, the isolated soluble fusion protein complexes comprise an amino acid sequence having at least about 70% (such as at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater) sequence identity to SEQ ID NO: 8.

In some embodiments, the isolated soluble fusion protein complexes comprise an amino acid sequence having at least about 70% (such as at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater) sequence identity to SEQ ID NO: 10.

In some embodiments, the isolated soluble fusion protein complexes comprise an amino acid sequence having at least about 70% (such as at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater) sequence identity to SEQ ID NO: 12.

In some embodiments, the isolated soluble fusion protein complexes comprise an amino acid sequence having at least about 70% (such as at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater) sequence identity to SEQ ID NO: 14.

In some embodiments, the isolated soluble fusion protein complexes comprise an amino acid sequence having at least about 70% (such as at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater) sequence identity to SEQ ID NO: 20.

In some embodiments, the isolated soluble fusion protein complexes comprise an amino acid sequence having at least about 70% (such as at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater) sequence identity to SEQ ID NO: 21.

In some embodiments, the isolated soluble fusion protein complexes comprise an amino acid sequence having at least about 70% (such as at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater) sequence identity to SEQ ID NO: 22.

In some embodiments, the isolated soluble fusion protein complexes comprise an amino acid sequence having at least about 70% (such as at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater) sequence identity to SEQ ID NO: 23.

In some embodiments, the isolated soluble fusion protein complexes comprise an amino acid sequence having at least about 70% (such as at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater) sequence identity to SEQ ID NO: 24.

In some embodiments, the isolated soluble fusion protein complexes comprise an amino acid sequence having at least about 70% (such as at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater) sequence identity to SEQ ID NO: 25.

In some embodiments, the isolated soluble fusion protein complexes comprise an amino acid sequence having at least about 70% (such as at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater) sequence identity to SEQ ID NO: 26.

In some embodiments, the isolated soluble fusion protein complexes comprise an amino acid sequence having at least about 70% (such as at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater) sequence identity to SEQ ID NO: 27.

In some embodiments, the isolated soluble fusion protein complexes comprise an amino acid sequence having at least about 70% (such as at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater) sequence identity to SEQ ID NO: 28.

In some embodiments, the isolated soluble fusion protein complexes comprise an amino acid sequence having at least about 70% (such as at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater) sequence identity to SEQ ID NO: 29.

In some embodiments, the isolated soluble fusion protein complexes comprise an amino acid sequence having at least about 70% (such as at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater) sequence identity to SEQ ID NO: 302.

In some embodiments, the isolated soluble fusion protein complexes comprise an amino acid sequence having at least about 70% (such as at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater) sequence identity to SEQ ID NO: 31.

In some embodiments, the isolated soluble fusion protein complexes comprise an amino acid sequence having at least about 70% (such as at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater) sequence identity to SEQ ID NO: 32.

In some embodiments, the isolated soluble fusion protein complexes comprise an amino acid sequence having at least about 70% (such as at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater) sequence identity to SEQ ID NO: 33.

In some embodiments, the isolated soluble fusion protein complexes comprise an amino acid sequence having at least about 70% (such as at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater) sequence identity to SEQ ID NO: 34.

Also provided is a soluble fusion protein complex comprising a first soluble fusion protein complex covalently linked to a second soluble fusion protein complex. For example, the soluble fusion protein complexes of the invention are multimerized, e.g., dimerized, trimerized, or otherwise multimerized (e.g., 4 complexes, 5 complexes, etc.). For example, the multimers are homomultimers or heteromultimers. The soluble fusion protein complexes are joined by covalent bonds, e.g., disulfide bonds, chemical cross-linking agents. In some cases, one soluble fusion protein is covalently linked to another soluble fusion protein by a disulfide bond linking the Fc domain of the first soluble protein to the Fc domain of the second soluble protein.

The Fc domain or functional fragment thereof includes an Fc domain selected from the group consisting of IgG Fc domain, human IgG1 Fc domain, human IgG2 Fc domain, human IgG3 Fc domain, human IgG4 Fc domain, IgA Fc domain, IgD Fc domain, IgE Fc domain, and IgM Fc domain; mouse IgG2A domain, or any combination thereof. Optionally, the Fc domain includes an amino acid change that results in an Fc domain with altered complement or Fc receptor binding properties or altered dimerization or glycosylation profiles. Amino acid changes to produce an Fc domain with altered complement or Fc receptor binding properties or altered dimerization or glycosylation profiles are known in the art. For example, a substitution of leucine residues at positions 234 and 235 of the IgG1 CH2 (numbering based on antibody consensus sequence) (i.e., … P E L L G G …) with alanine residues (i.e., … P E A A G G …) results in a loss of Fc gamma receptor binding, whereas the substitution of the lysine residue at position 322 of the IgG1 CH2 (numbering based on antibody consensus sequence) (i.e., … K C K S L …) with an alanine residue (i.e., … K C A S L …) results in a loss of complement activation. In some examples, such mutations are combined.

In some aspects, the binding domain and/or the cytokine receptor domain are covalently linked to an IL-15 polypeptide (or functional fragment thereof) by a polypeptide linker sequence. Similarly, the binding domain and/or the cytokine receptor domain are covalently linked to an IL-15Rα polypeptide (or functional fragment thereof) by polypeptide linker sequence. Optionally, the IL-15Rα polypeptide (or functional fragment thereof) is covalently linked to the Fc domain (or functional fragment thereof) by polypeptide linker sequence. Each polypeptide linker sequence can be selected independently. Optionally, the polypeptide linker sequences are the same. Alternatively, they are different.

Optionally, the soluble fusion protein complexes of the invention are provided wherein at least one of the soluble fusion proteins comprise a detectable label. Detectable labels include, but are not limited to, biotin, streptavidin, an enzyme, or catalytically active fragment thereof, a radionuclide, a nanoparticle, a paramagnetic metal ion, or a fluorescent, phosphorescent, or chemiluminescent molecule, or any combination thereof.

The invention provides method for making the soluble fusion protein complexes of the invention. The method includes the steps of: a) introducing into a first host cell a DNA vector with appropriate control sequences encoding the first protein, b) culturing the first host cell in media under conditions sufficient to express the first protein in the cell or the media; c) purifying the first protein from the host cells or media, d) introducing into a second host cell a DNA vector with appropriate control sequences encoding the second protein, e) culturing the second host cell in media under conditions sufficient to express the second protein in the cell or the media; and f) purifying the second protein from the host cells or media, and g) mixing the first and second proteins under conditions sufficient to allow binding between IL-15 domain of a first protein and the soluble IL-15Rα domain of a second protein to form the soluble fusion protein complex.

In some cases, the method further includes mixing the first and second protein under conditions sufficient to allow formation of a disulfide bond between the polypeptides expressed from the expression vectors.

Alternatively, methods for making soluble fusion protein complexes of the invention are carried out by a) introducing into a host cell a DNA vector with appropriate control sequences encoding the first protein and a DNA vector with appropriate control sequences encoding the second protein, b) culturing the host cell in media under conditions sufficient to express the proteins in the cell or the media and allow association between IL-15 domain of a first protein and the soluble IL-15Rα domain of a second protein to form the soluble fusion protein complex; and c) purifying the soluble fusion protein complex from the host cells or media.

In one aspect, the method further includes mixing the first and second protein under conditions sufficient to allow formation of a disulfide bond between the polypeptides expressed from the expression vectors.

Also provided are methods for making soluble fusion protein complexes comprising a) introducing into a host cell a DNA vector with appropriate control sequences encoding the first and second proteins, b) culturing the host cell in media under conditions sufficient to express the proteins in the cell or the media and allow association between IL-15 domain of a first protein and the soluble IL-15Rα domain of a second protein to form the soluble fusion protein complex, and to allow formation of a disulfide bond between the polypeptides; and c) purifying the soluble fusion protein complex from the host cells or media.

Optionally, the method further includes mixing the first and second protein under conditions sufficient to allow formation of a disulfide bond between the polypeptides expressed from the expression vectors.

Methods for treating a neoplasia, infectious disease, or autoimmune disease in a subject in need thereof are carried out by administering to a subject an effective amount of a pharmaceutical composition comprising a soluble fusion protein complex described herein, e.g., a soluble anti-PD-L1 scAb/IL-15N72D:TGFβRII/IL-15RαSu/Fc fusion protein complex, thereby treating the neoplasia, infectious disease, or autoimmune disease. For example, methods for treating solid or hematological malignancies in a subject in need thereof are carried out by administering to a subject an effective amount of a pharmaceutical composition comprising a soluble TGFβRII dimer/huIL-15N72D:anti-human PD-L1 scAb/huIL-15RαSu/huIgG1 Fc fusion protein complex, thereby treating the malignancy.

Suitable neoplasias for treatment with the methods described herein include a glioblastoma, prostate cancer, acute myeloid leukemia, B-cell neoplasm, multiple myeloma, B-cell lymphoma, B cell non-Hodgkin's lymphoma, Hodgkin's lymphoma, chronic lymphocytic leukemia, acute myeloid leukemia, cutaneous T-cell lymphoma, T-cell lymphoma, a solid tumor, urothelial/bladder carcinoma, melanoma, lung cancer, renal cell carcinoma, breast cancer, gastric and esophageal cancer, head and neck cancer, prostate cancer, pancreatic cancer, colorectal cancer, ovarian cancer, non-small cell lung carcinoma, and squamous cell head and neck carcinoma.

The pharmaceutical composition comprising a fusion protein complex is administered in an effective amount. For example, an effective amount of the pharmaceutical composition is between about 1 μg/kg and 100 μg/kg, e.g., 1, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100 μg/kg. Alternatively, TxM complex is administered as a fixed dose or based on body surface area (i.e., per m^2).

The pharmaceutical composition comprising the fusion protein complex is administered at least one time per month, e.g., twice per month, once per week, twice per week, once per day, twice per day, every 8 hours, every 4 hours, every 2 hours, or every hour. Suitable modes of administration for the pharmaceutical composition include systemic administration, intravenous administration, local administration, subcutaneous administration, intramuscular administration, intratumoral administration, inhalation, and intraperitoneal administration.

Preferably, the fusion protein complex increases serum levels of interferon gamma (IFN-γ), and/or stimulates $CD4^+$ and $CD8^+$ T cells and NK cells to kill diseased cells or tumor cells in a subject.

In certain embodiments, a method of inducing antibody-dependent cell-mediated cytotoxicity (ADCC) or antibody-dependent cell-mediated phagocytosis (ADCP) in a subject in need thereof is provided for, comprising administering to a subject in need thereof, an effective amount of a soluble fusion protein complex embodied herein.

In certain embodiments, a method of inhibiting transforming growth factor beta (TGFβ) activity *in vitro* or *in vivo*, comprising contacting a TGFβ-responsive cell *in vitro* or administering to a subject in need thereof, an effective amount of a soluble fusion protein complex embodied herein.

In certain embodiments, a method of decreasing the amount of transforming growth factor beta (TGFβ) *in vivo*, comprising administering to a subject in need thereof, an effective amount of a soluble fusion protein complex embodied herein.

In certain embodiments, a method of inhibiting transforming growth factor beta (TGFβ) mediated phosphorylation and activation of SMAD polypeptides *in vivo*, comprising administering to a subject in need thereof, a therapeutically effective amount of a soluble fusion protein complex embodied herein.

In certain aspects of the soluble fusion protein complexes of the invention, the IL-15 polypeptide is an IL-15 variant having a different amino acid sequence than native IL-15 polypeptide. The human IL-15 polypeptide is referred to herein as huIL-15, hIL-15, huIL15, hIL15, IL-15 wild type (wt), and variants thereof are referred to using the native amino acid, its position in the mature sequence and the variant amino acid. For example, huIL15N72D refers to human IL-15 comprising a substitution of N to D at position 72. In one aspect, the IL-15 variant functions as an IL-15 agonist as demonstrated, e.g., by increased binding activity for the IL-15/IL-2 $\beta\gamma_C$ receptors (IL-15R) compared to the native IL-15 polypeptide. Alternatively, the IL-15 variant functions as an IL-15 antagonist as demonstrated by e.g., decreased binding activity for the IL-15R compared to the native IL-15 polypeptide.

Methods for killing a target cell are carried out by a) contacting a plurality of cells with a soluble fusion protein complex of the invention, wherein the plurality of cells further include immune cells bearing the IL-15R chains recognized by the IL-15 domain, or immune cells bearing checkpoint and/or cytokine receptors or signaling molecules modulated by the checkpoint inhibitor, TGFβ molecules or immune agonist binding domains, and the target disease cells; b) activating the immune cells via the IL-15R or signaling molecules, via inhibiting TGFβ immunosuppression or via blockade of the checkpoint molecules; and c) killing the target disease cells by the activated immune cells. For example, the target disease cells are tumor cells, autoimmune cells, or virally infected cells. In some cases, the binding domain comprises an anti-PD-L1 antibody.

Methods for killing a target cell further comprise a) contacting a plurality of cells with a soluble fusion protein complex of the invention, wherein the plurality of cells further include immune cells bearing Fc receptor chains recognized by the Fc domain, and the target disease cells bearing an antigen recognized by binding domain such as an antigen-specific scab and/or a immunostimulatory cytokines or receptors thereof; b) forming a specific binding complex (bridge) between the antigen on the target disease cells and Fc receptor chains on the immune cells and an immunostimulatory cytokines or receptors thereof sufficient to bind and activate the immune cells; and c) killing the target disease cells by the bound activated immune cells. For example, the target disease cells are tumor cells, autoimmune cells, or virally infected cells. In some cases, the binding domain comprises an anti-PD-L1 antibody.

Also provided are methods for preventing or treating disease in a patient, the method including the steps of: a) administering to the patient a soluble fusion protein complex of the invention; b) activating the immune cells in the patient; and c) damaging or killing the disease cells via the activated immune cells sufficient to prevent or treat the disease in the patient.

The invention also provides methods for preventing or treating disease in a patient in the method including the steps of: a) mixing immune cells bearing IL-15R chains, cytokine receptors and/ or checkpoint or signaling molecules with a soluble fusion protein complex of the invention; b) activating the immune cells; c) administering to the patient the activated immune cells; and d) damaging or killing the disease cells via the activated immune cells sufficient to prevent or treat the disease in the patient. The immune cells can also be contacted with specific antigen to expand the number of activated immune cells.

Administration of the fusion protein complexes of the invention induces an immune response in a subject. For example, administration of the fusion protein complexes of the invention induces an immune response against cells associated with neoplasia, infectious disease, or autoimmune disease. In one aspect, the fusion protein complex of the invention increases immune cell proliferation.

The invention provides methods of stimulating immune responses in a mammal by administering to the mammal an effective amount of the soluble fusion protein complex of the invention. The invention also provides methods of suppressing immune responses in a mammal by administering to the mammal an effective amount of the soluble fusion protein complex of any one of the invention.

In one aspect, the invention provides an isolated soluble fusion protein complex comprising at least a first soluble protein and a second soluble protein, wherein the first soluble protein has at least 85% sequence identity to the amino acid sequence of SEQ ID NO:2, and wherein the second soluble protein has at least 85% sequence identity to the amino acid sequence of SEQ ID NO:4, and wherein an interleukin-15 (IL-15) domain of the first soluble protein binds to an IL-15 receptor alpha sushi-binding domain (IL-15RαSu) domain of the second soluble protein to form the soluble fusion protein complex.

In another aspect, the invention provides an isolated soluble fusion protein complex comprising at least a first soluble protein and a second soluble protein, wherein the first soluble protein has at least 85% sequence identity to the amino acid sequence of SEQ ID NO:6, wherein the second soluble protein has at least 85% sequence identity to the amino acid sequence of SEQ ID NO:8, and wherein an interleukin-15 (IL-15) domain of the first fusion protein binds to an IL-15 receptor alpha sushi-binding domain (IL-15RαSu) domain of the second fusion protein to form the soluble fusion protein complex.

Date Reçue/Date Received 2021-09-16

In another aspect, the invention provides a nucleic acid comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 16, 17, 18 and 19.

In another aspect, the invention provides an expression vector comprising the nucleic acid sequence of the nucleic acid of the invention.

In another aspect, the invention provides a pharmaceutical composition comprising the soluble fusion protein complex of the invention, the nucleic acid of the invention, or the expression vector of the invention; and an excipient.

In another aspect, the invention provides a method of preparing immune cells for infusion in a subject for treatment of neoplasia in the subject comprising: isolating and separating immune cells from a biological sample; contacting the immune cells *in vitro* with the soluble fusion protein complex of the invention.

In another aspect, the invention provides a use of the soluble fusion protein complex of the invention or the pharmaceutical composition comprising the soluble fusion protein complex of the invention, for treatment of neoplasia.

In another aspect, the invention provides a use of the soluble fusion protein complex of the invention for the manufacture of a medicament for treatment of neoplasia.

In another aspect, the invention provides the soluble fusion protein complex of the invention, or the pharmaceutical composition comprising the soluble fusion protein complex of the invention, for use in treatment of neoplasia.

In another aspect, the invention provides a method of inhibiting transforming growth factor beta (TGFβ) activity *in vitro*, comprising contacting a cell *in vitro* with the soluble fusion protein complex of the invention, the nucleic acid of the invention, the expression vector of the invention or the pharmaceutical composition of the invention, thereby inhibiting transforming growth factor beta (TGFβ) activity *in vitro*.

Date Reçue/Date Received 2022-04-26

In another aspect, the invention provides a use of the soluble fusion protein complex of the invention, the nucleic acid of the invention, the expression vector of the invention or the pharmaceutical composition of the invention, for inhibiting transforming growth factor beta (TGFβ) activity.

In another aspect, the invention provides a use of the soluble fusion protein complex of the invention, the nucleic acid of the invention, or the expression vector of the invention, for the manufacture of a medicament for inhibiting transforming growth factor beta (TGFβ) activity.

In another aspect, the invention provides the soluble fusion protein complex of the invention, the nucleic acid of the invention, the expression vector of the invention or the pharmaceutical composition of the invention, for use in inhibiting transforming growth factor beta (TGFβ) activity.

In another aspect, the invention provides a use of the soluble fusion protein complex of the invention, the nucleic acid of the invention, the expression vector of the invention or the pharmaceutical composition of the invention, for decreasing the amount of transforming growth factor beta (TGFβ) *in vivo*.

In another aspect, the invention provides a use of the soluble fusion protein complex of the invention, the nucleic acid of the invention, or the expression vector of the invention, for the manufacture of a medicament for decreasing the amount of transforming growth factor beta (TGFβ) *in vivo*.

In another aspect, the invention provides the soluble fusion protein complex of the invention, the nucleic acid of the invention, the expression vector of the invention or the pharmaceutical composition of the invention, for use in decreasing the amount of transforming growth factor beta (TGFβ) *in vivo*.

In another aspect, the invention provides a use of the soluble fusion protein complex of the invention, the nucleic acid of the invention, the expression vector of the invention or the pharmaceutical composition of the invention, for inducing antibody-dependent cell-mediated cytotoxicity in a subject in need thereof.

In another aspect, the invention provides a use of the soluble fusion protein complex of the invention, the nucleic acid of the invention, or the expression vector of the invention, for the manufacture of a medicament for inducing antibody-dependent cell-mediated cytotoxicity in a subject in need thereof.

Date Reçue/Date Received 2021-09-16

In another aspect, the invention provides the soluble fusion protein complex of the invention, the nucleic acid of the invention, the expression vector of the invention or the pharmaceutical composition of the invention, for use in inducing antibody-dependent cell-mediated cytotoxicity in a subject in need thereof.

In another aspect, the invention provides a use of the soluble fusion protein complex of the invention, the nucleic acid of the invention, the expression vector of the invention or the pharmaceutical composition of the invention, for inhibiting transforming growth factor beta (TGFβ) mediated phosphorylation and activation of SMAD polypeptides *in vivo*.

In another aspect, the invention provides a use of the soluble fusion protein complex of the invention, the nucleic acid of the invention, or the expression vector of the invention, for the manufacture of a medicament for inhibiting transforming growth factor beta (TGFβ) mediated phosphorylation and activation of SMAD polypeptides *in vivo*.

In another aspect, the invention provides the soluble fusion protein complex of the invention, the nucleic acid of the invention, the expression vector of the invention or the pharmaceutical composition of the invention, for use in inhibiting transforming growth factor beta (TGFβ) mediated phosphorylation and activation of SMAD polypeptides *in vivo*.

Unless defined otherwise, all technical and scientific terms used herein have the meaning commonly understood by a person skilled in the art to which this invention belongs. The following references provide one of skill with a general definition of many of the terms used in this invention: Singleton *et al.*, Dictionary of Microbiology and Molecular Biology (2nd ed. 1994); The Cambridge Dictionary of Science and Technology (Walker ed., 1988); The Glossary of Genetics, 5th Ed., R. Rieger *et al.* (eds.), Springer Verlag (1991); and Hale & Marham, The Harper Collins Dictionary of Biology (1991). As used herein, the following terms have the meanings ascribed to them below, unless specified otherwise.

By "agent" is meant a peptide, nucleic acid molecule, or small compound.

By "TxM" is meant a complex comprising an IL-15N72D:IL-15RαSu/Fc scaffold linked to a binding domain. An exemplary TxM is an IL-15N72D:IL-15RαSu/Fc complex comprising a fusion to a binding domain that specifically recognizes PD-L1 (PD-L1 TxM).

Date Reçue/Date Received 2021-09-16

By "ameliorate" is meant decrease, suppress, attenuate, diminish, arrest, or stabilize the development or progression of a disease.

By "analog" is meant a molecule that is not identical, but has analogous functional or structural features. For example, a polypeptide analog retains the biological activity of a corresponding naturally-occurring polypeptide, while having certain biochemical modifications that enhance the analog's function relative to a naturally occurring polypeptide. Such biochemical modifications could increase the analog's protease resistance, membrane permeability, or half-life, without altering, for example, ligand binding. An analog may include an unnatural amino acid.

The term "binding domain" is intended to encompass an antibody, single chain antibody, Fab, Fv, T-cell receptor binding domain, ligand binding domain, receptor binding domain, or other antigen-specific polypeptides known in the art.

The invention includes antibodies or fragments of such antibodies, so long as they exhibit the desired biological activity. Also included in the invention are chimeric antibodies, such as humanized antibodies. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source that is non-human. Humanization can be performed, for example, using methods described in the art, by substituting at least a portion of a rodent complementarity-determining region for the corresponding regions of a human antibody.

The term "antibody" or "immunoglobulin" is intended to encompass both polyclonal and monoclonal antibodies. The preferred antibody is a monoclonal antibody reactive with the antigen. The term "antibody" is also intended to encompass mixtures of more than one antibody reactive with the antigen (e.g., a cocktail of different types of monoclonal antibodies reactive with the antigen). The term "antibody" is further intended to encompass whole antibodies, biologically functional fragments thereof, single-chain antibodies, and genetically altered antibodies such as chimeric antibodies comprising portions from more than one species, bifunctional antibodies, antibody conjugates, humanized and human antibodies. Biologically functional antibody fragments, which can also be used, are those peptide fragments derived from an antibody that are sufficient for binding to the antigen. "Antibody" as used herein is meant to include the entire antibody as well as any antibody fragments (e.g. $F(ab')_2$, Fab', Fab, Fv) capable of binding the epitope, antigen, or antigenic fragment of interest.

By "binding to" a molecule is meant having a physicochemical affinity for that molecule.

"Detect" refers to identifying the presence, absence, or amount of the analyte to be detected.

By "disease" is meant any condition or disorder that damages or interferes with the normal function of a cell, tissue, or organ. Examples of diseases include neoplasias, autoimmune diseases and viral infections.

By the terms "effective amount" and "therapeutically effective amount" of a formulation or formulation component is meant a sufficient amount of the formulation or component, alone or in a combination, to provide the desired effect. For example, by "an effective amount" is meant an amount of a compound, alone or in a combination, required to ameliorate the symptoms of a disease relative to an untreated patient. The effective amount of active compound(s) used to practice the present invention for therapeutic treatment of a disease varies depending upon the manner of administration, the age, body weight, and general health of the subject. Ultimately, the attending physician or veterinarian will decide the appropriate amount and dosage regimen. Such amount is referred to as an "effective" amount.

By "fragment" is meant a portion of a polypeptide or nucleic acid molecule. This portion contains, preferably, at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, or 90% of the entire length of the reference nucleic acid molecule or polypeptide. For example, a fragment may contain 10, 20, 30, 40, 50, 60, 70, 80, 90, or 100, 200, 300, 400, 500, 600, 700, 800, 900, or 1000 nucleotides or amino acids. However, the invention also comprises polypeptides and nucleic acid fragments, so long as they exhibit the desired biological activity of the full-length polypeptides and nucleic acid, respectively. A nucleic acid fragment of almost any length is employed. For example, illustrative polynucleotide segments with total lengths of about 10,000, about 5,000, about 3,000, about 2,000, about 1,000, about 500, about 200, about 100, about 50 base pairs in length (including all intermediate lengths) are included in many implementations of this invention. Similarly, a polypeptide fragment of almost any length is employed. For example, illustrative polypeptide segments with total lengths of about 10,000, about 5,000, about 3,000, about 2,000, about 1,000, about 5,000, about 1,000, about 500, about 200, about 100, or about 50 amino acids in length (including all intermediate lengths) are included in many implementations of this invention.

The terms "isolated", "purified", or "biologically pure" refer to material that is free to varying degrees from components which normally accompany it as found in its native state. "Isolate" denotes a degree of separation from original source or surroundings. "Purify" denotes a degree of separation that is higher than isolation.

A "purified" or "biologically pure" protein is sufficiently free of other materials such that any impurities do not materially affect the biological properties of the protein or cause other adverse consequences. That is, a nucleic acid or peptide of this invention is purified if it is substantially free of cellular material, viral material, or culture medium when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. Purity and homogeneity are typically determined using analytical chemistry techniques, for example, polyacrylamide gel electrophoresis or high-performance liquid chromatography. The term "purified" can denote that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. For a protein that can be subjected to modifications, for example, phosphorylation or glycosylation, different modifications may give rise to different isolated proteins, which can be separately purified.

Similarly, by "substantially pure" is meant a nucleotide or polypeptide that has been separated from the components that naturally accompany it. Typically, the nucleotides and polypeptides are substantially pure when they are at least 60%, 70%, 80%, 90%, 95%, or even 99%, by weight, free from the proteins and naturally-occurring organic molecules with they are naturally associated.

By "isolated nucleic acid" is meant a nucleic acid that is free of the genes which flank it in the naturally-occurring genome of the organism from which the nucleic acid is derived. The term covers, for example: (a) a DNA which is part of a naturally occurring genomic DNA molecule, but is not flanked by both of the nucleic acid sequences that flank that part of the molecule in the genome of the organism in which it naturally occurs; (b) a nucleic acid incorporated into a vector or into the genomic DNA of a prokaryote or eukaryote in a manner, such that the resulting molecule is not identical to any naturally occurring vector or genomic DNA; (c) a separate molecule such as a cDNA, a genomic fragment, a fragment produced by polymerase chain reaction (PCR), or a restriction fragment; and (d) a recombinant nucleotide sequence that is part of a hybrid gene, i.e., a gene encoding a fusion protein. Isolated nucleic acid molecules according to the present invention further include molecules produced synthetically, as well as any nucleic acids that have been altered chemically and/or that have modified backbones. For example, the isolated nucleic acid is a purified cDNA or RNA polynucleotide. Isolated nucleic acid molecules also include messenger ribonucleic acid (mRNA) molecules.

By an "isolated polypeptide" is meant a polypeptide of the invention that has been separated from components that naturally accompany it. Typically, the polypeptide is isolated when it is at least 60%, by weight, free from the proteins and naturally-occurring organic molecules with which it is naturally associated. Preferably, the preparation is at least 75%, more preferably at least 90%, and most preferably at least 99%, by weight, a polypeptide of the invention. An isolated polypeptide of the invention may be obtained, for example, by extraction from a natural source, by expression of a recombinant nucleic acid encoding such a polypeptide; or by chemically synthesizing the protein. Purity can be measured by any appropriate method, for example, column chromatography, polyacrylamide gel electrophoresis, or by HPLC analysis.

By "marker" is meant any protein or polynucleotide having an alteration in expression level or activity that is associated with a disease or disorder.

By "neoplasia" is meant a disease or disorder characterized by excess proliferation or reduced apoptosis. Illustrative neoplasms for which the invention can be used include, but are not limited to leukemias (e.g., acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, acute myeloblastic leukemia, acute promyelocytic leukemia, acute myelomonocytic leukemia, acute monocytic leukemia, acute erythroleukemia, chronic leukemia, chronic myelocytic leukemia, chronic lymphocytic leukemia), polycythemia vera, lymphoma (Hodgkin's disease, non-Hodgkin's disease), Waldenstrom's macroglobulinemia, heavy chain disease, and solid tumors such as sarcomas and carcinomas (e.g., fibrosarcoma, myxosarcoma, liposarcoma, chondrosarcoma, osteogenic sarcoma, chordoma, angiosarcoma, endotheliosarcoma, lymphangiosarcoma, lymphangioendotheliosarcoma, synovioma, mesothelioma, Ewing's tumor, leiomyosarcoma, rhabdomyosarcoma, colon carcinoma, pancreatic cancer, breast cancer, ovarian cancer, prostate cancer, squamous cell carcinoma, basal cell carcinoma, adenocarcinoma, sweat gland carcinoma, sebaceous gland carcinoma, papillary carcinoma, papillary adenocarcinomas, cystadenocarcinoma, medullary carcinoma, bronchogenic carcinoma, renal cell carcinoma, hepatoma, nile duct carcinoma, choriocarcinoma, seminoma, embryonal carcinoma, Wilm's tumor, cervical cancer, uterine cancer, testicular cancer, lung carcinoma, small cell lung carcinoma, bladder carcinoma, epithelial carcinoma, glioma, glioblastoma multiforme, astrocytoma, medulloblastoma, craniopharyngioma, ependymoma, pinealoma, hemangioblastoma, acoustic neuroma, oligodenroglioma, schwannoma, meningioma, melanoma, neuroblastoma, and retinoblastoma). In particular embodiments, the neoplasia is multiple myeloma, beta-cell lymphoma, urothelial/bladder carcinoma, or melanoma. As used herein, "obtaining" as in "obtaining an agent" includes synthesizing, purchasing, or otherwise acquiring the agent.

By "reduces" is meant a negative alteration of at least 5%, 10%, 25%, 50%, 75%, or 100%.

By "reference" is meant a standard or control condition.

A "reference sequence" is a defined sequence used as a basis for sequence comparison. A reference sequence may be a subset of or the entirety of a specified sequence; for example, a segment of a full-length cDNA or gene sequence, or the complete cDNA or gene sequence. For polypeptides, the length of the reference polypeptide sequence will generally be at least about 16 amino acids, preferably at least about 20 amino acids, more preferably at least about 25 amino acids, and even more preferably about 35 amino acids, about 50 amino acids, or about 100 amino acids. For nucleic acids, the length of the reference nucleic acid sequence will generally be at least about 50 nucleotides, preferably at least about 60 nucleotides, more preferably at least about 75 nucleotides, and even more preferably about 100 nucleotides or about 300 nucleotides or any integer thereabout or therebetween.

By "specifically binds" is meant a compound or antibody that recognizes and binds a polypeptide of the invention, but which does not substantially recognize and bind other molecules in a sample, for example, a biological sample, which naturally includes a polypeptide of the invention.

Nucleic acid molecules useful in the methods of the invention include any nucleic acid molecule that encodes a polypeptide of the invention or a fragment thereof. Such nucleic acid molecules need not be 100% identical with an endogenous nucleic acid sequence, but will typically exhibit substantial identity. Polynucleotides having "substantial identity" to an endogenous sequence are typically capable of hybridizing with at least one strand of a double-stranded nucleic acid molecule. Nucleic acid molecules useful in the methods of the invention include any nucleic acid molecule that encodes a polypeptide of the invention or a fragment thereof. Such nucleic acid molecules need not be 100% identical with an endogenous nucleic acid sequence, but will typically exhibit substantial identity. Polynucleotides having "substantial identity" to an endogenous sequence are typically capable of hybridizing with at least one strand of a double-stranded nucleic acid molecule. By "hybridize" is meant pair to form a double-stranded molecule between complementary polynucleotide sequences (e.g., a gene described herein), or portions thereof, under various conditions of stringency. (See, e.g., Wahl, G. M. and S. L. Berger (1987) Methods Enzymol. 152:399; Kimmel, A. R. (1987) Methods Enzymol. 152:507).

For example, stringent salt concentration will ordinarily be less than about 750 mM NaCl and 75 mM trisodium citrate, preferably less than about 500 mM NaCl and 50 mM trisodium citrate, and more preferably less than about 250 mM NaCl and 25 mM trisodium citrate. Low stringency hybridization can be obtained in the absence of organic solvent, e.g., formamide, while high stringency hybridization can be obtained in the presence of at least about 35% formamide, and more preferably at least about 50% formamide. Stringent temperature conditions will ordinarily include temperatures of at least about 30° C, more preferably of at least about 37° C, and most preferably of at least about 42° C. Varying additional parameters, such as hybridization time, the concentration of detergent, e.g., sodium dodecyl sulfate (SDS), and the inclusion or exclusion of carrier DNA, are well known to those skilled in the art. Various levels of stringency are accomplished by combining these various conditions as needed. In a preferred: embodiment, hybridization will occur at 30° C in 750 mM NaCl, 75 mM trisodium citrate, and 1% SDS. In a more preferred embodiment, hybridization will occur at 37° C in 500 mM NaCl, 50 mM trisodium citrate, 1% SDS, 35% formamide, and 100 .mu.g/ml denatured salmon sperm DNA (ssDNA). In a most preferred embodiment, hybridization will occur at 42° C in 250 mM NaCl, 25 mM trisodium citrate, 1% SDS, 50% formamide, and 200 μg/ml ssDNA. Useful variations on these conditions will be readily apparent to those skilled in the art.

For most applications, washing steps that follow hybridization will also vary in stringency. Wash stringency conditions can be defined by salt concentration and by temperature. As above, wash stringency can be increased by decreasing salt concentration or by increasing temperature. For example, stringent salt concentration for the wash steps will preferably be less than about 30 mM NaCl and 3 mM trisodium citrate, and most preferably less than about 15 mM NaCl and 1.5 mM trisodium citrate. Stringent temperature conditions for the wash steps will ordinarily include a temperature of at least about 25° C, more preferably of at least about 42° C, and even more preferably of at least about 68° C. In a preferred embodiment, wash steps will occur at 25° C in 30 mM NaCl, 3 mM trisodium citrate, and 0.1% SDS. In a more preferred embodiment, wash steps will occur at 42 C in 15 mM NaCl, 1.5 mM trisodium citrate, and 0.1% SDS. In a more preferred embodiment, wash steps will occur at 68° C in 15 mM NaCl, 1.5 mM trisodium citrate, and 0.1% SDS. Additional variations on these conditions will be readily apparent to those skilled in the art. Hybridization techniques are well known to those skilled in the art and are described, for example, in Benton and Davis (Science 196:180, 1977); Grunstein and Hogness (Proc. Natl. Acad. Sci., USA 72:3961, 1975); Ausubel *et al.* (Current Protocols in Molecular Biology, Wiley Interscience, New York, 2001); Berger and Kimmel (Guide to Molecular Cloning Techniques, 1987, Academic Press, New York); and Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, New York.

By "substantially identical" is meant a polypeptide or nucleic acid molecule exhibiting at least 50% identity to a reference amino acid sequence (for example, any one of the amino acid sequences described herein) or nucleic acid sequence (for example, any one of the nucleic acid sequences described herein). Preferably, such a sequence is at least 60%, more preferably 80% or 85%, and more preferably 90%, 95% or even 99% identical at the amino acid level or nucleic acid to the sequence used for comparison.

Sequence identity is typically measured using sequence analysis software (for example, Sequencher, Gene Codes Corporation, 775 Technology Drive, Ann Arbor, MI; Vector NTI, Life Technologies, 3175 Staley Rd. Grand Island, NY). Such software matches identical or similar sequences by assigning degrees of homology to various substitutions, deletions, and/or other modifications. Conservative substitutions typically include substitutions within the following groups: glycine, alanine; valine, isoleucine, leucine; aspartic acid, glutamic acid, asparagine, glutamine; serine, threonine; lysine, arginine; and phenylalanine, tyrosine. In an exemplary approach to determining the degree of identity, a BLAST program may be used, with a probability score between e^{-3} and e^{-100} indicating a closely related sequence.

By "subject" is meant a mammal, including, but not limited to, a human or non-human mammal, such as a bovine, equine, canine, ovine, or feline. The subject is preferably a mammal in need of such treatment, e.g., a subject that has been diagnosed with B cell lymphoma or a predisposition thereto. The mammal is any mammal, e.g., a human, a primate, a mouse, a rat, a dog, a cat, a horse, as well as livestock or animals grown for food consumption, e.g., cattle, sheep, pigs, chickens, and goats. In a preferred embodiment, the mammal is a human.

Ranges provided herein are understood to be shorthand for all of the values within the range. For example, a range of 1 to 50 is understood to include any number, combination of numbers, or sub-range from the group consisting 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50.

The terms "treating" and "treatment" as used herein refer to the administration of an agent or formulation to a clinically symptomatic individual afflicted with an adverse condition, disorder, or disease, so as to affect a reduction in severity and/or frequency of symptoms, eliminate the symptoms and/or their underlying cause, and/or facilitate improvement or remediation of damage. It will be appreciated that, although not precluded, treating a disorder or condition does not require that the disorder, condition, or symptoms associated therewith be completely eliminated.

The terms "preventing" and "prevention" refer to the administration of an agent or composition to a clinically asymptomatic individual who is susceptible or predisposed to a particular adverse condition, disorder, or disease, and thus relates to the prevention of the occurrence of symptoms and/or their underlying cause.

Unless specifically stated or obvious from context, as used herein, the term "or" is understood to be inclusive. Unless specifically stated or obvious from context, as used herein, the terms "a", "an", and "the" are understood to be singular or plural.

Unless specifically stated or obvious from context, as used herein, the term "about" is understood as within a range of normal tolerance in the art, for example within 2 standard deviations of the mean. About can be understood as within 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1%, 0.5%, 0.1%, 0.05%, or 0.01% of the stated value. Unless otherwise clear from context, all numerical values provided herein are modified by the term about.

The recitation of a listing of chemical groups in any definition of a variable herein includes definitions of that variable as any single group or combination of listed groups. The recitation of an embodiment for a variable or aspect herein includes that embodiment as any single embodiment or in combination with any other embodiments or portions thereof.

Any compositions or methods provided herein can be combined with one or more of any of the other compositions and methods provided herein.

The transitional term "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. By contrast, the transitional phrase "consisting of" excludes any element, step, or ingredient not specified in the claim. The transitional phrase "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.

Other features and advantages of the invention will be apparent from the following description of the preferred embodiments thereof, and from the claims. Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below.

In the case of conflict with references cited herein, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

BRIEF DESCRIPTION OF THE DRAWINGS

The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.

FIG. 1 is a schematic diagram illustrating an embodiment of a structure of the construct: αPDL1/ TGFβRII /TXM.

FIG.2 is an analytical Size Exclusion Chromatography (SEC) of αPDL1/TGFβRII/TXM after rProtein A purification.

FIG. 3 is a scan of a photograph showing reduced SDS PAGE results of αPDL1/TGFβRII/TXM.

Date Reçue/Date Received 2021-09-16

FIG. 4 is schematic diagram illustrating an embodiment of a structure of construct: TGFβRII /αPDL1/TXM.

FIG. 5 is an analytical SEC of TGFβRII/αPDL1/TXM after rProtein A purification.

FIG. 6 is a scan of a photograph showing reduced SDS PAGE results of TGFβRII/αPDL1/TXM.

FIG. 7 is schematic diagram illustrating embodiments of a structure of construct: αPDL1/TxM/TGFβRII.

FIG. 8 shows the reduced SDS-PAGE results for TGFβRII/αPDL1/TxM and αPDL1/TGFβRII/TxM.

FIG. 9 is a table and a schematic representation of the early protein characterization.

FIG. 10 is a graph and a table depicting results obtained using an IL-15 activity assay comparing αPDL1/TxM/TGFβRII, αPDL1/TGFβRII/TxM, TGFβRII/αPDL1/TxM and ALT-803.

FIG. 11 is a graph and a table depicting results obtained using a TGFβ activity blocking assay comparing αPDL1/TxM/TGFβRII, TGFβRII/αPDL1/TxM and αPDL1/TGFβRII/TxM.

FIG. 12 is a graph and a table depicting results obtained using PDL1 binding assays comparing αPDL1/TxM/TGFβRII, TGFβRII/αPDL1/TxM, and αPDL1/TGFβRII/TxM.

FIG. 13 is a table showing the overall comparison between TGFβRII/αPDL1/TXM and αPDL1/TGFβRII/TXM.

FIG. 14A is a graph showing cell proliferation after stimulation with hTGFβRII/αPDL1/TxM or ALT-803. IL-15 dependent 32Dβ cells were stimulated for 3 days with hTGFβRII/αPDL1/TxM or ALT-803 and cell proliferation was assessed using PrestoBlue. The EC_{50} of IL-15 was calculated by using ALT-803 as a positive control. The results that hαPDL1/TGFβRII/TxM has IL-15 activities, with an EC50 approximately 188 pM.

FIG. 14B is a graph showing cell proliferation after stimulation with hαPDL1/TGFβRII/TxM or ALT-803. IL-15 dependent 32Dβ cells were stimulated for 3 days with hαPDL1/TGFβRII/TxM or ALT-803 and cell proliferation was assessed using PrestoBlue. The EC_{50} of IL-15 was calculated by using ALT-803 as a positive control. The results that hαPDL1/TGFβRII/TxM has IL-15 activities, with an EC_{50} approximately 376.5 pM.

FIG. 15A is a graph showing results obtained from binding of TGFβRII/αPDL1/TxM to human lung papillary adenocarcinoma cells. Binding of TGFβRII/αPDL1/TxM to $PDL1^+$ H441 human lung papillary adenocarcinoma cells was analyzed by flow cytometry using APC labeled antibody specific for the Fc portion of hIgG. The results show TGFβRII/αPDL1/TxM has binding activity for PDL1.

FIG. 15B is a graph showing results obtained from binding of hαPDL1/TGFβRII/TxM to human lung papillary adenocarcinoma cells. Binding of hαPDL1/TGFβRII/TxM to $PDL1^+$ H441 human lung papillary adenocarcinoma cells was analyzed by flow cytometry using APC labeled antibody specific for the Fc portion of hIgG. The results show that hαPDL1/TGFβRII/TxM has binding activity for PDL1.

FIG. 16A is a graph showing results obtained from blocking of TGFβ1 mediated Smad2/3 phosphorylation by hTGFβRII/αPDL1/TxM. Blocking of Smad2/3 phosphorylation induced by TGFβ1 (100ng/mL) using hTGFβRII/αPDL1/TxM was assessed with HEK293 cells containing TGF/SMAD Signaling Pathway SBE Reporter (BPS Bioscience). TGFβRII fused to IgG Fc was used as control. The results show that hTGFβRII/αPDL1/TxM can effectively block Smad phosphorylation mediated by TGFβ1, with a IC_{50} approximately 2.35 nM.

FIG. 16B is a graph showing results obtained from blocking of TGFβ1 mediated Smad2/3 phosphorylation by hαPDL1/TGFβRII/TxM. Blocking of Smad2/3 phosphorylation induced by TGFβ1 (100ng/mL) using hαPDL1/TGFβRII/TxM was assessed with HEK293 cells containing TGF/SMAD Signaling Pathway SBE Reporter (BPS Bioscience). TGFβRII fused to IgG Fc was used as control. The results show that hαPDL1/TGFβRII/TxM can effectively block Smad phosphorylation mediated by TGFβ1, with a IC_{50} approximately 0.38nM.

FIG. 17A is a graph showing results obtained from blocking of TGFβ3 mediated Smad2/3 phosphorylation by hTGFβRII/αPDL1/TxM. Blocking of Smad2/3 phosphorylation induced by TGFβ3 (100ng/mL) using hTGFβRII/αPDL1/TxM was assessed with HEK293 cells containing TGF/SMAD Signaling Pathway SBE Reporter (BPS Bioscience). TGFβRII fused to IgG Fc was used as control. The results show that hTGFβRII/αPDL1/TxM can effectively block Smad phosphorylation mediated by TGFβ3, with a IC_{50} approximately 0.355nM.

FIG. 17B is a graph showing results obtained from blocking of TGFβ3 mediated Smad2/3 phosphorylation by hαPDL1/TGFβRII/TxM. Blocking of Smad2/3 phosphorylation induced by TGFβ3 (100ng/mL) using hαPDL1/TGFβRII/TxM was assessed with HEK293 cells containing TGF/SMAD Signaling Pathway SBE Reporter (BPS Bioscience). TGFβRII fused to IgG Fc was used as control. The results show that hαPDL1/TGFβRII/TxM can effectively block Smad phosphorylation mediated by TGFβ3, with a IC_{50} approximately 0.029nM.

FIG. 18A is a graph showing results obtained from binding of hTGFβRII/αPDL1/TXM to TGF-β1. ELISAs were performed to assess binding of hTGFβRII/αPDL1/TXM to TGF-β1. Wells were first coated with TGFβ1 (0.5 µg/ml) overnight and then incubated with hTGFβRII/αPDL1/TXM in serial dilution. Protein binding was detected using anti-hIgG-horseradish peroxidase (HRP). The results show that hTGFβRII/αPDL1/TXM can bind to plate bound TGF-β1, with an EC50 of 1.28nM.

FIG. 18B is a graph showing results obtained from binding of hαPDL1/TGFβRII/TXM to TGF-β1. ELISAs were performed to assess binding of hαPDL1/TGFβRII/TXM to TGF-β1. Wells were first coated with TGFβ1 (0.5ug/ml) overnight and then incubated with hαPDL1/TGFβRII/TXM in serial dilution. Protein binding was detected using anti-hIgG-horseradish peroxidase (HRP). The results show that hαPDL1/TGFβRII/TXM can bind to plate bound TGF-β1, with an EC50 of 0.49nM.

FIG. 19A is a graph showing results obtained from binding of hTGFβRII/αPDL1/TXM to TGF-β3. ELISAs were performed to assess binding of hTGFβRII/αPDL1/TXM to TGF-β1. Wells were first coated with TGFβ3 (0.5 µg/ml) overnight and then incubated with hTGFβRII/αPDL1/TXM in serial dilution. Protein binding was detected using anti-hIgG-horseradish peroxidase (HRP). The results show that hTGFβRII/αPDL1/TXM can bind to plate bound TGFβ3, with an EC50 of 3.617nM.

FIG. 19B is a graph showing results obtained from binding of hαPDL1/TGFβRII/TXM to TGF-β3. ELISAs were performed to assess binding of hαPDL1/TGFβRII/TXM to TGF-β3. Wells were first coated with TGFβ3 (0.5µg/ml) overnight and then incubated with hαPDL1/TGFβRII/TXM in serial dilution. Protein binding was detected using anti-hIgG-horseradish peroxidase (HRP). The results show that hαPDL1/TGFβRII/TXM can bind to plate bound TGFβ3, with an EC_{50} of 2.447nM.

FIG. 20 is a graph showing results obtained from experiments assessing the anti-tumor activity of hTGFβRII/αPDL1/TXM. To assess the anti-tumor activity of hTGFβRII/αPDL1/TXM protein, CellTrace labeled PD-L1$^+$ H441 lung tumor cells were incubated with human NK cells at E: T ratio of 10:1 for 20 hrs at 37^{o}C in the presence of different proteins as indicated. Cells was then washed and resuspended in 2μg/ml PI solution. The percentage of dead PI$^+$ CellTrace$^+$ H441 tumor cells was determined by flow cytometry and represents NK cell dependent killing of tumor cells mediated by the different proteins. The results showed that hTGFβRII/αPDL1/TXM protein can induce ADCC against tumor cells.

FIG. 21 is a graph showing results obtained from experiments assessing the anti-tumor activity of hαPDL1/TGFβRII/TXM. To assess the anti-tumor activity of hαPDL1/TGFβRII/TXM protein, CellTrace labeled PD-L1$^+$ H441 lung tumor cells were incubated with human NK cells at E: T ratio of 10:1 for 20 hrs at 37^{o}C in the presence of different proteins as indicated. Cells was then washed and resuspended in 2 μg/ml PI solution. The percentage of dead PI$^+$ CellTrace$^+$ H441 tumor cells was determined by flow cytometry and represents NK cell dependent killing of tumor cells mediated by the different proteins. The results showed that hαPDL1/TGFβRII/TXM protein can induce ADCC against tumor cells.

FIG. 22A is a schematic representation of the αPDL1/TxM/TGFβRII construct. FIG. 22B: αPD-L1/TxM, αPDL1/TxM/TGFβRII, and a control antibody were run on SDS-PAGE in reduced (left) and non-reduced conditions (right). FIG. 22C is the SPR analysis of αPDL1/TxM/TGFβRII and Rsbc6 (αPDL1 Ab). αPDL1/TxM/TGFβRII and Rsbc6 were immobilized onto the SPR sensor by Fc capture. Binding affinity to PD-L1 was determined by OneStep kinetic analysis on Pioneer FE (Fortebio). FIG. 22D are results from a SEC-HPLC of αPDL1/TxM/TGFβRII showing 93% purity. FIG. 22E demonstrate the ADCC activity of αPD-L1/TxM, Avelumab, Rsbc6 (Anti-PD-L1), αPDL1/TxM/TGFβRIIR against PD-L1-positve tumor cells (MDA-MB-231 breast tumor cells). αPD-L1/TxM shows a maximal killing of ~85% whereas αPDL1/TxM/TGFβRII shows a maximal killing of ~30%.

FIG. 23 is a series of plots showing a surface plasmon resonance (SPR) analysis of TGFβ1, TGFβ2 and TGFβ3 binding on αPDL1/TxM/TGFβRII. αPDL1/TxM/TGFβRII was immobilized onto the SPR sensor by Fc capture. Binding affinities to TGFβ1 (left panel), TGFβ2 (middle panel) and TGFβ3 (right panel) were determine by OneStep kinetic analysis on Pioneer FE (Fortebio).

FIG. 24 is a schematic diagram of a standardize PD-L1 blockade assay to evaluate immune checkpoint activity of proteins.

FIG. 25A is a graph showing results obtained from blocking of PD-L1 mediated immune cell suppression by hαPDL1/TGFβRII/TxM and hTGFβRII/αPDL1/TxM compared to αPDL1 Ab. FIG. 25B is a graph showing results obtained from blocking of PD-L1 mediated immune cell suppression by hαPDL1/TxM/TGFβRII and hTGFβRII/αPDL1/TxM compared to αPDL1 Ab. Increasing concentrations of hαPDL1/TGFβRII/TxM , hTGFβRII/αPDL1/TxM and hαPDL1/TxM/TGFβRII were added to a standardized cell-based PD-L1 blockade assay (FIG. 24). The ability of the complexes to block immune suppression was measured by T cell activation resulting in NFAT-RE-mediated luminescence. Anti-PD-L1 antibody and PD-L1/TxM protein complexes (similar to TGFβRII/αPDL1/TXM and αPDL1/TGFβRII/TXM complexes but lacking the TGFβRII domains) served as positive controls.

FIGS. 26A and 26B are graphs demonstrating the human TGFβ specific blocking activity for each molecule (N-810, FIG. 26A) compared against the activity of the parental control molecule (αPDL1/TxM, FIG. 26B). A stable cellular luciferase-based reporter system (HEK-293T-luc2P/SBE) was used in order to assess the specific TGFβ-blocking activity. Cultured cells were stimulated for 20 hours with 0.0175 nM of recombinant human TGFβ1 in the presence or absence of the blocking reagent. Response to hTGFβ1 was expressed by Relative Luminescence Units (RLU) ± SD.

FIGS. 27A and 27B are graphs demonstrating specific hTGFβ1 blocking activity for each molecule (N-810 Sorrento-Fc, Fig 27A) compared against the activity of the parental control molecule (αPDL1/TxM, FIG. 27B). A stable cellular luciferase-based reporter system (HEK-293T-luc2P/SBE) was used in order to assess the specific TGFβ-blocking activity. Cultured cells were stimulated for 20 hours with 0.0175 nM of recombinant human TGFβ1 in the presence or absence of the blocking reagent. Response to hTGFβ1 was expressed by Relative Luminescence Units (RLU) ± SD.

FIGS. 28A and 28B are graphs demonstrating specific hTGFβ1 blocking activity for each molecule (N-810 ΔC, FIG. 28A) compared against the activity of the parental control molecule (αPDL1/TxM, FIG. 28B). A stable cellular luciferase-based reporter system (HEK-293T-luc2P/SBE) was used in order to assess the specific TGFβ-blocking activity. Cultured cells were stimulated for 20 hours with 0.0175 nM of recombinant human TGFβ1 in the presence or absence of the blocking reagent. Response to hTGFβ1 was expressed by Relative Luminescence Units (RLU) ± SD.

FIGS. 29A and 29B are graphs demonstrating specific hTGFβ1 blocking activity for each molecule (N-810D, FIG. 29A) compared against the activity of the parental control molecule (αPDL1/TxM, FIG. 29B). A stable cellular luciferase-based reporter system (HEK-293T-luc2P/SBE) was used in order to assess the specific TGFβ-blocking activity. Cultured cells were stimulated for 20 hours with 0.0175 nM of recombinant human TGFβ1 in the presence or absence of the blocking reagent. Response to hTGFβ1 was expressed by Relative Luminescence Units (RLU) ± SD.

FIG. 30 is a graph demonstrating the antibody-dependent cellular cytotoxicity (ADCC) of the TxM constructs in mammary adenocarcinoma cells (MDA-MB-231). Antibody-Dependent Cellular Cytotoxicity (ADCC) was used in order to determine the specific αPD-L1 activity. Effector cells: haNK (NK-92 derivative).

FIGS. 31A-31H are schematic representations showing the various constructs. FIG. 31A: N-810A. FIG. 31B: N-810A aglycosylated. FIG. 31C: N-810A aglycosylated, Δ free cysteine. FIG. 31D: N-810A Δ hinge. FIG. 31E: N-810A (IL15-K41Q, L45S, I67T, N79Y, E93A). The mutations in IL15 enhance the solubility and expression of the molecule. FIG. 31F: N-810A (IL15-L45S). The mutations in IL15 enhance solubility and expression of the molecule. FIG. 31G: N-810D. FIG. 31H: N-810E.

FIG. 32 is a table demonstrating that IL15 mutations increase protein yield and decrease aggregation. N-810D variation also increases yield and decreases aggregation.

DETAILED DESCRIPTION

The invention is based, at least in part, on the surprising discovery that multi-specific IL-15-based protein complexes enhance the activity of immune cells and promote their activity against disease cells, thereby resulting in reduction or prevention of disease. These protein complexes also show increased binding to disease and target antigens. Provided herein are multi-specific protein complexes with one domain comprising IL-15 or a functional variant, a cytokine receptor or cytokine ligand, and a binding domain comprising a disease-specific binding domain, immune checkpoint inhibitor or immune agonist. Such protein complexes have utility in methods for treating a neoplasia, infectious disease, or autoimmune disease in a subject. Thus, provided herein are compositions featuring PD-L1/TGFβRII/TxM and methods of using such compositions to enhance an immune response against a neoplasia (e.g., solid and hematologic tumors).

As described herein, the use of proteins with the capability of targeting diseased cells for host immune recognition and response is an effective strategy for treating cancer, infectious diseases, and autoimmune diseases. As described in U.S. Patent No. 8,507,222, a protein scaffold comprising IL-15 and IL-15 receptor α domains has been used to generate multi-specific proteins capable of recognizing antigens on disease cells and receptors on immune cells. *See*, U.S. Patent No. 8,507,222 at Example 15. Described herein is the generation of soluble multi-specific protein complexes comprising IL-15 and IL-15 receptor α linked to one or more binding domains recognizing immune checkpoint or signaling molecules. In some cases, these complexes also comprise binding domains that recognize antigens, such as PD-L1, ssDNA, CD20, HER2, EGFR, CD19, CD38, CD52, GD2, CD33, Notch1, intercellular adhesion molecule 1 (ICAM-1), tissue factor, HIV envelope or other tumor antigens, expressed on disease cells.

In some cases, the binding domain comprises a single chain antibody wherein an immunoglobulin light chain variable domain covalently linked to an immunoglobulin heavy chain variable domain by a polypeptide linker sequence. The single chain antibody domain can be arranged in either the VH-linker-VL or VL-linker-VH format. Alternatively, the binding domain comprises a soluble or extracellular ligand or receptor domain capable of acting as an immune checkpoint inhibitor or immune agonist. The binding domains recognizing an immune checkpoint or signaling molecule are linked to either the N- or C-termini of the IL-15 or IL-15 receptor α proteins with or without an additional linker sequence so long as binding activity is maintained. Preferably, the binding domain is linked to the N-terminus of the human IL-15N72D superagonist protein (huIL-15N72D). Alternatively, the binding domain is linked to the C-terminus of the human IL-15N72D protein. Preferably, the binding domain is linked to the N-terminus of the human IL-15 receptor α sushi domain (huIL-15RαSu). Alternatively, the binding domain is linked to the C-terminus of the huIL-15RαSuFc protein. In some cases, the multi-specific protein complexes of the invention further comprise an IgG Fc domain for protein dimerization and

Date Reçue/Date Received 2021-09-16

recognition of CD16 receptors on immune cells. Such a domain mediates stimulation of antibody-dependent cellular cytotoxicity (ADCC), antibody-dependent cellular phagocytosis (ADCP) and complement-dependent cytotoxicity (CDC) against target cells. In some examples, it is useful to employ Fc domains with enhanced or decreased CD16 binding activity. In one aspect, the Fc domain contains amino acid substitutions L234A and L235A (LALA) (number based on Fc consensus sequence) that reduce ADCC activity, but retain the ability to form disulfide-bound dimers.

Accordingly, in certain embodiments, an isolated soluble fusion protein complex comprises at least two soluble protein complexes, a first soluble protein complex comprises an interleukin-15 (IL-15) polypeptide domain and a second soluble protein comprises a soluble IL-15 receptor alpha sushi-binding domain (IL-15RαSu) fused to an immunoglobulin Fc domain, wherein the immunoglobulin Fc domain is fused or linked to a transforming growth factor-beta receptor type 2 (TGFβRII) domain; the first and/or second soluble protein further comprises a binding domain that specifically binds to a disease antigen, immune checkpoint molecule or immune signaling molecule, and the IL-15 domain of the first soluble protein binds to the IL-15RαSu domain of the second soluble protein to form a soluble fusion protein complex. In certain aspects, the immunoglobulin Fc domain is linked to a transforming growth factor-beta receptor type 2 (TGFβRII) domain via a linker molecule.

In certain embodiments, a soluble fusion complex comprises at least two soluble proteins a first fusion protein and a second fusion protein, wherein the first fusion protein comprises a transforming growth factor-beta receptor type 2 (TGFβRII) dimer comprising a first TGFβRII domain linked to a second TGFβRII domain wherein the TGFβRII dimer is fused or linked to an interleukin-15 (IL-15) polypeptide domain; the second fusion protein comprises a soluble IL-15 receptor alpha sushi-binding domain (IL-15RαSu) fused to an immunoglobulin Fc domain; wherein the second fusion protein further comprises a binding domain that specifically binds to a disease antigen, immune checkpoint molecule or immune signaling molecule, and wherein the IL-15 domain of the first fusion protein binds to the IL-15RαSu domain of the second fusion protein to form a soluble fusion protein complex.

In certain embodiments, a soluble fusion complex comprises at least two soluble proteins a first fusion protein and a second fusion protein, wherein the first fusion protein comprises an interleukin-15 (IL-15) polypeptide domain fused to a binding domain that specifically binds to a disease antigen, immune checkpoint molecule or immune signaling molecule; the second fusion protein comprises a transforming growth factor-beta receptor type 2 (TGFβRII) dimer comprising a first TGFβRII domain linked to a second TGFβRII domain wherein the TGFβRII dimer and a soluble IL-15 receptor alpha sushi-binding domain (IL-15RαSu) fused to an immunoglobulin Fc domain; wherein the first or second TGFβRII domain is fused to the IL-15RαSu domain wherein the IL-15 polypeptide domain of the first fusion protein binds to the IL-15RαSu domain of the second fusion protein to form a soluble fusion protein complex.

In certain embodiments, one of the first or second soluble protein further comprises a second binding domain that specifically binds to a disease antigen, immune checkpoint molecule, or immune signaling molecule.

In certain embodiments, the IL-15 polypeptide is an IL-15 variant comprising an N72D mutation (IL-15N72D).

In certain embodiments, the binding domain comprises an immunoglobulin light chain variable domain covalently linked to an immunoglobulin heavy chain variable domain by a polypeptide linker sequence.

In certain embodiments, the binding domain specifically binds to one or more molecules comprising: programmed death ligand 1 (PD-L1), programmed death 1 (PD-1), cytotoxic T-lymphocyte associated protein 4 (CTLA-4), cluster of differentiation 33 (CD33), cluster of differentiation 47 (CD47), glucocorticoid-induced tumor necrosis factor receptor (TNFR) family related gene (GITR), lymphocyte function-associated antigen 1 (LFA-1), tissue factor (TF), delta-like protein 4 (DLL4), single strand DNA or T-cell immunoglobulin and mucin-domain containing-3 (Tim-3).

In certain embodiments, the binding domain specifically binds to one or more molecules comprising: programmed death ligand 1 (PD-L1). In certain embodiments, the TGFβRII domain binds to transforming factor beta (TGFβ).

In certain embodiments, a first fusion protein complex is covalently linked to a second fusion protein complex by a disulfide bond linking the Fc domain of the first soluble fusion protein complex to the Fc domain of the second soluble fusion protein complex.

<u>Interleukin-15</u>

Interleukin-15 (IL-15) is an important cytokine for the development, proliferation, and activation of effector NK cells and $CD8^+$ memory T cells. IL-15 binds to the IL-15 receptor α (IL-15Rα) and is presented in *trans* to the IL-2/IL-15 receptor β - common γ chain (IL-

15Rβγc) complex on effector cells. IL-15 and IL-2 share binding to the IL-15Rβγc, and signal through STAT3 and STAT5 pathways. However, unlike IL-2, IL-15 does not support maintenance of $CD4^+CD25^+FoxP3^+$ regulatory T (Treg) cells or induce cell death of activated $CD8^+$ T cells, effects that may have limited the therapeutic activity of IL-2 against multiple myeloma. Additionally, IL-15 is the only cytokine known to provide anti-apoptotic signaling to effector $CD8^+$ T cells. IL-15, either administered alone or as a complex with the IL-15Rα, exhibits potent anti-tumor activities against well-established solid tumors in experimental animal models and, thus, has been identified as one of the most promising immunotherapeutic drugs that could potentially cure cancer. A first-in-human clinical trial found that patients administered recombinant human (rh)IL-15 showed significant increases in γδ T cells, $CD8^+$ T cells, and NK cells, but the high doses resulted in toxicities and limited tumor responses.[2] A relatively short half-life of the prokaryotic rhIL-15 was also observed.[23]

To facilitate clinical development of an IL-15-based cancer therapeutic, an IL-15 mutant (IL-15N72D) with increased biological activity compared to IL-15 was identified (Zhu *et al.*, J Immunol, 183: 3598-3607, 2009). The pharmacokinetics and biological activity of this IL-15 super-agonist (IL-15N72D) was further improved by the creation of IL-15N72D:IL-15Rα/Fc fusion complex (ALT-803), such that the super agonist complex has at least 25-times the activity of the native cytokine *in vivo* (Han *et al.*, Cytokine, 56: 804-810, 2011).

Immune Checkpoint Inhibitor and Immune Agonist Domains

In other embodiments, the binding domain is specific to an immune checkpoint or signaling molecule or its ligand and acts as an inhibitor of immune checkpoint suppressive activity or as an agonist of immune stimulatory activity. Such immune checkpoint and signaling molecules and ligands include PD-1, PD-L1, PD-L2, CTLA-4, CD28, CD80, CD86, B7-H3, B7-H4, B7-H5, ICOS-L, ICOS, BTLA, CD137L, CD137, HVEM, KIR, 4-1BB, OX40L, CD70, CD27, CD47, CIS, OX40, GITR, IDO, TIM3, GAL9, VISTA, CD155, TIGIT, LIGHT, LAIR-1, Siglecs and A2aR (Pardoll DM. 2012. Nature Rev Cancer 12:252-264, Thaventhiran T, *et al.* 2012. J Clin Cell Immunol S12:004). Additionally, preferred antibody domains of the invention may include ipilimumab and/or tremelimumab (anti-CTLA4), nivolumab, pembrolizumab, pidilizumab, TSR-042, ANB011, AMP-514 and AMP-224 (a ligand-Fc fusion) (anti-PD1), atezolizumab (MPDL3280A), avelumab (MSB0010718C), durvalumab (MEDI4736), MEDI0680, and BMS-9365569 (anti-PDL1), MEDI6469 (anti-OX40 agonist), BMS-986016, IMP701, IMP731, IMP321 (anti-LAG3) and GITR ligand.

Cytokine Receptors and Cytokines

Cytokine receptors which are fused or linked to the IL-15 molecules embodied herein bind to immunostimulatory cytokines which result in the augmentation of immune activity. Examples of cytokines include but are not limited to the IL-2 family, interferon (IFN), IL-10, IL-1, IL-17, TGF and TNF cytokine families, and to IL-1 through IL-35, IFN-α, IFN-β, IFNγ, TGF-β, TNF-α, and TNFβ. An exemplary receptor is the transforming growth factor beta receptor II (TGFβRII) which binds to TGFβ. The protein encoded by this gene is a transmembrane protein that has a protein kinase domain, forms a heterodimeric complex with TGF-beta receptor type-1, and binds TGF-beta. This receptor/ligand complex phosphorylates proteins, which then enter the nucleus and regulate the transcription of genes related to cell proliferation, cell cycle arrest, wound healing, immunosuppression, and tumorigenesis. Mutations in this gene have been associated with Marfan Syndrome, Loeys-Deitz Aortic Aneurysm Syndrome, and the development of various types of tumors. The extracellular domain of TGFβRII can bind to TGF-β and block its activity. Within the tumor microenvironment, TGF-β acts to promote tumor progression via stromal modification, angiogenesis, and induction of epithelial-mesenchymal transition (EMT). TGF-β1 can directly suppress T cell proliferation and responses and natural killer (NK) cell activity. Moreover, TGF-β signaling in myeloid cells is critical in driving metastasis.

Antigen-specific Binding Domains

Antigen-specific binding domains consist of polypeptides that specifically bind to targets on diseased cells. Alternatively, these domains may bind to targets on other cells that support the diseased state, such as targets on stromal cells that support tumor growth or targets on immune cells that support disease-mediated immunosuppression. Antigen-specific binding domains include antibodies, single chain antibodies, Fabs, Fv, T-cell receptor binding domains, ligand binding domains, receptor binding domains, domain antibodies, single domain antibodies, minibodies, nanobodies, peptibodies, or various other antibody mimics (such as affimers, affitins, alphabodies, atrimers, CTLA4-based molecules, adnectins, anticalins, Kunitz domain-based proteins, avimers, knottins, fynomers, darpins, affibodies, affilins, monobodies and armadillo repeat protein-based proteins (Weidle, UH, *et al.* 2013. Cancer Genomics & Proteomics 10: 155-168)) known in the art.

In certain embodiments, the antigen for the antigen-specific binding domain comprises a cell surface receptor or ligand. In a further embodiment, the antigen comprises a CD antigen, cytokine or chemokine receptor or ligand, growth factor receptor or ligand, tissue factor, cell adhesion molecule, MHC/MHC-like molecules, Fc receptor, Toll-like receptor, NK receptor, TCR, BCR, positive/negative co-stimulatory receptor or ligand, death receptor or ligand, tumor associated antigen, or virus encoded antigen.

Preferably, the antigen-specific binding domain is capable of binding to an antigen on a tumor cell. Tumor-specific binding domain may be derived from antibodies approved for treatment of patients with cancer include rituximab, ofatumumab, and obinutuzumab (anti-CD20 Abs); trastuzumab and pertuzumab (anti-HER2 Abs); cetuximab and panitumumab (anti-EGFR Abs); and alemtuzumab (anti-CD52 Ab). Similarly, binding domains from approved antibody-effector molecule conjugates specific to CD20 (^{90}Y-labeled ibritumomab tiuxetan, ^{131}I-labeled tositumomab), HER2 (ado-trastuzumab emtansine), CD30 (brentuximab vedotin) and CD33 (gemtuzumab ozogamicin) (Sliwkowski MX, Mellman I. 2013 Science 341:1192) could be used.

Additionally, preferred binding domains of the invention may include various other tumor-specific antibody domains known in the art. The antibodies and their respective targets for treatment of cancer include but are not limited to nivolumab (anti-PD-1 Ab), TA99 (anti-gp75), 3F8 (anti-GD2), 8H9 (anti-B7-H3), abagovomab (anti-CA-125 (imitation)), adecatumumab (anti-EpCAM), afutuzumab (anti-CD20), alacizumab pegol (anti-VEGFR2), altumomab pentetate (anti-CEA), amatuximab (anti-mesothelin), AME-133 (anti-CD20), anatumomab mafenatox (anti-TAG-72), apolizumab (anti-HLA-DR), arcitumomab (anti-CEA), bavituximab (anti-phosphatidylserine), bectumomab (anti-CD22), belimumab (anti-BAFF), besilesomab (anti-CEA-related antigen), bevacizumab (anti-VEGF-A), bivatuzumab mertansine (anti-CD44 v6), blinatumomab (anti-CD19), BMS-663513 (anti-CD137), brentuximab vedotin (anti-CD30 (TNFRSF8)), cantuzumab mertansine (anti-mucin CanAg), cantuzumab ravtansine (anti-MUC1), capromab pendetide (anti-prostatic carcinoma cells), carlumab (anti-MCP-1), catumaxomab (anti-EpCAM, CD3), cBR96-doxorubicin immunoconjugate (anti-Lewis-Y antigen), CC49 (anti-TAG-72), cedelizumab (anti-CD4), Ch.14.18 (anti-GD2), ch-TNT (anti-DNA associated antigens), citatuzumab bogatox (anti-EpCAM), cixutumumab (anti-IGF-1 receptor), clivatuzumab tetraxetan (anti-MUC1), conatumumab (anti-TRAIL-R2), CP-870893 (anti-CD40), dacetuzumab (anti-CD40), daclizumab (anti-CD25), dalotuzumab (anti-insulin-like growth factor I receptor), daratumumab (anti-CD38 (cyclic ADP ribose hydrolase)), demcizumab (anti-DLL4), detumomab (anti-B-lymphoma cell), drozitumab (anti-DR5), duligotumab (anti-HER3), dusigitumab (anti-ILGF2), ecromeximab (anti-GD3 ganglioside), edrecolomab (anti-EpCAM), elotuzumab (anti-SLAMF7), elsilimomab (anti-IL-6), enavatuzumab (anti-TWEAK receptor), enoticumab (anti-DLL4), ensituximab (anti-5AC), epitumomab cituxetan (anti-episialin), epratuzumab (anti-CD22), ertumaxomab (anti-HER2/neu, CD3), etaracizumab (anti-integrin αvβ3), faralimomab (anti-Interferon receptor), farletuzumab (anti-folate receptor 1), FBTA05 (anti-CD20), ficlatuzumab (anti-HGF), figitumumab (anti-IGF-1 receptor), flanvotumab (anti-TYRP1(glycoprotein 75)), fresolimumab (anti-TGF β), futuximab (anti-EGFR), galiximab (anti-CD80), ganitumab (anti-IGF-I), gemtuzumab ozogamicin (anti-CD33), girentuximab (anti-carbonic anhydrase 9 (CA-IX)), glembatumumab vedotin (anti-GPNMB), guselkumab (anti-IL13), ibalizumab (anti-CD4), ibritumomab tiuxetan (anti-CD20), icrucumab (anti-VEGFR-1), igovomab (anti-CA-125), IMAB362 (anti-CLDN18.2), IMC-CS4 (anti-CSF1R), IMC-TR1 (TGFβRII), imgatuzumab (anti-EGFR), inclacumab (anti-selectin P), indatuximab ravtansine (anti-SDC1), inotuzumab ozogamicin (anti-CD22), intetumumab (anti-CD51), ipilimumab (anti-CD152), iratumumab (anti-CD30 (TNFRSF8)), KM3065 (anti-CD20), KW-0761 (anti-CD194), LY2875358 (anti-MET) labetuzumab (anti-CEA), lambrolizumab (anti-PDCD1), lexatumumab (anti-TRAIL-R2), lintuzumab (anti-CD33), lirilumab (anti-KIR2D), lorvotuzumab mertansine (anti-CD56), lucatumumab (anti-CD40), lumiliximab (anti-CD23 (IgE receptor)), mapatumumab (anti-TRAIL-R1), margetuximab (anti-ch4D5), matuzumab (anti-EGFR), mavrilimumab (anti-GMCSF receptor α-chain), milatuzumab (anti-CD74), minretumomab (anti-TAG-72), mitumomab (anti-GD3 ganglioside), mogamulizumab (anti-CCR4), moxetumomab pasudotox (anti-CD22), nacolomab tafenatox (anti-C242 antigen), naptumomab estafenatox (anti-5T4), narnatumab (anti-RON), necitumumab (anti-EGFR), nesvacumab (anti-angiopoietin 2), nimotuzumab (anti-EGFR), nivolumab (anti-IgG4), nofetumomab merpentan, ocrelizumab (anti-CD20), ocaratuzumab (anti-CD20), olaratumab (anti-PDGF-R α), onartuzumab (anti-c-MET), ontuxizumab (anti-TEM1), oportuzumab monatox (anti-EpCAM), oregovomab (anti-CA-125), otlertuzumab (anti-CD37), pankomab (anti-tumor specific glycosylation of MUC1), parsatuzumab (anti-EGFL7), pascolizumab (anti-IL-4), patritumab (anti-HER3), pemtumomab (anti-MUC1), pertuzumab (anti-HER2/neu), pidilizumab (anti-PD-1), pinatuzumab vedotin (anti-CD22), pintumomab (anti-adenocarcinoma antigen), polatuzumab vedotin (anti-CD79B), pritumumab (anti-vimentin), PRO131921 (anti-CD20), quilizumab (anti-IGHE), racotumomab (anti-N-glycolylneuraminic acid), radretumab (anti-fibronectin extra domain-B), ramucirumab (anti-VEGFR2), rilotumumab (anti-HGF), robatumumab (anti-IGF-1 receptor), roledumab (anti-RHD), rovelizumab (anti-CD11 & CD18), samalizumab (anti-CD200), satumomab pendetide (anti-TAG-72), seribantumab (anti-ERBB3), SGN-CD19A (anti-CD19), SGN-CD33A (anti-CD33), sibrotuzumab (anti-FAP), siltuximab (anti-IL-6), solitomab (anti-EpCAM), sontuzumab (anti-episialin), tabalumab (anti-BAFF), tacatuzumab tetraxetan (anti-alpha-fetoprotein), taplitumomab paptox (anti-CD19), telimomab aritox, tenatumomab (anti-tenascin C), teneliximab (anti-CD40), teprotumumab (anti-CD221), TGN1412 (anti-CD28), ticilimumab (anti-CTLA-4), tigatuzumab (anti-TRAIL-R2), TNX-650 (anti-IL-13), tositumomab (anti-CS20), tovetumab (anti-CD140a), TRBS07 (anti-GD2), tregalizumab (anti-CD4), tremelimumab (anti-CTLA-4), TRU-016 (anti-CD37), tucotuzumab celmoleukin (anti-EpCAM), ublituximab (anti-CD20), urelumab (anti-4-1BB), vantictumab (anti-Frizzled receptor), vapaliximab (anti-AOC3 (VAP-1)), vatelizumab (anti-ITGA2), veltuzumab (anti-CD20), vesencumab (anti-NRP1), visilizumab (anti-CD3), volociximab (anti-integrin α5β1), vorsetuzumab mafodotin (anti-CD70), votumumab (anti-tumor antigen CTAA16.88), zalutumumab (anti-EGFR), zanolimumab (anti-CD4), zatuximab (anti-HER1), ziralimumab (anti-CD147 (basigin)), RG7636 (anti-ETBR), RG7458 (anti-MUC16), RG7599 (anti-NaPi2b), MPDL3280A (anti-PD-L1), RG7450 (anti-STEAP1), and GDC-0199 (anti-Bcl-2).

Other antibody domains or tumor target binding proteins useful in the invention (e.g. TCR domains) include, but are not limited to, those that bind the following antigens (note, the cancer indications indicated represent non-limiting examples): aminopeptidase N (CD13), annexin Al, B7-H3 (CD276, various cancers), CA125 (ovarian cancers), CA15-3 (carcinomas), CA19-9 (carcinomas), L6 (carcinomas), Lewis Y (carcinomas), Lewis X (carcinomas), alpha fetoprotein (carcinomas), CA242 (colorectal cancers), placental alkaline phosphatase (carcinomas), prostate specific antigen (prostate), prostatic acid phosphatase (prostate), epidermal growth factor (carcinomas), CD2 (Hodgkin's disease, NHL lymphoma, multiple myeloma), CD3 epsilon (T cell lymphoma, lung, breast, gastric, ovarian cancers, autoimmune diseases, malignant ascites), CD19 (B cell malignancies), CD20 (non-Hodgkin's lymphoma, B-cell neoplasmas, autoimmune diseases), CD21 (B-cell lymphoma), CD22 (leukemia, lymphoma, multiple myeloma, SLE), CD30 (Hodgkin's lymphoma), CD33 (leukemia, autoimmune diseases), CD38 (multiple myeloma), CD40 (lymphoma, multiple myeloma, leukemia (CLL)), CD51 (metastatic melanoma, sarcoma), CD52 (leukemia), CD56 (small cell lung cancers, ovarian cancer, Merkel cell carcinoma, and the liquid tumor, multiple myeloma), CD66e (carcinomas), CD70 (metastatic renal cell carcinoma and non-Hodgkin lymphoma), CD74 (multiple myeloma), CD80 (lymphoma), CD98 (carcinomas), CD123 (leukemia), mucin (carcinomas), CD221 (solid tumors), CD227 (breast, ovarian cancers), CD262 (NSCLC and other cancers), CD309 (ovarian cancers), CD326 (solid tumors), CEACAM3 (colorectal, gastric cancers), CEACAM5 (CEA, CD66e) (breast, colorectal and lung cancers), DLL4 (A-like-4), EGFR (various cancers), CTLA4 (melanoma), CXCR4 (CD 184, heme-oncology, solid tumors), Endoglin (CD 105, solid tumors), EPCAM (epithelial cell adhesion molecule, bladder, head, neck, colon, NHL prostate, and ovarian cancers), ERBB2 (lung, breast, prostate cancers), FCGR1 (autoimmune diseases), FOLR (folate receptor, ovarian cancers), FGFR (carcinomas), GD2 ganglioside (carcinomas), G-28 (a cell surface antigen glycolipid, melanoma), GD3 idiotype (carcinomas), heat shock proteins (carcinomas), HER1 (lung, stomach cancers), HER2 (breast, lung and ovarian cancers), HLA-DR10 (NHL), HLA-DRB (NHL, B cell leukemia), human chorionic gonadotropin (carcinomas), IGF1R (solid tumors, blood cancers), IL-2 receptor (T-cell leukemia and lymphomas), IL-6R (multiple myeloma, RA, Castleman's disease, IL6 dependent tumors), integrins ($\alpha v\beta 3$, $\alpha 5\beta 1$, $\alpha 6\beta 4$, $\alpha 11\beta 3$, $\alpha 5\beta 5$, $\alpha v\beta 5$, for various cancers), MAGE-1 (carcinomas), MAGE-2 (carcinomas), MAGE-3 (carcinomas), MAGE 4 (carcinomas), anti-transferrin receptor (carcinomas), p97 (melanoma), MS4A1 (membrane-spanning 4-domains subfamily A member 1, Non-Hodgkin's B cell lymphoma, leukemia), MUC1 (breast, ovarian, cervix, bronchus and gastrointestinal cancer), MUC16 (CA125) (ovarian cancers), CEA (colorectal cancer), gp100 (melanoma), MARTI (melanoma), MPG (melanoma), MS4A1 (membrane-spanning 4-domains subfamily A, small cell lung cancers, NHL), nucleolin, Neu oncogene product (carcinomas), P21 (carcinomas), nectin-4 (carcinomas), paratope of anti-(N- glycolylneuraminic acid, breast, melanoma cancers), PLAP-like testicular alkaline phosphatase (ovarian, testicular cancers), PSMA (prostate tumors), PSA (prostate), ROB04, TAG 72 (tumour associated glycoprotein 72, AML, gastric, colorectal, ovarian cancers), T cell transmembrane protein (cancers), Tie (CD202b), tissue factor, TNFRSF10B (tumor necrosis factor receptor superfamily member 10B, carcinomas), TNFRSF13B (tumor necrosis factor receptor superfamily member 13B, multiple myeloma, NHL, other cancers, RA and SLE), TPBG (trophoblast glycoprotein, renal cell carcinoma), TRAIL-R1 (tumor necrosis apoptosis inducing ligand receptor 1, lymphoma, NHL, colorectal, lung cancers), VCAM-1 (CD106, Melanoma), VEGF, VEGF-A, VEGF-2 (CD309) (various cancers). Some other tumor associated antigen targets have been reviewed (Gerber, *et al*, mAbs 2009 1:247-253; Novellino *et al*, Cancer Immunol Immunother. 2005

54:187-207, Franke, *et al*, Cancer Biother Radiopharm. 2000, 15:459-76, Guo, *et al.*, Adv Cancer Res. 2013; 119: 421–475, Parmiani *et al.* J Immunol. 2007 178:1975-9). Examples of these antigens include Cluster of Differentiations (CD4, CD5, CD6, CD7, CD8, CD9, CD10, CDl la, CDl lb, CDl lc, CD12w, CD14, CD15, CD16, CDwl7, CD18, CD21, CD23, CD24, CD25, CD26, CD27, CD28, CD29, CD31, CD32, CD34, CD35, CD36, CD37, CD41, CD42, CD43, CD44, CD45, CD46, CD47, CD48, CD49b, CD49c, CD53, CD54, CD55, CD58, CD59, CD61, CD62E, CD62L, CD62P, CD63, CD68, CD69, CD71, CD72, CD79, CD81, CD82, CD83, CD86, CD87, CD88, CD89, CD90, CD91, CD95, CD96, CD100, CD103, CD105, CD106, CD109, CD117, CD120, CD127, CD133, CD134, CD135, CD138, CD141, CD142, CD143, CD144, CD147, CD151, CD152, CD154, CD156, CD158, CD163, CD166, .CD168, CD184, CDwl86, CD195, CD202 (a, b), CD209, CD235a, CD271, CD303, CD304), annexin Al, nucleolin, endoglin (CD105), ROB04, amino-peptidase N, -like-4 (DLL4), VEGFR-2 (CD309), CXCR4 (CD184), Tie2, B7-H3, WT1, MUC1, LMP2, HPV E6 E7, EGFRvIII, HER-2/neu, idiotype, MAGE A3, p53 nonmutant, NY-ESO-1, GD2, CEA, MelanA/MARTl, Ras mutant, gp100, p53 mutant, proteinase3 (PR1), bcr-abl, tyrosinase, survivin, hTERT, sarcoma translocation breakpoints, EphA2, PAP, ML-IAP, AFP, EpCAM, ERG (TMPRSS2 ETS fusion gene), NA17, PAX3, ALK, androgen receptor, cyclin B l, polysialic acid, MYCN, RhoC, TRP-2, GD3, fucosyl GMl , mesothelin, PSCA, MAGE Al, sLe(a), CYPIB I, PLACl, GM3, BORIS, Tn, GloboH, ETV6-AML, NY-BR-1, RGS5, SART3, STn, carbonic anhydrase IX, PAX5, OY-TES1, sperm protein 17, LCK, HMWMAA, AKAP-4, SSX2, XAGE 1, B7H3, legumain, Tie 2, Page4, VEGFR2, MAD-CT-1, FAP, PDGFR-β, MAD-CT-2, Notch1, ICAM1 and Fos-related antigen 1.

Additionally, preferred binding domains of the invention include those specific to antigens and epitope targets associated with infected cells that are known in the art. Such targets include but are not limited those derived from the following infectious agents are of interest: HIV virus (particularly antigens derived from the HIV envelope spike and/or gp120 and gp41 epitopes), Human papilloma virus (HPV), *Mycobacterium tuberculosis*, *Streptococcus agalactiae*, methicillin-resistant *Staphylococcus aureus*, *Legionella pneumophilia*, *Streptococcus pyogenes*, *Escherichia coli*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pneumococcus*, *Cryptococcus neoformans*, *Histoplasma capsulatum*, -*influenzae* B, *Treponema pallidum*, Lyme disease spirochetes, *Pseudomonas aeruginosa*, *Mycobacterium leprae*, *Brucella abortus*, rabies virus, *influenza virus*, *cytomegalovirus*, herpes simplex virus I, herpes simplex virus II, human serum parvo-like virus, respiratory syncytial virus, varicella-zoster virus, hepatitis B virus, hepatitis C virus, measles virus, adenovirus, human T-cell leukemia viruses, Epstein-Barr virus, murine leukemia virus, mumps virus, vesicular stomatitis virus, sindbis virus, lymphocytic choriomeningitis virus, wart virus, blue tongue virus, Sendai virus, feline leukemia virus, reovirus, polio virus, simian virus 40, mouse mammary tumor virus, dengue virus, rubella virus, West Nile virus, *Plasmodium falciparum*, *Plasmodium vivax*, *Toxoplasma gondii*, *Trypanosoma rangeli*, *Trypanosoma cruzi*, *Trypanosoma rhodesiensei*, *Trypanosoma brucei*, *Schistosoma mansoni*, *Schistosoma japonicum*, *Babesia bovis*, *Elmeria tenella*, *Onchocerca volvulus*, *Leishmania tropica*, *Trichinella spiralis*, *Theileria parva*, *Taenia hydatigena*, *Taenia ovis*, *Taenia saginata*, *Echinococcus granulosus*, *Mesocestoides corti*, *Mycoplasma arthritidis*, *M. hyorhinis*, *M. orale*, *M arginini*, *Acholeplasma laidlawii*, *M. salivarium* and *M. pneumoniae*.

T-Cell Receptors (TCRs)

T-cells are a subgroup of cells which together with other immune cell types (polymorphonuclear cells, eosinophils, basophils, mast cells, B-cells, NK cells), constitute the cellular component of the immune system. Under physiological conditions, T-cells function in immune surveillance and in the elimination of foreign antigen. However, under pathological conditions, there is compelling evidence that T-cells play a major role in the causation and propagation of disease. In these disorders, breakdown of T-cell immunological tolerance, either central or peripheral is a fundamental process in the causation of autoimmune disease.

The TCR complex is composed of at least seven transmembrane proteins. The disulfide-linked ($\alpha\beta$ or $\gamma\delta$) heterodimer forms the monotypic antigen recognition unit, while the invariant chains of CD3, consisting of ε, γ, δ, ζ, and η chains, are responsible for coupling the ligand binding to signaling pathways that result in T-cell activation and the elaboration of the cellular immune responses. Despite the gene diversity of the TCR chains, two structural features are common to all known subunits. First, they are transmembrane proteins with a single transmembrane spanning domain--presumably alpha-helical. Second, all TCR chains have the unusual feature of possessing a charged amino acid within the predicted transmembrane domain. The invariant chains have a single negative charge, conserved between the mouse and human, and the variant chains possess one (TCR-β) or two (TCR-α) positive charges. The transmembrane sequence of TCR-α is highly conserved in a number of species and thus phylogenetically may serve an important functional role. The octapeptide sequence containing the hydrophilic amino acids arginine and lysine is identical between the species.

A T-cell response is modulated by antigen binding to a TCR. One type of TCR is a membrane bound heterodimer consisting of an α and β chain resembling an immunoglobulin variable (V) and constant (C) region. The TCR α chain includes a covalently linked V-α and C-α chain, whereas the β chain includes a V-β chain covalently linked to a C-β chain. The V-α and V-β chains form a pocket or cleft that can bind a superantigen or antigen in the context of a major histocompatibility complex (MHC) (known in humans as an HLA complex). See, Davis *Ann. Rev. of Immunology* 3: 537 (1985); *Fundamental Immunology* 3rd Ed., W. Paul Ed. Rsen Press LTD. New York (1993).

The extracellular domains of the TCR chains (αβ or γδ) can also engineered as fusions to heterologous transmembrane domains for expression on the cell surface. Such TCRs may include fusions to CD3, CD28, CD8, 4-1BB and/or chimeric activation receptor (CAR) transmembrane or activation domains. TCRs can also be the soluble proteins comprising one or more of the antigen binding domains of αβ or γδ chains. Such TCRs may include the TCR variable domains or function fragments thereof with or without the TCR constant domains. Soluble TCRs may be heterodimeric or single-chain molecules.

Fc Domain

Protein complexes of the invention may contain an Fc domain. For example, PD-L1 TxM comprises an anti-PD-L1 scAb/huIL-15N72D:anti-PD-L1 scAb/huIL-15RαSu/huIgG1 Fc fusion complex. Fusion proteins that combine the Fc regions of IgG with the domains of another protein, such as various cytokines and soluble receptors have been reported (see, for example, Capon *et al.*, Nature, 337:525-531, 1989; Chamow *et al.*, Trends Biotechnol., 14:52-60, 1996); U.S. Pat. Nos. 5,116,964 and 5,541,087). The prototype fusion protein is a homodimeric protein linked through cysteine residues in the hinge region of IgG Fc, resulting in a molecule similar to an IgG molecule without the heavy chain variable and C_{H1} domains and light chains. The dimeric nature of fusion proteins comprising the Fc domain may be advantageous in providing higher order interactions (i.e. bivalent or bispecific binding) with other molecules. Due to the structural homology, Fc fusion proteins exhibit an *in vivo* pharmacokinetic profile comparable to that of human IgG with a similar isotype. Immunoglobulins of the IgG class are among the most abundant proteins in human blood, and their circulation half-lives can reach as long as 21 days. To extend the circulating half-life of IL-15 or an IL-15 fusion protein and/or to increase its biological activity, fusion protein complexes containing the IL-15 domain non-covalently bound to IL-15Rα covalently linked to the Fc portion of the human heavy chain IgG protein are described herein.

The term "Fc" refers to the fragment crystallizable region which is the constant region of an antibody that interacts with cell surface receptors called Fc receptors and some proteins of the complement system. Such an "Fc" is in dimeric form. The original immunoglobulin source of the native Fc is preferably of human origin and may be any of the immunoglobulins, although IgG1 and IgG2 are preferred. Native Fc's are made up of monomeric polypeptides that may be linked into dimeric or multimeric forms by covalent (i.e., disulfide bonds) and non-covalent association. The number of intermolecular disulfide bonds between monomeric subunits of native Fc molecules ranges from 1 to 4 depending on class (e.g., IgG, IgA, IgE) or subclass (e.g., IgG1, IgG2, IgG3, IgA1, IgGA2). One example of a native Fc is a disulfide-bonded dimer resulting from papain digestion of an IgG (see Ellison *et al.* (1982), Nucleic Acids Res. 10: 4071-9). The term "native Fc" as used herein is generic to the monomeric, dimeric, and multimeric forms. Fc domains containing binding sites for Protein A, Protein G, various Fc receptors and complement proteins. In some embodiments, Fc domain of the complex is capable of interacting with Fc receptors to mediate antibody-dependent cell-mediated cytotoxicity (ADCC) and/or antibody dependent cellular phagocytosis (ADCP). In other applications, the complex comprises an Fc domain (e.g., IgG4 Fc) that is incapable of effectively mediating ADCC or ADCP.

In some embodiments, the term "Fc variant" refers to a molecule or sequence that is modified from a native Fc, but still comprises a binding site for the salvage receptor, FcRn. International applications WO 97/34631 and WO 96/32478 describe exemplary Fc variants, as well as interaction with the salvage receptor. Thus, the term "Fc variant" comprises a molecule or sequence that is humanized from a non-human native Fc. Furthermore, a native Fc comprises sites that may be removed because they provide structural features or biological activity that are not required for the fusion molecules of the present invention. Thus, in certain embodiments, the term "Fc variant" comprises a molecule or sequence that alters one or more native Fc sites or residues that affect or are involved in (1) disulfide bond formation, (2) incompatibility with a selected host cell (3) N-terminal heterogeneity upon expression in a selected host cell, (4) glycosylation, (5) interaction with complement, (6) binding to an Fc receptor other than a salvage receptor, (7) antibody-dependent cellular cytotoxicity (ADCC) or (8) antibody-dependent cellular

Date Reçue/Date Received 2021-09-16

phagocytosis (ADCP). Such alterations can increase or decrease any one or more of these Fc properties. In certain embodiments, the Fc region is a human IgG Fc region and comprises one or more amino acid substitution, deletion, insertion or modification (e.g., carbohydrate chemical modification) introduced at any position within the Fc region. In certain embodiments a human IgG Fc variant comprises one or more amino acid residue mutants and has an increased binding affinity for an FcRn as compared to the wild type Fc region not comprising the one or more amino acid residue mutants. Fc binding interactions are essential for hinging to neonatal receptor, but not limited to, increasing serum half-life of IgG. Accordingly, in certain embodiments, human IgG Fc variants exhibit altered binding affinity for at least one or more Fc ligands (e.g., FcRns) relative to an antibody having the same amino acid sequence but not comprising the one or more amino acid substitution, deletion, insertion or modification (referred to herein as a "comparable molecule") such as, for example, an unmodified Fc region containing naturally occurring amino acid residues at the corresponding position in the Fc region. Fc variants are described in further detail hereinafter.

The term "Fc domain" encompasses native Fc and Fc variant molecules and sequences as defined above. As with Fc variants and native Fc's, the term "Fc domain" includes molecules in monomeric or multimeric form, whether digested from whole antibody or produced by recombinant gene expression or by other means.

Fusions Protein Complexes

The invention provides for fusion protein complexes. In some cases, the first protein comprises a first biologically active polypeptide covalently linked to interleukin-15 (IL-15) or functional fragment thereof; and the second protein comprises a second biologically active polypeptide covalently linked to soluble interleukin-15 receptor alpha (IL-15Rα) polypeptide or functional fragment thereof, where the IL-15 domain of a first protein binds to the soluble IL-15Rα domain of the second protein to form a soluble fusion protein complex. Fusion protein complexes of the invention also comprise immunoglobulin Fc domain or a functional fragment thereof linked to one or both of the first and second proteins. Preferably, the Fc domains linked to the fusion proteins interact to form a fusion protein complex. Such a complex may be stabilized by disulfide bond formation between the immunoglobulin Fc domains. In one aspect, the soluble fusion protein complexes of the invention include an IL-15 polypeptide, IL-15 variant or a functional fragment thereof and a soluble IL-15Rα polypeptide or a functional fragment thereof, wherein one or both of the IL-15 and IL-15Rα polypeptides further include an immunoglobulin Fc domain or a functional fragment thereof.

In certain examples, one or both of the first and second proteins comprises an antibody or functional fragment thereof. For example, one of the binding domain comprises a soluble anti-PD-L1 single chain antibody or functional fragment thereof. In another example, the other or second binding domain comprises an anti-CTLA4 single chain antibody or a disease antigen-specific antibody or functional fragment thereof. In one embodiment, the invention provides PD-L1 TxM, comprising a soluble anti-PD-L1 scAb/huIL-15N72D:anti-PD-L1 scAb/huIL-15RαSu/huIgG1 Fc fusion protein complex. In this complex, the huIL-15N72D and huIL-15RαSu domains interact and the huIgG1 Fc domains on two anti-PD-L1 scAb/huIL-15RαSu/huIgG1 Fc fusion protein to form a multichain fusion protein complex.

As used herein, the term "biologically active polypeptide" or "effector molecule" is meant an amino acid sequence such as a protein, polypeptide, or peptide; a sugar or polysaccharide; a lipid or a glycolipid, glycoprotein, or lipoprotein that can produce the desired effects as discussed herein. Effector molecules also include chemical agents. Also contemplated are effector molecule nucleic acids encoding a biologically active or effector protein, polypeptide, or peptide. Thus, suitable molecules include regulatory factors, enzymes, antibodies, or drugs as well as DNA, RNA, and oligonucleotides. The biologically active polypeptides or effector molecule can be naturally occurring or it can be synthesized from known components, e.g., by recombinant or chemical synthesis and can include heterologous components. A biologically active polypeptide or effector molecule is generally between about 0.1 to 100 KD or greater up to about 1000 KD, preferably between about 0.1, 0.2, 0.5, 1, 2, 5, 10, 20, 30 and 50 KD as judged by standard molecule sizing techniques such as centrifugation or SDS-polyacrylamide gel electrophoresis. Desired effects of the invention include, but are not limited to, for example, forming a fusion protein complex of the invention with increased binding activity, killing a target cell, e.g. either to induce cell proliferation or cell death, initiate an immune response, in preventing or treating a disease, or to act as a detection molecule for diagnostic purposes. For such detection, an assay could be used, for example an assay that includes sequential steps of culturing cells to proliferate same, and contacting the cells with a fusion complex of the invention and then evaluating whether the fusion complex inhibits further development of the cells.

Covalently linking the effector molecule to the fusion protein complexes of the invention in accordance with the invention provides a number of significant advantages. Fusion protein complexes of the invention can be produced that contain a single effector molecule, including a peptide of known structure. Additionally, a wide variety of effector molecules can be produced in similar DNA vectors. That is, a library of different effector molecules can be linked to the fusion protein complexes for recognition of infected or diseased cells. Further, for therapeutic applications, rather than administration of a fusion protein complex of the invention to a subject, a DNA expression vector coding for the fusion protein complex can be administered for *in vivo* expression of the fusion protein complex. Such an approach avoids costly purification steps typically associated with preparation of recombinant proteins and avoids the complexities of antigen uptake and processing associated with conventional approaches.

As noted, components of the fusion proteins disclosed herein, e.g., effector molecule such as cytokines, chemokines, growth factors, protein toxins, immunoglobulin domains or other bioactive molecules and any peptide linkers, can be organized in nearly any fashion provided that the fusion protein has the function for which it was intended. In particular, each component of the fusion protein can be spaced from another component by at least one suitable peptide linker sequence if desired. Additionally, the fusion proteins may include tags, e.g., to facilitate modification, identification and/or purification of the fusion protein. More specific fusion proteins are in the Examples described below.

Linkers

In certain embodiments, the fusion complexes of the invention also include a flexible linker sequence interposed between the IL-15 or IL-15Rα domains and the biologically active polypeptide. The linker sequence should allow effective positioning of the biologically active polypeptide with respect to the IL-15 or IL-15Rα domains to allow functional activity of both domains.

In certain cases, the soluble fusion protein complex has a linker wherein the first biologically active polypeptide is covalently linked to IL-15 (or functional fragment thereof) by polypeptide linker sequence. In other aspects, the soluble fusion protein complex as described herein has a linker wherein the second biologically active polypeptide is covalently linked to IL-15Rα polypeptide (or functional fragment thereof) by polypeptide linker sequence.

The linker sequence is preferably encoded by a nucleotide sequence resulting in a peptide that can effectively position the binding groove of a TCR molecule for recognition of a presenting antigen or the binding domain of an antibody molecule for recognition of an antigen. As used herein, the phrase "effective positioning of the biologically active polypeptide with respect to the IL-15 or IL-15Rα domains", or other similar phrase, is intended to mean the biologically active polypeptide linked to the IL-15 or IL-15Rα domains is positioned so that the IL-15 or IL-15Rα domains are capable of interacting with each other to form a protein complex. For example, the IL-15 or IL-15Rα domains are effectively positioned to allow interactions with immune cells to initiate or inhibit an immune reaction, or to inhibit or stimulate cell development.

The fusion complexes of the invention preferably also include a flexible linker sequence interposed between the IL-15 or IL-15Rα domains and the immunoglobulin Fc domain. The linker sequence should allow effective positioning of the Fc domain, biologically active polypeptide and IL-15 or IL-15Rα domains to allow functional activity of each domain. For example, the Fc domains are effectively positioned to allow proper fusion protein complex formation and/or interactions with Fc receptors on immune cells or proteins of the complement system to stimulate Fc-mediated effects including opsonization, cell lysis, degranulation of mast cells, basophils, and eosinophils, and other Fc receptor-dependent processes; activation of the complement pathway; and enhanced *in vivo* half-life of the fusion protein complex.

Linker sequences can also be used to link two or more polypeptides of the biologically active polypeptide to generate a single-chain molecule with the desired functional activity.

Preferably, the linker sequence comprises from about 7 to 20 amino acids, more preferably from about 10 to 20 amino acids. The linker sequence is preferably flexible so as not hold the biologically active polypeptide or effector molecule in a single undesired conformation. The linker sequence can be used, e.g., to space the recognition site from the fused molecule. Specifically, the peptide linker sequence can be positioned between the biologically active polypeptide and the effector molecule, e.g., to chemically cross-link same and to provide molecular flexibility. The linker preferably predominantly comprises amino acids with small side chains, such as glycine, alanine, and serine, to provide for flexibility. Preferably, about 80 or 90 percent or greater of the linker sequence comprises glycine, alanine, or serine residues, particularly glycine and serine residues.

Different linker sequences could be used including any of a number of flexible linker designs that have been used successfully to join antibody variable regions together (see, Whitlow, M. *et al*., (1991) Methods: A Companion to Methods in Enzymology, 2:97-105).

Pharmaceutical Therapeutics

The invention provides pharmaceutical compositions comprising fusion protein complexes for use as a therapeutic. In one aspect, fusion protein complex of the invention is administered systemically, for example, formulated in a pharmaceutically-acceptable buffer such as physiological saline. Preferable routes of administration include, for example, instillation into the bladder, subcutaneous, intravenous, intraperitoneal, intramuscular, intratumoral or intradermal injections that provide continuous, sustained, or effective levels of the composition in the patient. Treatment of human patients or other animals is carried out using a therapeutically effective amount of a therapeutic identified herein in a physiologically-acceptable carrier. Suitable carriers and their formulation are described, for example, in Remington's Pharmaceutical Sciences by E. W. Martin. The amount of the therapeutic agent to be administered varies depending upon the manner of administration, the age and body weight of the patient, and with the clinical symptoms of the neoplasia. Generally, amounts will be in the range of those used for other agents used in the treatment of other diseases associated with neoplasia, autoimmune or infectious diseases, although in certain instances lower amounts will be needed because of the increased specificity of the compound. A compound is administered at a dosage that enhances an immune response of a subject, or that reduces the proliferation, survival, or invasiveness of a neoplastic, infected, or autoimmune cell as determined by a method known to one skilled in the art.

Formulation of Pharmaceutical Compositions

The administration of the fusion protein complex of the invention for the treatment of a neoplasia, infectious or autoimmune disease is by any suitable means that results in a concentration of the therapeutic that, combined with other components, is effective in ameliorating, reducing, or stabilizing said neoplasia, infectious or autoimmune disease. The fusion protein complex of the invention may be contained in any appropriate amount in any suitable carrier substance, and is generally present in an amount of 1-95% by weight of the total weight of the composition. The composition may be provided in a dosage form that is suitable for parenteral (e.g., subcutaneous, intravenous, intramuscular, intravesicular, intratumoral or intraperitoneal) administration route. For example, the pharmaceutical compositions are formulated according to conventional pharmaceutical practice (see, e.g., Remington: The Science and Practice of Pharmacy (20th ed.), ed. A. R. Gennaro, Lippincott Williams & Wilkins, 2000 and Encyclopedia of Pharmaceutical Technology, eds. J. Swarbrick and J. C. Boylan, 1988-1999, Marcel Dekker, New York).

Human dosage amounts are initially determined by extrapolating from the amount of compound used in mice or non-human primates, as a skilled artisan recognizes it is routine in the art to modify the dosage for humans compared to animal models. For example, the dosage may vary from between about 1 μg compound/kg body weight to about 5000 mg compound/kg body weight; or from about 5 mg/kg body weight to about 4,000 mg/kg body weight or from about 10 mg/kg body weight to about 3,000 mg/kg body weight; or from about 50 mg/kg body weight to about 2000 mg/kg body weight; or from about 100 mg/kg body weight to about 1000 mg/kg body weight; or from about 150 mg/kg body weight to about 500 mg/kg body weight. For example, the dose is about 1, 5, 10, 25, 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1,000, 1,050, 1,100, 1,150, 1,200, 1,250, 1,300, 1,350, 1,400, 1,450, 1,500, 1,600, 1,700, 1,800, 1,900, 2,000, 2,500, 3,000, 3,500, 4,000, 4,500, or 5,000 mg/kg body weight. Alternatively, doses are in the range of about 5 mg compound/Kg body weight to about 20 mg compound/kg body weight. In another example, the doses are about 8, 10, 12, 14, 16 or 18 mg/kg body weight. Preferably, the fusion protein complex is administered at 0.5 mg/kg-about 10 mg/kg (e.g., 0.5, 1, 3, 5, 10 mg/kg). Of course, this dosage amount may be adjusted upward or downward, as is routinely done in such treatment protocols, depending on the results of the initial clinical trials and the needs of a particular patient.

Pharmaceutical compositions are formulated with appropriate excipients into a pharmaceutical composition that, upon administration, releases the therapeutic in a controlled manner. Examples include single or multiple unit tablet or capsule compositions, oil solutions, suspensions, emulsions, microcapsules, microspheres, molecular complexes, nanoparticles, patches, and liposomes. Preferably, the fusion protein complex is formulated in an excipient suitable for parenteral administration.

Parenteral Compositions

The pharmaceutical composition comprising a fusion protein complex of the invention are administered parenterally by injection, infusion, or implantation (subcutaneous, intravenous, intramuscular, intratumoral, intravesicular, intraperitoneal) in dosage forms, formulations, or via suitable delivery devices or implants containing conventional, non-toxic pharmaceutically acceptable carriers and adjuvants. The formulation and preparation of such compositions are well known to those skilled in the art of pharmaceutical formulation. Formulations can be found in Remington: The Science and Practice of Pharmacy, supra.

Compositions comprising a fusion protein complex of the invention for parenteral use are provided in unit dosage forms (e.g., in single-dose ampoules). Alternatively, the composition is provided in vials containing several doses and in which a suitable preservative may be added (see below). The composition is in the form of a solution, a suspension, an emulsion, an infusion device, or a delivery device for implantation, or it is presented as a dry powder to be reconstituted with water or another suitable vehicle before use. Apart from the active agent that reduces or ameliorates a neoplasia, infectious or autoimmune disease, the composition includes suitable parenterally acceptable carriers and/or excipients. The active therapeutic agent(s) may be incorporated into microspheres, microcapsules, nanoparticles, liposomes for controlled release. Furthermore, the composition may include suspending, solubilizing, stabilizing, pH-adjusting agents, tonicity adjusting agents, and/or dispersing, agents.

As indicated above, the pharmaceutical compositions comprising a fusion protein complex of the invention may be in a form suitable for sterile injection. To prepare such a composition, the suitable active therapeutic(s) are dissolved or suspended in a parenterally acceptable liquid vehicle. Among acceptable vehicles and solvents that may be employed are water, water adjusted to a suitable pH by addition of an appropriate amount of hydrochloric acid, sodium hydroxide or a suitable buffer, 1,3-butanediol, Ringer's solution, and isotonic sodium chloride solution and dextrose solution. The aqueous formulation may also contain one or more preservatives (e.g., methyl, ethyl, or n-propyl p-hydroxybenzoate). In cases where one of the compounds is only sparingly or slightly soluble in water, a dissolution enhancing or solubilizing agent can be added, or the solvent may include 10-60% w/w of propylene glycol.

The present invention provides methods of treating neoplasia, infectious or autoimmune diseases or symptoms thereof which comprise administering a therapeutically effective amount of a pharmaceutical composition comprising a compound of the formulae herein to a subject (e.g., a mammal such as a human). Thus, one embodiment is a method of treating a subject suffering from or susceptible to a neoplasia, infectious or autoimmune disease or symptom thereof. The method includes the step of administering to the mammal a therapeutic amount of an amount of a compound herein sufficient to treat the disease or disorder or symptom thereof, under conditions such that the disease or disorder is treated.

The methods herein include administering to the subject (including a subject identified as in need of such treatment) an effective amount of a compound described herein, or a composition described herein to produce such effect. Identifying a subject in need of such treatment can be in the judgment of a subject or a health care professional and can be subjective (e.g. opinion) or objective (e.g. measurable by a test or diagnostic method).

The therapeutic methods of the invention (which include prophylactic treatment) in general comprise administration of a therapeutically effective amount of the compounds herein, such as a compound of the formulae herein to a subject (e.g., animal, human) in need thereof, including a mammal, particularly a human. Such treatment will be suitably administered to subjects, particularly humans, suffering from, having, susceptible to, or at risk for a neoplasia, infectious disease, autoimmune disease, disorder, or symptom thereof. Determination of those subjects "at risk" can be made by any objective or subjective determination by a diagnostic test or opinion of a subject or health care provider (e.g., genetic test, enzyme or protein marker, Marker (as defined herein), family history, and the like). The fusion protein complexes of the invention may be used in the treatment of any other disorders in which an increase in an immune response is desired.

The invention also provides a method of monitoring treatment progress. The method includes the step of determining a level of diagnostic marker (Marker) (e.g., any target delineated herein modulated by a compound herein, a protein or indicator thereof, etc.) or diagnostic measurement (e.g., screen, assay) in a subject suffering from or susceptible to a disorder or symptoms thereof associated with neoplasia in which the subject has been administered a therapeutic amount of a compound herein sufficient to treat the disease or symptoms thereof. The level of Marker determined in the method can be compared to known levels of Marker in either healthy normal controls or in other afflicted patients to establish the subject's disease status. In some cases, a second level of Marker in the subject is determined at a time point later than the determination of the first level, and the two levels are compared to monitor the course of disease or the efficacy of the therapy. In certain aspects, a pre-treatment level of Marker in the subject is determined prior to beginning treatment according to this invention; this pre-treatment level of Marker can then be compared to the level of Marker in the subject after the treatment commences, to determine the efficacy of the treatment.

Combination Therapies

Optionally, the fusion protein complex of the invention is administered in combination with any other standard therapy; such methods are known to the skilled artisan and described in Remington's Pharmaceutical Sciences by E. W. Martin. If desired, fusion protein complexes of the invention is administered in combination with any conventional anti-neoplastic therapy, including but not limited to, immunotherapy, therapeutic antibodies, targeted therapy, surgery, radiation therapy, or chemotherapy.

Kits or Pharmaceutical Systems

Pharmaceutical compositions comprising the fusion protein complex of the invention may be assembled into kits or pharmaceutical systems for use in ameliorating a neoplasia, infectious or autoimmune disease. Kits or pharmaceutical systems according to this aspect of the invention comprise a carrier means, such as a box, carton, tube, having in close confinement therein one or more container means, such as vials, tubes, ampoules, bottles, and the like. The kits or pharmaceutical systems of the invention may also comprise associated instructions for using the fusion protein complex of the invention.

Recombinant Protein Expression

In general, preparation of the fusion protein complexes of the invention (e.g., components of a TxM complex) can be accomplished by procedures disclosed herein and by recognized recombinant DNA techniques.

In general, recombinant polypeptides are produced by transformation of a suitable host cell with all or part of a polypeptide-encoding nucleic acid molecule or fragment thereof in a suitable expression vehicle. Those skilled in the field of molecular biology will understand that any of a wide variety of expression systems may be used to provide the recombinant protein. The precise host cell used is not critical to the invention. A recombinant polypeptide may be produced in virtually any eukaryotic host (e.g., *Saccharomyces cerevisiae*, insect cells, e.g., Sf21 cells, or mammalian cells, e.g., NIH 3T3, HeLa, or preferably COS cells). Such cells are available from a wide range of sources (e.g., the American Type Culture Collection, Rockland, Md.; also, see, e.g., Ausubel *et al.*, Current Protocol in Molecular Biology, New York: John Wiley and Sons, 1997). The method of transfection and the choice of expression vehicle will depend on the host system selected. Transformation methods are described, e.g., in Ausubel *et al.* (supra); expression vehicles may be chosen from those provided, e.g., in Cloning Vectors: A Laboratory Manual (P. H. Pouwels *et al.*, 1985, Supp. 1987).

A variety of expression systems exist for the production of recombinant polypeptides. Expression vectors useful for producing such polypeptides include, without limitation, chromosomal, episomal, and virus-derived vectors, e.g., vectors derived from bacterial plasmids, from bacteriophage, from transposons, from yeast episomes, from insertion elements, from yeast chromosomal elements, from viruses such as baculoviruses, papova viruses, such as SV40, vaccinia viruses, adenoviruses, fowl pox viruses, pseudorabies viruses and retroviruses, and vectors derived from combinations thereof.

Once the recombinant polypeptide is expressed, it is isolated, e.g., using affinity chromatography. In one example, an antibody (e.g., produced as described herein) raised against the polypeptide may be attached to a column and used to isolate the recombinant polypeptide. Lysis and fractionation of polypeptide-harboring cells prior to affinity chromatography may be performed by standard methods (see, e.g., Ausubel *et al.*, supra). Once isolated, the recombinant protein can, if desired, be further purified, e.g., by high performance liquid chromatography (see, e.g., Fisher, Laboratory Techniques in Biochemistry and Molecular Biology, eds., Work and Burdon, Elsevier, 1980).

As used herein, biologically active polypeptides or effector molecules of the invention may include factors such as cytokines, chemokines, growth factors, protein toxins, immunoglobulin domains or other bioactive proteins such as enzymes. Also, biologically active polypeptides may include conjugates to other compounds such as non-protein toxins, cytotoxic agents, chemotherapeutic agents, detectable labels, radioactive materials, and such.

Cytokines of the invention are defined by any factor produced by cells that affect other cells and are responsible for any of a number of multiple effects of cellular immunity. Examples of cytokines include but are not limited to the IL-2 family, interferon (IFN), IL-10, IL-1, IL-17, TGF and TNF cytokine families, and to IL-1 through IL-35, IFN-α, IFN-β, IFNγ, TGF-β, TNF-α, and TNFβ.

In an aspect of the invention, the first protein comprises a first biologically active polypeptide covalently linked to interleukin-15 (IL-15) domain or a functional fragment thereof. IL-15 is a cytokine that affects T-cell activation and proliferation. IL-15 activity in affecting immune cell activation and proliferation is similar in some respects to IL-2, although fundamental differences have been well characterized (Waldmann, T A, 2006, *Nature Rev. Immunol.* 6:595-601).

In another aspect of the invention, the first protein comprises an interleukin-15 (IL-15) domain that is an IL-15 variant (also referred to herein as IL-15 mutant). The IL-15 variant preferably comprises a different amino acid sequence that the native (or wild type) IL-15 protein. The IL-15 variant preferably binds the IL-15Rα polypeptide and functions as an IL-15 agonist or antagonist. Preferably, IL-15 variants with agonist activity have super agonist activity. The IL-15 variant can function as an IL-15 agonist or antagonist independent of its association with IL-15Rα. IL-15 agonists are exemplified by comparable or increased biological activity compared to wild type IL-15. IL-15 antagonists are exemplified by decreased biological activity compared to wild type IL-15 or by the ability to inhibit IL-15-mediated responses. In some examples, the IL-15 variant binds with increased or decreased activity to the IL-15RβγC receptors. In some cases, the sequence of the IL-15 variant has at least one amino acid change, e.g. substitution or deletion, compared to the native IL-2 sequence, such changes resulting in IL-15 agonist or antagonist activity. Preferably, the amino acid substitutions/deletions are in the domains of IL-15 that interact with IL-15Rβ and/or γC. More preferably, the amino acid substitutions/deletions do not affect binding to the IL-15Rα polypeptide or the ability to produce the IL-15 variant. Suitable amino acid substitutions/deletions to generate IL-15 variants can be identified based on putative or known IL-15 structures, comparisons of IL-15 with homologous molecules such as IL-2 with known structure, through rational or random mutagenesis and functional assays, as provided herein, or other empirical methods. Additionally, suitable amino acid substitutions can be conservative or non-conservative changes and insertions of additional amino acids. Preferably, IL-15 variants of the invention contain one or more than one amino acid substitutions/deletions at position 6, 8, 10, 61, 65, 72, 92, 101, 104, 105, 108, 109, 111, or 112 of the mature human IL-15 sequence; particularly, D8N ("D8" refers to the amino acid and residue position in the native mature human IL-15 sequence and "N" refers to the substituted amino acid residue at that position in the IL-15 variant), I6S, D8A, D61A, N65A, N72R, V104P or Q108A substitutions result in IL-15 variants with antagonist activity and N72D substitutions result in IL-15 variants with agonist activity.

Chemokines, similar to cytokines, are defined as any chemical factor or molecule which when exposed to other cells are responsible for any of a number of multiple effects of cellular immunity. Suitable chemokines may include but are not limited to the CXC, CC, C, and CX_3C chemokine families and to CCL-1 through CCL-28, CXC-1 through CXC-17, XCL-1, XCL-2, CX3CL1, MIP-1b, IL-8, MCP-1, and Rantes.

Growth factors include any molecules which when exposed to a particular cell induce proliferation and/or differentiation of the affected cell. Growth factors include proteins and chemical molecules, some of which include: GM-CSF, G-CSF, human growth factor and stem cell growth factor. Additional growth factors may also be suitable for uses described herein.

Toxins or cytotoxic agents include any substance that has a lethal effect or an inhibitory effect on growth when exposed to cells. More specifically, the effector molecule can be a cell toxin of, e.g., plant or bacterial origin such as, e.g., diphtheria toxin (DT), shiga toxin, abrin, cholera toxin, ricin, saporin, pseudomonas exotoxin (PE), pokeweed antiviral protein, or gelonin. Biologically active fragments of such toxins are well known in the art and include, e.g., DT A chain and ricin A chain. Additionally, the toxin can be an agent active at the cell surface such as, e.g., phospholipase enzymes (e.g., phospholipase C).

Further, the effector molecule can be a chemotherapeutic drug such as, e.g., vindesine, vincristine, vinblastin, methotrexate, adriamycin, bleomycin, or cisplatin.

Additionally, the effector molecule can be a detectably-labeled molecule suitable for diagnostic or imaging studies. Such labels include biotin or streptavidin/avidin, a detectable nanoparticles or crystal, an enzyme or catalytically active fragment thereof, a fluorescent label such as green fluorescent protein, FITC, phycoerythrin, cychome, texas red or quantum dots; a radionuclide e.g., iodine-131, yttrium-90, rhenium-188 or bismuth-212; phosphorescent or chemiluminescent molecules or a label detectable by PET, ultrasound, or MRI such as Gd-- or paramagnetic metal ion-based contrast agents. See e.g., Moskaug, *et al. J. Biol. Chem.* 264, 15709 (1989); Pastan, I. *et al. Cell* 47, 641, 1986; Pastan *et al.*, Recombinant Toxins as Novel Therapeutic Agents, *Ann. Rev. Biochem.* 61, 331, (1992); “Chimeric Toxins” *Olsnes and Phil, Pharmac. Ther.*, 25, 355 (1982); published PCT application no. WO 94/29350; published PCT application no. WO 94/04689; published PCT application no. WO2005046449 and U.S. Pat. No. 5,620,939 for disclosure relating to making and using proteins comprising effectors or tags.

A protein fusion or conjugate complex that includes a covalently linked IL-15 and IL-15Rα domains has several important uses. For example, the protein fusion or conjugate complex comprising an anti-PD-L1 scAb can be employed to deliver the IL-15:IL-15Rα complex to certain cells, e.g., tumor cells that express PD-L1. Accordingly, the protein fusion or conjugate complex provides means of selectively damaging or killing cells comprising the ligand. Examples of cells or tissue capable of being damaged or killed by the protein fusion or conjugate complexes include tumors and virally or bacterially infected cells expressing one or more ligands. Cells or tissue susceptible to being damaged or killed can be readily assayed by the methods disclosed herein.

The IL-15 and IL-15Rα polypeptides of the invention suitably correspond in amino acid sequence to naturally occurring IL-15 and IL-15Rα molecules, e.g. IL-15 and IL-15Rα molecules of a human, mouse or other rodent, or other mammals. Sequences of these polypeptides and encoding nucleic acids are known in the literature, including human interleukin 15 (IL15) mRNA - GenBank: U14407.1, Mus musculus interleukin 15 (IL15) mRNA - GenBank: U14332.1, human interleukin-15 receptor alpha chain precursor (IL15RA) mRNA - GenBank: U31628.1, Mus musculus interleukin 15 receptor, alpha chain - GenBank: BC095982.1.

In some settings, it can be useful to make the protein fusion or conjugate complexes of the present invention polyvalent, e.g., to increase the valency of the sc-antibody. In particular, interactions between the IL-15 and IL-15Rα domains of the fusion protein complex provide a means of generating polyvalent complexes. In addition, the polyvalent fusion protein can be made by covalently or non-covalently linking together between one and four proteins (the same or different) by using e.g., standard biotin-streptavidin labeling techniques, or by conjugation to suitable solid supports such as latex beads. Chemically cross-linked proteins (for example cross-linked to dendrimers) are also suitable polyvalent species. For example, the protein can be modified by including sequences encoding tag sequences that can be modified such as the biotinylation BirA tag or amino acid residues with chemically reactive side chains such as Cys or His. Such amino acid tags or chemically reactive amino acids may be positioned in a variety of positions in the fusion protein, preferably distal to the active site of the biologically active polypeptide or effector molecule. For example, the C-terminus of a soluble fusion protein can be covalently linked to a tag or other fused protein which includes such a reactive amino acid(s). Suitable side chains can be included to chemically link two or more fusion proteins to a suitable dendrimer or other nanoparticle to give a multivalent molecule. Dendrimers are synthetic chemical polymers that can have any one of a number of different functional groups of their surface (D. Tomalia,

Date Reçue/Date Received 2021-09-16

Aldrichimica Acta, 26:91:101 (1993)). Exemplary dendrimers for use in accordance with the present invention include e.g. E9 starburst polyamine dendrimer and E9 combust polyamine dendrimer, which can link cystine residues. Exemplary nanoparticles include liposomes, core-shell particles, or PLGA-based particles.

In another aspect, one or both of the polypeptides of the fusion protein complex comprises an immunoglobulin domain. Alternatively, the protein binding domain-IL-15 fusion protein can be further linked to an immunoglobulin domain. The preferred immunoglobulin domains comprise regions that allow interaction with other immunoglobulin domains to form multichain proteins as provided above. For example, the immunoglobulin heavy chain regions, such as the IgG1 C_H2-C_H3, are capable of stably interacting to create the Fc region. Preferred immunoglobulin domains including Fc domains also comprise regions with effector functions, including Fc receptor or complement protein binding activity, and/or with glycosylation sites. In some aspects, the immunoglobulin domains of the fusion protein complex contain mutations that reduce or augment Fc receptor or complement binding activity or glycosylation or dimerization, thereby affecting the biological activity of the resulting protein. For example, immunoglobulin domains containing mutations that reduce binding to Fc receptors could be used to generate fusion protein complex of the invention with lower binding activity to Fc receptor-bearing cells, which may be advantageous for reagents designed to recognize or detect specific antigens.

<u>Nucleic Acids and Vectors</u>

The invention further provides nucleic acid sequences and particularly DNA sequences that encode the present fusion proteins (e.g., components of TxM). Preferably, the DNA sequence is carried by a vector suited for extrachromosomal replication such as a phage, virus, plasmid, phagemid, cosmid, YAC, or episome. In particular, a DNA vector that encodes a desired fusion protein can be used to facilitate preparative methods described herein and to obtain significant quantities of the fusion protein. The DNA sequence can be inserted into an appropriate expression vector, i.e., a vector that contains the necessary elements for the transcription and translation of the inserted protein-coding sequence. A variety of host-vector systems may be utilized to express the protein-coding sequence. These include mammalian cell systems infected with virus (e.g., vaccinia virus, adenovirus, etc.); insect cell systems infected with virus (e.g., baculovirus); microorganisms such as yeast containing yeast vectors, or bacteria transformed with bacteriophage DNA, plasmid DNA or cosmid DNA. Depending on the host-vector system utilized, any one of a number of suitable transcription and translation elements may be used. See, Sambrook *et al.*, supra and Ausubel *et al.*, supra.

Included in the invention are methods for making a soluble fusion protein complex, the method comprising introducing into a host cell a DNA vector as described herein encoding the first and second proteins, culturing the host cell in media under conditions sufficient to express the fusion proteins in the cell or the media and allow association between IL-15 domain of a first protein and the soluble IL-15Rα domain of a second protein to form the soluble fusion protein complex, purifying the soluble fusion protein complex from the host cells or media.

In general, a preferred DNA vector according to the invention comprises a nucleotide sequence linked by phosphodiester bonds comprising, in a 5' to 3' direction a first cloning site for introduction of a first nucleotide sequence encoding a biologically active polypeptide, operatively linked to a sequence encoding an effector molecule.

The fusion protein components encoded by the DNA vector can be provided in a cassette format. By the term "cassette" is meant that each component can be readily substituted for another component by standard recombinant methods. In particular, a DNA vector configured in a cassette format is particularly desirable when the encoded fusion complex is to be used against pathogens that may have or have capacity to develop serotypes.

To make the vector coding for a fusion protein complex, the sequence coding for the biologically active polypeptide is linked to a sequence coding for the effector peptide by use of suitable ligases. DNA coding for the presenting peptide can be obtained by isolating DNA from natural sources such as from a suitable cell line or by known synthetic methods, e.g. the phosphate triester method. See, e.g., Oligonucleotide Synthesis, IRL Press (M. J. Gait, ed., 1984). Synthetic oligonucleotides also may be prepared using commercially available automated oligonucleotide synthesizers. Once isolated, the gene coding for the biologically active polypeptide can be amplified by the polymerase chain reaction (PCR) or other means known in the art. Suitable PCR primers to amplify the biologically active polypeptide gene may add restriction sites to the PCR product. The PCR product preferably includes splice sites for the effector peptide and leader sequences necessary for proper expression and secretion of the biologically active polypeptide-effector fusion complex. The PCR product also preferably includes a sequence coding for the linker sequence, or a restriction enzyme site for ligation of such a sequence.

The fusion proteins described herein are preferably produced by standard recombinant DNA techniques. For example, once a DNA molecule encoding the biologically active polypeptide is isolated, sequence can be ligated to another DNA molecule encoding the effector polypeptide. The nucleotide sequence coding for a biologically active polypeptide may be directly joined to a DNA sequence coding for the effector peptide or, more typically, a DNA sequence coding for the linker sequence as discussed herein may be interposed between the sequence coding for the biologically active polypeptide and the sequence coding for the effector peptide and joined using suitable ligases. The resultant hybrid DNA molecule can be expressed in a suitable host cell to produce the fusion protein complex. The DNA molecules are ligated to each other in a 5' to 3' orientation such that, after ligation, the translational frame of the encoded polypeptides is not altered (i.e., the DNA molecules are ligated to each other in-frame). The resulting DNA molecules encode an in-frame fusion protein.

Other nucleotide sequences also can be included in the gene construct. For example, a promoter sequence, which controls expression of the sequence coding for the biologically active polypeptide fused to the effector peptide, or a leader sequence, which directs the fusion protein to the cell surface or the culture medium, can be included in the construct or present in the expression vector into which the construct is inserted. An immunoglobulin or CMV promoter is particularly preferred.

In obtaining variant biologically active polypeptide, IL-15, IL-15Rα or Fc domain coding sequences, those of ordinary skill in the art will recognize that the polypeptides may be modified by certain amino acid substitutions, additions, deletions, and post-translational modifications, without loss or reduction of biological activity. In particular, it is well-known that conservative amino acid substitutions, that is, substitution of one amino acid for another amino acid of similar size, charge, polarity, and conformation, are unlikely to significantly alter protein function. The 20 standard amino acids that are the constituents of proteins can be broadly categorized into four groups of conservative amino acids as follows: the nonpolar (hydrophobic) group includes alanine, isoleucine, leucine, methionine, phenylalanine, proline, tryptophan and valine; the polar (uncharged, neutral) group includes asparagine, cysteine, glutamine, glycine, serine, threonine and tyrosine; the positively charged (basic) group contains arginine, histidine and lysine; and the negatively charged (acidic) group contains aspartic acid and glutamic acid. Substitution in a protein of one amino acid for another within the same group is unlikely to have an adverse effect on the biological activity of the protein. In other instance, modifications to amino acid positions can be made to reduce or enhance the biological activity of the protein. Such changes can be introduced randomly or via site-specific mutations based on known or presumed structural or functional properties of targeted residue(s). Following expression of the variant protein, the changes in the biological activity due to the modification can be readily assessed using binding or functional assays.

Homology between nucleotide sequences can be determined by DNA hybridization analysis, wherein the stability of the double-stranded DNA hybrid is dependent on the extent of base pairing that occurs. Conditions of high temperature and/or low salt content reduce the stability of the hybrid, and can be varied to prevent annealing of sequences having less than a selected degree of homology. For instance, for sequences with about 55% G-C content, hybridization, and wash conditions of 40-50 C, 6 x SSC (sodium chloride/sodium citrate buffer) and 0.1% SDS (sodium dodecyl sulfate) indicate about 60-70% homology, hybridization, and wash conditions of 50-65 C, 1 x SSC and 0.1% SDS indicate about 82-97% homology, and hybridization, and wash conditions of 52 C, 0.1 x SSC and 0.1% SDS indicate about 99-100% homology. A wide range of computer programs for comparing nucleotide and amino acid sequences (and measuring the degree of homology) are also available, and a list providing sources of both commercially available and free software is found in Ausubel *et al.* (1999). Readily available sequence comparison and multiple sequence alignment algorithms are, respectively, the Basic Local Alignment Search Tool (BLAST) (Altschul *et al.*, 1997) and ClustalW programs. BLAST is available on the world wide web at ncbi.nlm.nih.gov and a version of ClustalW is available at 2.ebi.ac.uk.

The components of the fusion protein can be organized in nearly any order provided each is capable of performing its intended function. For example, in one embodiment, the biologically active polypeptide is situated at the C or N terminal end of the effector molecule.

Preferred effector molecules of the invention will have sizes conducive to the function for which those domains are intended. The effector molecules of the invention can be made and fused to the biologically active polypeptide by a variety of methods including well-known chemical cross-linking methods. See, e.g., Means, G. E. and Feeney, R. E. (1974) in *Chemical Modification of Proteins*, Holden-Day. See also, S. S. Wong (1991) in *Chemistry of Protein Conjugation and Cross-Linking*, CRC Press. However, it is generally preferred to use recombinant manipulations to make the in-frame fusion protein.

As noted, a fusion molecule or a conjugate molecule in accord with the invention can be organized in several ways. In an exemplary configuration, the C-terminus of the biologically active polypeptide is operatively linked to the N-terminus of the effector molecule. That linkage can be achieved by recombinant methods if desired. However, in another configuration, the N-terminus of the biologically active polypeptide is linked to the C-terminus of the effector molecule.

Alternatively, or in addition, one or more additional effector molecules can be inserted into the biologically active polypeptide or conjugate complexes as needed.

Vectors and Expression

A number of strategies can be employed to express the components of fusion protein complex of the invention (e.g., TxM). For example, a construct encoding one or more components of fusion protein complex of the invention can be incorporated into a suitable vector using restriction enzymes to make cuts in the vector for insertion of the construct followed by ligation. The vector containing the gene construct is then introduced into a suitable host for expression of the fusion protein. See, generally, Sambrook *et al.*, *supra*. Selection of suitable vectors can be made empirically based on factors relating to the cloning protocol. For example, the vector should be compatible with, and have the proper replicon for the host that is being employed. The vector must be able to accommodate the DNA sequence coding for the fusion protein complex that is to be expressed. Suitable host cells include eukaryotic and prokaryotic cells, preferably those cells that can be easily transformed and exhibit rapid growth in culture medium. Specifically, preferred hosts cells include prokaryotes such as *E. coli, Bacillus subtillus*, etc. and eukaryotes such as animal cells and yeast strains, e.g., *S. cerevisiae*. Mammalian cells are generally preferred, particularly J558, NSO, SP2-O or CHO. Other suitable hosts include, e.g., insect cells such as Sf9. Conventional culturing conditions are employed. See, Sambrook, *supra*. Stable transformed or transfected cell lines can then be selected. Cells expressing a fusion protein complex of the invention can be determined by known procedures. For example, expression of a fusion protein complex linked to an immunoglobulin can be determined by an ELISA specific for the linked immunoglobulin and/or by immunoblotting. Other methods for detecting expression of fusion proteins comprising biologically active polypeptides linked to IL-15 or IL-15Rα domains are disclosed in the Examples section which follows.

As mentioned generally above, a host cell can be used for preparative purposes to propagate nucleic acid encoding a desired fusion protein. Thus, a host cell can include a prokaryotic or eukaryotic cell in which production of the fusion protein is specifically intended. Thus, host cells specifically include yeast, fly, worm, plant, frog, mammalian cells and organs that are capable of propagating nucleic acid encoding the fusion. Non-limiting examples of mammalian cell lines which can be used include CHO dhfr-cells (Urlaub and Chasm, *Proc. Natl. Acad. Sci. USA*, 77:4216 (1980)), 293 cells (Graham *et al.*, *J Gen. Virol.*, 36:59 (1977)) or myeloma cells like SP2 or NSO (Galfre and Milstein, *Meth. Enzymol.*, 73(B):3 (1981)).

Host cells capable of propagating nucleic acid encoding a desired fusion protein complexes encompass non-mammalian eukaryotic cells as well, including insect (e.g., *Sp. frugiperda*), yeast (e.g., *S. cerevisiae, S. pombe, P. pastoris., K. lactis, H. polymorpha*; as generally reviewed by Fleer, R., *Current Opinion in Biotechnology*, 3(5):486496 (1992)), fungal and plant cells. Also contemplated are certain prokaryotes such as *E. coli* and *Bacillus*.

Nucleic acid encoding a desired fusion protein can be introduced into a host cell by standard techniques for transfecting cells. The term "transfecting" or "transfection" is intended to encompass all conventional techniques for introducing nucleic acid into host cells, including calcium phosphate co-precipitation, DEAE-dextran-mediated transfection, lipofection, electroporation, microinjection, viral transduction and/or integration. Suitable methods for transfecting host cells can be found in Sambrook *et al.* supra, and other laboratory textbooks.

Various promoters (transcriptional initiation regulatory region) may be used according to the invention. The selection of the appropriate promoter is dependent upon the proposed expression host. Promoters from heterologous sources may be used as long as they are functional in the chosen host.

Promoter selection is also dependent upon the desired efficiency and level of peptide or protein production. Inducible promoters such as tac are often employed in order to dramatically increase the level of protein expression in *E. coli*. Overexpression of proteins may be harmful to the host cells. Consequently, host cell growth may be limited. The use of inducible promoter systems allows the host cells to be cultivated to acceptable densities prior to induction of gene expression, thereby facilitating higher product yields.

Various signal sequences may be used according to the invention. A signal sequence which is homologous to the biologically active polypeptide coding sequence may be used. Alternatively, a signal sequence which has been selected or designed for efficient secretion and processing in the expression host may also be used. For example, suitable signal sequence/host cell pairs include the *B. subtilis* sacB signal sequence for secretion in *B. subtilis*, and the *Saccharomyces cerevisiae* α-mating factor or *P. pastoris* acid phosphatase phoI signal sequences for *P. pastoris* secretion. The signal sequence may be joined directly through the sequence encoding the signal peptidase cleavage site to the protein coding sequence, or through a short nucleotide bridge consisting of usually fewer than ten codons, where the bridge ensures correct reading frame of the downstream TCR sequence.

Elements for enhancing transcription and translation have been identified for eukaryotic protein expression systems. For example, positioning the cauliflower mosaic virus (CaMV) promoter 1,000 bp on either side of a heterologous promoter may elevate transcriptional levels by 10- to 400-fold in plant cells. The expression construct should also include the appropriate translational initiation sequences. Modification of the expression construct to include a Kozak consensus sequence for proper translational initiation may increase the level of translation by 10-fold.

A selective marker is often employed, which may be part of the expression construct or separate from it (e.g., carried by the expression vector), so that the marker may integrate at a site different from the gene of interest. Examples include markers that confer resistance to antibiotics (e.g., bla confers resistance to ampicillin for *E. coli* host cells, nptII confers kanamycin resistance to a wide variety of prokaryotic and eukaryotic cells) or that permit the host to grow on minimal medium (e.g., HIS4 enables *P. pastoris* or His$^-$ *S. cerevisiae* to grow in the absence of histidine). The selectable marker has its own transcriptional and translational initiation and termination regulatory regions to allow for independent expression of the marker. If antibiotic resistance is employed as a marker, the concentration of the antibiotic for selection will vary depending upon the antibiotic, generally ranging from 10 to 600 μg of the antibiotic/mL of medium.

The expression construct is assembled by employing known recombinant DNA techniques (Sambrook *et al.*, 1989; Ausubel *et al.*, 1999). Restriction enzyme digestion and ligation are the basic steps employed to join two fragments of DNA. The ends of the DNA fragment may require modification prior to ligation, and this may be accomplished by filling in overhangs, deleting terminal portions of the fragment(s) with nucleases (e.g., ExoIII), site directed mutagenesis, or by adding new base pairs by PCR. Polylinkers and adaptors may be employed to facilitate joining of selected fragments. The expression construct is typically assembled in stages employing rounds of restriction, ligation, and transformation of *E. coli*. Numerous cloning vectors suitable for construction of the expression construct are known in the art (λZAP and pBLUESCRIPT SK-1, Stratagene, La Jolla, CA, pET, Novagen Inc., Madison, WI, cited in Ausubel *et al*., 1999) and the particular choice is not critical to the invention. The selection of cloning vector will be influenced by the gene transfer system selected for introduction of the expression construct into the host cell. At the end of each stage, the resulting construct may be analyzed by restriction, DNA sequence, hybridization, and PCR analyses.

The expression construct may be transformed into the host as the cloning vector construct, either linear or circular, or may be removed from the cloning vector and used as is or introduced onto a delivery vector. The delivery vector facilitates the introduction and maintenance of the expression construct in the selected host cell type. The expression construct is introduced into the host cells by any of a number of known gene transfer systems (e.g., natural competence, chemically mediated transformation, protoplast transformation, electroporation, biolistic transformation, transfection, or conjugation) (Ausubel *et al*., 1999; Sambrook *et al*., 1989). The gene transfer system selected depends upon the host cells and vector systems used.

For instance, the expression construct can be introduced into *S. cerevisiae* cells by protoplast transformation or electroporation. Electroporation of *S. cerevisiae* is readily accomplished, and yields transformation efficiencies comparable to spheroplast transformation.

The present invention further provides a production process for isolating a fusion protein of interest. In the process, a host cell (e.g., a yeast, fungus, insect, bacterial or animal cell), into which has been introduced a nucleic acid encoding the protein of the interest operatively linked to a regulatory sequence, is grown at production scale in a culture medium to stimulate transcription of the nucleotides sequence encoding the fusion protein of interest. Subsequently, the fusion protein of interest is isolated from harvested host cells or from the culture medium. Standard protein purification techniques can be used to isolate the protein of interest from the medium or from the harvested cells. In particular, the purification techniques can be used to express and purify a desired fusion protein on a large-scale (i.e. in at least milligram quantities) from a variety of implementations including roller bottles, spinner flasks, tissue culture plates, bioreactor, or a fermentor.

An expressed protein fusion complex can be isolated and purified by known methods. Typically, the culture medium is centrifuged or filtered and then the supernatant is purified by affinity or immunoaffinity chromatography, e.g. Protein-A or Protein-G affinity chromatography or an immunoaffinity protocol comprising use of monoclonal antibodies that bind the expressed fusion complex. The fusion proteins of the present invention can be separated and purified by appropriate combination of known techniques. These methods include, for example, methods utilizing solubility such as salt precipitation and solvent precipitation, methods utilizing the difference in molecular weight such as dialysis, ultra-filtration, gel-filtration, and SDS-polyacrylamide gel electrophoresis, methods utilizing a difference in electrical charge such as ion-exchange column chromatography, methods utilizing specific affinity such as affinity chromatography, methods utilizing a difference in hydrophobicity such as reverse-phase high performance liquid chromatography and methods utilizing a difference in isoelectric point, such as isoelectric focusing electrophoresis, metal affinity columns such as Ni-NTA. See generally Sambrook *et al.* and Ausubel *et al.* supra for disclosure relating to these methods.

It is preferred that the fusion proteins of the present invention be substantially pure. That is, the fusion proteins have been isolated from cell substituents that naturally accompany it so that the fusion proteins are present preferably in at least 80% or 90% to 95% homogeneity (w/w). Fusion proteins having at least 98 to 99% homogeneity (w/w) are most preferred for many pharmaceutical, clinical and research applications. Once substantially purified the fusion protein should be substantially free of contaminants for therapeutic applications. Once purified partially or to substantial purity, the soluble fusion proteins can be used therapeutically, or in performing *in vitro* or *in vivo* assays as disclosed herein. Substantial purity can be determined by a variety of standard techniques such as chromatography and gel electrophoresis.

The present fusion protein complexes are suitable for *in vitro* or *in vivo* use with a variety of cells that are cancerous or are infected or that may become infected by one or more diseases.

Human interleukin-15 (huIL-15) is trans-presented to immune effector cells by the human IL-15 receptor α chain (huIL-15Rα) expressed on antigen presenting cells. IL-15Rα binds huIL-15 with high affinity (38 pM) primarily through the extracellular sushi domain (huIL-15RαSu). As described herein, the huIL-15 and huIL-15RαSu domains can be used as a scaffold to construct multi-domain fusion complexes.

IgG domains, particularly the Fc fragment, have been used successfully as dimeric scaffolds for a number of therapeutic molecules including approved biologic drugs. For example, etanercept is a dimer of soluble human p75 tumor necrosis factor-α (TNF-α) receptor (sTNFR) linked to the Fc domain of human IgG1. This dimerization allows etanercept to be up to 1,000 times more potent at inhibiting TNF-α activity than the monomeric sTNFR and provides the fusion with a five-fold longer serum half-life than the monomeric form. As a result, etanercept is effective at neutralization of the pro-inflammatory activity of TNF-α *in vivo* and improving patient outcomes for a number of different autoimmune indications.

In addition to its dimerization activity, the Fc fragment also provides cytotoxic effector functions through the complement activation and interaction with Fcγ receptors displayed on natural killer (NK) cells, neutrophils, phagocytes, and dendritic cells. In the context of anti-cancer therapeutic antibodies and other antibody domain-Fc fusion proteins, these activities likely play an important role in efficacy observed in animal tumor models and in cancer patients. However, these cytotoxic effector responses may not be sufficient in a number of therapeutic applications. Thus, there has been considerable interest in improving and expanding on the effector activity of the Fc domain and developing other means of recruiting cytolytic immune responses, including T cell activity, to the disease site via targeted therapeutic molecules. IgG domains have been used as a scaffold to form bispecific antibodies to improve the quality and quantity of products generated by the traditional hybridoma fusion technology. Although these methods bypass the shortcomings of other scaffolds, it has been difficult to produce bispecific antibodies in mammalian cells at levels sufficient to support clinical development and use.

In an effort to develop human-derived immunostimulatory multimeric scaffold, human IL-15 (huIL-15) and IL-15 receptor domains were used. huIL-15 is a member of the small four α-helix bundle family of cytokines that associates with the huIL-15 receptor α-chain (huIL-15Rα) with a high binding affinity (equilibrium dissociation constant (KD) ~10^{-11} M). The resulting complex is then trans-presented to the human IL-2/15 receptor β/common γ chain (huIL-15RβγC) complexes displayed on the surface of T cells and NK cells. This cytokine/receptor interaction results in expansion and activation of effector T cells and NK cells, which play an important role in eradicating virally infected and malignant cells. Normally, huIL-15 and huIL-15Rα are co-produced in dendritic cells to form complexes intracellularly that are subsequently secreted and displayed as heterodimeric molecules on cell surfaces. Thus, the characteristics of huIL-15 and huIL-15Rα interactions suggest that these inter chain binding domains could serve as a human-derived immunostimulatory scaffold to make soluble dimeric molecules capable of target-specific binding.

As described in detail below, an huIL-15:huIL-15RαSu-based scaffold was used to create PD-L1/TGFβRII/TxM. The dimeric fusion protein complexes retained immunostimulatory and target-specific biological activity of their huIL-15 domains and binding domains, indicating that the addition of huIL-15 and huIL-15Rα did not significantly alter the spatial arrangement of the fusion domains and provided an adequate degree of conformational flexibility without impacting cytokine activity. Thus, this scaffold could be used to form multivalent fusion complexes, such as the PD-L1 TxM, to increase the overall binding affinity of molecules. The soluble fusion proteins were produced at relatively high levels in recombinant CHO cell culture (mgs per liter in cell culture supernatant without extensive cell line screening or optimization) and could be readily purified from the cell culture supernatants.

The practice of the present invention employs, unless otherwise indicated, conventional techniques of molecular biology (including recombinant techniques), microbiology, cell biology, biochemistry, and immunology, which are well within the purview of the skilled artisan. Such techniques are explained fully in the literature, such as, "Molecular Cloning: A Laboratory Manual", second edition (Sambrook, 1989); "Oligonucleotide Synthesis" (Gait, 1984); "Animal Cell Culture" (Freshney, 1987); "Methods in Enzymology" "Handbook of Experimental Immunology" (Weir, 1996); "Gene Transfer Vectors for Mammalian Cells" (Miller and Calos, 1987); "Current Protocols in Molecular Biology" (Ausubel, 1987); "PCR: The Polymerase Chain Reaction", (Mullis, 1994); "Current Protocols in Immunology" (Coligan, 1991). These techniques are applicable to the production of the polynucleotides and polypeptides of the invention, and, as such, may be considered in making and practicing the invention. Particularly useful techniques for particular embodiments will be discussed in the sections that follow.

<u>Lymphoma</u>

Lymphoma is a type of blood cancer that occurs when B or T lymphocytes divide faster than normal cells or live longer than intended. For example, B cell lymphomas include both Hodgkin's lymphomas and most non-Hodgkin's lymphomas. B cell lymphomas express CD20.

Lymphoma may develop in the lymph nodes, spleen, bone marrow, blood, or other organs. These malignant cells often originate in the lymph nodes, presenting as an enlargement of the node, i.e., a solid tumor of lymphoid cells. Lymphoma is definitively diagnosed by a lymph node biopsy, i.e., a partial or total excision of a lymph node, which is examined under a microscope. This examination may reveal histopathological features that may indicate lymphoma. Treatment might involve chemotherapy, radiotherapy, and/or bone marrow transplantation.

The following examples are put forth so as to provide those of ordinary skill in the art with a complete disclosure and description of how to make and use the assay, screening, and therapeutic methods of the invention, and are not intended to limit the scope of what the inventors regard as their invention.

EXAMPLES

Example 1: Generation and Characterization of Fusion Protein Complexes Comprising IL-15, anti-PDL1, and TGFβRII domains

An important therapeutic approach for treating cancer or infectious disease relies on augmenting immune cell activity against the diseased cells. This strategy includes stimulating immune cells ex vivo followed by adoptive transfer and/or directly increasing immune cell levels or activity *in vivo* in the patient. Immune cells involved in these approaches may be those of the innate (i.e., NK cells) or adaptive (i.e., T cells) immune system.

One approach for augmenting immune activity is to provide immunostimulatory cytokines to the immune cells. Such cytokines are known in the art and can be used alone or in combination with other cytokines or agents. As described in detail below, we generated fusion protein complexes comprising an IL-15N72D:IL-15RαSu/Fc scaffold fused to an antibody (Ab) or antibody binding fragment which can binds to an immune checkpoint protein Programmed Death Ligand 1 (PD-L1), and a TGFβRII domain which are capable of binding TGFβ. These fusion protein complexes have advantages in binding to NK cells and signaling cell responses via cytokine receptors. The Fc region of Ig molecules forms a dimer to provide a soluble multi-polypeptide complex, can bind Protein A for the purpose of purification and can interact with Fcγ receptors on NK cells and macrophages, capable of mediating ADCC and ADCP. Additionally, interactions between the IL-15N72D and IL-15RαSu domains provides a means to link the IL-15N72D, TGFβRII and anti-PDL1 antibody (Ab) domains (and possibly other protein domains or agents) into a single immunostimulatory fusion protein complex.

Specifically, constructs were made linking a TGFβRII monomer or dimer or a single chain of anti-PDL1 Ab to the IL-15N72D and IL-15RαSu/Fc chains. In the case of TGFβRII dimer, the peptide consists of two TGFβRII that can be linked via a flexible linker sequence to generate an active single-chain form. In some cases, either TGFβRII dimer and/or anti-PDL1 Ab is linked to the N-terminus of the IL-15N72D and/or IL-15RαSu/Fc chains through genetically engineered fusions. In other cases, a TGFβRII polypeptide is linked to the C-terminus of IL-15RαSu/Fc chains with/without linker. Specific fusion protein complexes comprising an IL-15N72D:IL-15RαSu/Fc scaffold fused to TGFβRII and anti-PDL1binding domains are described below.

A: αPDL1/ TGFβRII /TXM (N-810C): A fusion protein complex was generated comprising TGFβRII dimer /IL-15RαSu/Fc and anti-PDL1-IL15N72D fusion proteins.

A1: TGFβRII /IL-15RαSu/Fc: the human TGFβRII coding sequences were obtained from the UniProt website and optimized for CHO cell lines transfection. Specifically, gene constructs were made by linking the coding sequence for a TGFβRII to another TGFβRII by a linker to generate sequence encoding a TGFβRII dimer, and then directly linking this sequence to one encoding the N-terminus of IL-15RαSu/Fc chain. DNA sequence of the construct was synthesized by Genewiz Inc and used for molecular cloning into the expression vector.

The nucleic acid sequence of the TGFβRII /IL-15RαSu/Fc construct (including signal peptide sequence) is as follows (SEQ ID NO: 1):

(Signal peptide)

atgaagtgggtgaccttcatcagcctgctgttcctgttctccagcgcctactcc

(Human TGFβRII*)*

atcccccccatgtgcaaaagagcgtgaacaacgatatgatcgtgaccgacaacaacggcgccgtgaagtttccccagctctgcaag
ttctgcgatgtcaggttcagcacctgcgataatcagaagtcctgcatgtccaactgcagcatcacctccatctgcgagaagccccaaga

agtgtgcgtggccgtgtggcggaaaaatgacgagaacatcaccctggagaccgtgtgtcacgaccccaagctcccttatcacgacttc attctggaggacgctgcctcccccaaatgcatcatgaaggagaagaagaagcccggagagaccttctttatgtgttcctgtagcagcg acgagtgtaacgacaacatcatcttcagcgaagagtacaacaccagcaaccctgat

(Linker)

ggaggtggcggatccggaggtggaggttctggtggaggtgggagt

(Human TGFβRII*)*

attcctccccacgtgcagaagagcgtgaataatgacatgatcgtgaccgataacaatggcgccgtgaaatttccccagctgtgcaaatt ctgcgatgtgaggttttccacctgcgacaaccagaagtcctgtatgagcaactgctccatcacctccatctgtgagaagcctcaggagg tgtgcgtggctgtctggcggaagaatgacgagaatatcaccctggaaaccgtctgccacgatcccaagctgccctaccacgatttcatc ctggaagacgccgccagccctaagtgcatcatgaaagagaaaaagaagcctggcgagaccttttcatgtgctcctgcagcagcgac gaatgcaacgacaatatcatctttagcgaggaatacaataccagcaaccccgac

(Human IL-15R α sushi domain)

atcacgtgtcctcctcctatgtccgtggaacacgcagacatctgggtcaagagctacagcttgtactccagggagcggtacatttgtaac tctggtttcaagcgtaaagccggcacgtccagcctgacggagtgcgtgttgaacaaggccacgaatgtcgcccactggacaaccccc agtctcaaatgcattaga

(Human IgG1 CH2-CH3 (Fc) domain)

gagccgaaatcttgtgacaaaactcacacatgcccaccgtgcccagcacctgaactcctggggggaccgtcagtcttcctcttccccc caaaacccaaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtc aagttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccgcgggaggagcagtacaacagcacgtaccgtg tggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagccc ccatcgagaaaaccatctccaaagccaaagggcagccccgagaaccacaggtgtacaccctgcccccatcccgggatgagctgac caagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggagtgggagagcaatgggcagccgg agaacaactacaagaccacgcctcccgtgctggactccgacggctccttcttcctctacagcaagctcaccgtggacaagagcaggt ggcagcaggggaacgtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagcctctccctgtctcctgg taaa

The amino acid sequence of the be TGFβRII /IL-15RαSu/Fc fusion protein (including signal peptide sequence) is as follows (SEQ ID NO: 2):

(Signal peptide)

MKWVTFISLLFLFSSAYS

(Human TGFβRII*)*

IPPHVQKSVNNDMIVTDNNGAVKFPQLCKFCDVRFSTCDNQKSCMSNCSITSICEKPQ
EVCVAVWRKNDENITLETVCHDPKLPYHDFILEDAASPKCIMKEKKKPGETFFMCSC
SSDECNDNIIFSEEYNTSNPD

(*Linker*)

GGGGSGGGGSGGGGS

(*Human* TGFβRII)

IPPHVQKSVNNDMIVTDNNGAVKFPQLCKFCDVRFSTCDNQKSCMSNCSITSICEKPQ
EVCVAVWRKNDENITLETVCHDPKLPYHDFILEDAASPKCIMKEKKKPGETFFMCSC
SSDECNDNIIFSEEYNTSNPD

(Human IL-15R α sushi domain)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWT
TPSLKCIR

(Human IgG1 CH2-CH3 (Fc) domain)

EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA
LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
SLSPGK

In some cases, the leader peptide is cleaved from the intact polypeptide to generate the mature form that may be soluble or secreted.

A2: Anti-PDL1-15N72D: Constructs were also made by linking the synthesized single chain anti-PDL1 antibody nucleotide sequence to the N-terminus coding region of IL-15N72D via overlapping PCR to generate anti-PDL1-15N72D. Specifically, the light chain and heavy chain variable domain sequences of anti-PDL1 Ab were linked by a sequence encoding flexible linker to form a single chain anti-PDL1 antibody construct, then the single chain anti-PD-L1 sequence was linked to the sequence encoding the N-terminus of IL-15N72D. The sequence of single chain anti-PDL1 Ab was synthesized by Genewiz Inc, and was then linked to the N-terminal coding region of IL-15N72D via overlapping PCR. The nucleic acid and protein sequences of a construct comprising single chain anti-PDL1 Ab linked to the N-terminus of IL15N72D are shown below.

The nucleic acid sequence of the anti-PDL1/IL-15N72D construct (including leader sequence) is as follows (SEQ ID NO: 3):

(Signal peptide)

atgaagtgggtgaccttcatcagcctgctgttcctgttctccagcgcctactcc

(anti-PDL1 single chain)

(anti-PDL1 light chain variable domain)

aacatccagatgacccagtcccctagctccgtgtccgcctccgtgggagatcgggtgaccatcacctgtagggcctcccaggacatct
ccaggtggctggcctggtaccagcagaagcccggcaaggcccccaagctgctgatctacgccgcctcctccctgcagtccggagtg
cctagcaggttctccggctccggatccggcacagacttcgccctgaccatctcctccctgcagcccgaggacttcgccacctactactg
ccagcaggccgactccaggttctccatcaccttcggccagggcaccaggctggagatcaagaggg

(Linker)

ggaggtggcggatccggaggtggaggttctggtggaggtgggagt

(anti-PDL1 heavy chain variable domain)

gaggtgcagctggtgcagtccggaggaggactggtgcagcctggcggatccctgaggctgtcctgtgccgcttccggcttcaccttc
agctcctactccatgaactgggtgaggcaggcccctggaaagggcctggagtgggtgtcctacatctccagctcctcctccaccatcc
agtacgccgactccgtgaagggcaggttcaccatctccagggacaacgccaagaactccctgtacctgcagatgaacagcctgagg
gacgaggacaccgccgtgtactactgcgccaggggcgactattactacggcatggacgtgtggggccagggaaccaccgtgaccg
tgtcctcc

(Human IL-15N72D)

aactgggttaacgtaataagtgatttgaaaaaaattgaagatcttattcaatctatgcatattgatgctactttatatacggaaagtgatgttc
accccagttgcaaagtaacagcaatgaagtgctttctcttggagttacaagttatttcacttgagtccggagatgcaagtattcatgataca
gtagaaaatctgatcatcctagcaaacgacagtttgtcttctaatgggaatgtaacagaatctggatgcaaagaatgtgaggaactggag
gaaaaaaatattaaagaatttttgcagagttttgtacatattgtccaaatgttcatcaacacttct

The amino acid sequence of the anti-PDL1/IL-15N72D fusion protein (including leader sequence) is as follows (SEQ ID NO: 4):

(Signal peptide)

MKWVTFISLLFLFSSAYS

(anti-PDL1 single chain)

(anti-PDL1 light chain variable domain)

NIQMTQSPSSVSASVGDRVTITCRASQDISRWLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFALTISSLQPEDFATYYCQQADSRFSITFGQGTRLEIKR

(Linker)

GGGGSGGGGSGGGGS

(anti-PDL1 heavy chain variable domain)

EVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYISSSSSTIQYADSVKGRFTISRDNAKNSLYLQMNSLRDEDTAVYYCARGDYYYGMDVWGQGTTVTVSS

(Human IL-15N72D)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANDSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

In some cases, the leader peptide is cleaved from the intact polypeptide to generate the mature form that may be soluble or secreted.

Co-transfection and protein purification. TGFβRII/IL-15RαSu/Fc and anti-PDL1-IL15N72D constructs were cloned into expression vectors as described previously (U.S. Patent No. 8,507,222, at Example 1), and the expression vectors were transfected into CHO cells. Co-expression of the two constructs in CHO cells allowed for formation and secretion of a soluble anti-PDL1-IL15N72D: TGFβRII /IL-15RαSu/Fc fusion protein complex (referred to as anti-PDL1/ TGFβRII /TxM). The anti-PDL1/ TGFβRII /TxM protein was purified from CHO cell culture supernatant by Protein A affinity chromatography and size exclusion chromatography resulting in soluble (non-aggregated) fusion protein complexes consisting of TGFβRII/IL-15RαSu/Fc dimers and anti-PDL1-IL15N72D fusion proteins (FIG. 2).

Reduced SDS-PAGE analysis of the Protein A-purified anti-PDL1-IL15N72D: TGFβRII /IL-15RαSu/Fc fusion protein complexes is shown in FIG. 3. Bands corresponding to the soluble anti-PDL1-IL15N72D: TGFβRII /IL-15RαSu/Fc fusion protein proteins at ~40 kDa and ~70kDa, respectively, were observed (FIGS. 3 and 8).

B: TGFβRII/ αPDL1/TXM (N-810B)

For a second approach, a similar fusion protein complex was generated comprising TGFβRII -IL15N72D: anti-PDL1-15RαSu/Fc fusion protein.

Date Reçue/Date Received 2021-09-16

B1: Anti-PDL1-15RαSu/Fc: The anti-PDL1-15RαSu/Fc gene construct was generated by linking the synthesized single chain anti-PDL1 Ab nucleotide sequence to the N-terminal coding region of IL-15RαSu/Fc via overlapping PCR. The nucleic acid and protein sequences of a construct comprising the anti-PDL1 Ab linked to the N-terminus of IL-15RαSu/Fc are shown below.

The nucleic acid sequence of the anti-PDL1/IL-15RαSu/Fc construct (including signal peptide sequence) is as follows (SEQ ID NO: 5):

(Signal peptide)

atgaagtgggtgaccttcatcagcctgctgttcctgttctccagcgcctactcc

(anti-PDL1 single chain)

(anti-PDL1 light chain variable domain)

aacatccagatgacccagtcccctagctccgtgtccgcctccgtgggagatcgggtgaccatcacctgtagggcctcccaggacatct
ccaggtggctggcctggtaccagcagaagcccggcaaggcccccaagctgctgatctacgccgcctcctccctgcagtccggagtg
cctagcaggttctccggctccggatccggcacagacttcgccctgaccatctcctccctgcagcccgaggacttcgccacctactactg
ccagcaggccgactccaggttctccatcaccttcggccagggcaccaggctggagatcaagagg

(Linker)

ggaggtggcggatccggaggtggaggttctggtggaggtgggagt

(anti-PDL1 heavy chain variable domain)

gaggtgcagctggtgcagtccggaggaggactggtgcagcctggcggatccctgaggctgtcctgtgccgcttccggcttcaccttc
agctcctactccatgaactgggtgaggcaggcccctggaaagggcctggagtgggtgtcctacatctccagctcctcctccaccatcc
agtacgccgactccgtgaagggcaggttcaccatctccagggacaacgccaagaactccctgtacctgcagatgaacagcctgagg
gacgaggacaccgccgtgtactactgcgccaggggcgactattactacggcatggacgtgtggggccagggaaccaccgtgaccg
tgtcctcc

(Human IL-15R α sushi domain)

atcacgtgtcctcctcctatgtccgtggaacacgcagacatctgggtcaagagctacagcttgtactccagggagcggtacatttgtaac
tctggtttcaagcgtaaagccggcacgtccagcctgacggagtgcgtgttgaacaaggccacgaatgtcgcccactggacaaccccc
agtctcaaatgcattaga

(Human IgG1 CH2-CH3 (Fc) domain)

gagccgaaatcttgtgacaaaactcacacatgcccaccgtgcccagcacctgaactcctggggggaccgtcagtcttcctcttccccc caaaacccaaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtc aagttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccgcgggaggagcagtacaacagcacgtaccgtg tggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagccc ccatcgagaaaaccatctccaaagccaaagggcagccccgagaaccacaggtgtacaccctgcccccatcccgggatgagctgac caagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggagtgggagagcaatgggcagccgg agaacaactacaagaccacgcctcccgtgctggactccgacggctccttcttcctctacagcaagctcaccgtggacaagagcaggt ggcagcaggggaacgtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagcctctccctgtctcctgg taaa

The amino acid sequence of the anti-PDL1/IL-15RαSu/Fc fusion protein (including signal peptide sequence) is as follows (SEQ ID NO: 6):

(Signal peptide)

MKWVTFISLLFLFSSAYS

(anti-PDL1 single chain)

(anti-PDL1 light chain variable domain)

NIQMTQSPSSVSASVGDRVTITCRASQDISRWLAWYQQKPGKAPKLLIYAASSLQSG VPSRFSGSGSGTDFALTISSLQPEDFATYYCQQADSRFSITFGQGTRLEIKR

(Linker)

GGGGSGGGGSGGGGS

(anti-PDL1 heavy chain variable domain)

EVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYISSSSST IQYADSVKGRFTISRDNAKNSLYLQMNSLRDEDTAVYYCARGDYYYGMDVWGQG TTVTVSS

(Human IL-15R α sushi domain)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWT TPSLKCIR

(Human IgG1 CH2-CH3 (Fc) domain)

EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA

LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
SLSPGK

In some cases, the leader peptide is cleaved from the intact polypeptide to generate the mature form that may be soluble or secreted.

B2: TGFβRII -IL15N72D: Specifically, constructs were made linking a TGFβRII to another TGFβRII by a linker to generate a TGFβRII dimer, and then directly linking the TGFβRII dimer sequence to the N-terminus of IL15N72D. The DNA fragment encoding TGFβRII -IL15N72D was synthesized by GENEWIZ.

The nucleic acid sequence of the TGFβRII -IL15N72D construct (including signal peptide sequence) is as follows (SEQ ID NO: 7):

(Signal peptide)

atgaagtgggtgaccttcatcagcctgctgttcctgttctccagcgcctactcc

(Human TGFβRII)

atccccccccatgtgcaaaagagcgtgaacaacgatatgatcgtgaccgacaacaacggcgccgtgaagtttccccagctctgcaag
ttctgcgatgtcaggttcagcacctgcgataatcagaagtcctgcatgtccaactgcagcatcacctccatctgcgagaagccccaaga
agtgtgcgtggccgtgtggcggaaaaatgacgagaacatcaccctggagaccgtgtgtcacgaccccaagctcccttatcacgacttc
attctggaggacgctgcctcccccaaatgcatcatgaaggagaagaagaagcccggagagaccttctttatgtgttcctgtagcagcg
acgagtgtaacgacaacatcatcttcagcgaagagtacaacaccagcaaccctgat

(Linker)

ggaggtggcggatccggaggtggaggttctggtggaggtgggagt

(Human TGFβRII)

attcctccccacgtgcagaagagcgtgaataatgacatgatcgtgaccgataacaatggcgccgtgaaatttccccagctgt
gcaaattctgcgatgtgaggttttccacctgcgacaaccagaagtcctgtatgagcaactgctccatcacctccatctgtgagaagcctc
aggaggtgtgcgtggctgtctggcggaagaatgacgagaatatcaccctggaaaccgtctgccacgatcccaagctgccctaccacg
atttcatcctggaagacgccgccagccctaagtgcatcatgaaagagaaaaagaagcctggcgagacctttttcatgtgctcctgcagc
agcgacgaatgcaacgacaatatcatctttagcgaggaatacaataccagcaaccccgac

(Human IL-15N72D)

aactgggttaacgtaataagtgatttgaaaaaaattgaagatcttattcaatctatgcatattgatgctactttatatacggaaagtgatgttc
accccagttgcaaagtaacagcaatgaagtgctttctcttggagttacaagttatttcacttgagtccggagatgcaagtattcatgataca

gtagaaaatctgatcatcctagcaaacgacagtttgtcttctaatgggaatgtaacagaatctggatgcaaagaatgtgaggaactggaggaaaaa aatattaaagaatttttgcagagttttgtacatattgtccaaatgttcatcaacacttct

The amino acid sequence of the TGFβRII -IL15N72D fusion protein (including leader sequence) is as follows (SEQ ID NO: 8):

(Signal peptide)

MKWVTFISLLFLFSSAYS

(Human TGFβRII)

IPPHVQKSVNNDMIVTDNNGAVKFPQLCKFCDVRFSTCDNQKSCMSNCSITSICEKPQEVCV AVWRKNDENITLETVCHDPKLPYHDFILEDAASPKCIMKEKKKPGETFFMCSCSSDECNDNII FSEEYNTSNPD

(*Linker*)

GGGGSGGGGSGGGGS

(Human TGFβRII)

IPPHVQKSVNNDMIVTDNNGAVKFPQLCKFCDVRFSTCDNQKSCMSNCSITSICEKPQEVCV AVWRKNDENITLETVCHDPKLPYHDFILEDAASPKCIMKEKKKPGETFFMCSCSSDECNDNII FSEEYNTSNPD

(Human IL-15N72D)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTV ENLIILANDSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

In some cases, the leader peptide is cleaved from the intact polypeptide to generate the mature form that may be soluble or secreted.

Co-transfection and protein purification: The TGFβRII dimer / IL-15N72D and αPDL1/IL-15RαSu/Fc constructs were cloned into expression vectors as described previously (U.S. Patent No. 8,507,222, at Example 1), and the expression vectors were transfected into CHO cells. Co-expression of the two constructs in CHO cells allowed for formation and secretion of the soluble TGFβRII /IL-15N72D: αPDL1/IL-15RαSu/Fc fusion protein complex (referred to as TGFβRII / αPDL1/TxM).

Date Reçue/Date Received 2021-09-16

The TGFβRII /anti-PDL1/TxM protein was purified from CHO cell culture supernatant by Protein A affinity chromatography and size exclusion chromatography resulting in soluble (non-aggregated) fusion protein complexes (FIG. 5).

Reduced SDS-PAGE analysis of the Protein A-purified TGFβRII /anti-PDL1/TxM fusion protein complexes is shown in FIG. 6. Bands corresponding to the soluble anti-PDL1-IL15N72D: TGFβRII /IL-15RαSu/Fc fusion protein proteins at ~50 kDa and ~60 kDa, respectively, were observed (FIGS. 6 and 8).

C: αPDL1/ TXM/ TGFβRII (N-810A)

Fusion protein complexes were also generated, which comprising IL15N72D and anti-PDL1/IL-15RαSu/Fc/ TGFβRII. In these constructs, TGFβRII was fused to C-terminal of anti-PDL1-IL-15RαSu/Fc with or without linker (FIG. 7).

C1: IL15N72D: IL15N72D construct was made as described previously (U.S. Patent No. 8,507,222, at Example 1).

The nucleic acid sequence of the IL15N72D construct (including signal peptide sequence) is as follows (SEQ ID NO: 9):

(Signal peptide)

atgaagtgggtgaccttcatcagcctgctgttcctgttctccagcgcctactcc

(Human IL-15N72D)

aactgggttaacgtaataagtgatttgaaaaaaattgaagatcttattcaatctatgcatattgatgctactttatatacggaaagtgatgttcaccccagt
tgcaaagtaacagcaatgaagtgctttctcttggagttacaagttatttcacttgagtccggagatgcaagtattcatgatacagtagaaaatctgatca
tcctagcaaacgacagtttgtcttctaatgggaatgtaacagaatctggatgcaaagaatgtgaggaactggaggaaaaaaatattaaagaatttttg
cagagttttgtacatattgtccaaatgttcatcaacacttct

The amino acid sequence of the IL15N72D protein (including leader sequence) is as follows (SEQ ID NO: 10):

(Signal peptide)

MKWVTFISLLFLFSSAYS

(Human IL-15N72D)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTV
ENLIILANDSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Date Reçue/Date Received 2021-09-16

In some cases, the leader peptide is cleaved from the intact polypeptide to generate the mature form that may be soluble or secreted.

C2: anti-PDL1/IL-15RαSu/Fc/ TGFβRII: Two constructs were made for this fusion protein (FIG. 7). In the first construct, TGFβRII was fused directly to C-terminal of anti-PDL1/IL-15RαSu/Fc. In the second construct, a linker was added between TGFβRII and anti-PDL1/IL-15RαSu/Fc to increase the flexibility. Both of the constructs, the nucleic acid sequences encoding anti-PDL1/IL-15RαSu/Fc/ TGFβRII were synthesized by Genewiz. A nucleic acid mutation was made at position 27 (G to T) of the TGFβRII sequence to generate a *Hap1* restriction enzyme cutting site at that position, however, there was no amino acid sequence change.

C2A: anti-PDL1/IL-15RαSu/Fc/ TGFβRII – no linker: The nucleic acid sequence of the anti-PDL1/IL-15RαSu/Fc/ TGFβRII construct without linker (including signal peptide sequence) is as follows (SEQ ID NO: 11):

(Signal peptide)

atgaagtgggtgaccttcatcagcctgctgttcctgttctccagcgcctactcc

(Signal peptide)

atgaagtgggtgaccttcatcagcctgctgttcctgttctccagcgcctactcc

(anti-PDL1 single chain)

(anti-PDL1 light chain variable domain)

aacatccagatgacccagtcccctagctccgtgtccgcctccgtgggagatcgggtgaccatcacctgtagggcctcccaggacatct ccaggtggctggcctggtaccagcagaagcccggcaaggcccccaagctgctgatctacgccgcctcctccctgcagtccggagtg cctagcaggttctccggctccggatccggcacagacttcgccctgaccatctcctccctgcagcccgaggacttcgccacctactactg ccagcaggccgactccaggttctccatcaccttcggccagggcaccaggctggagatcaagagg

(Linker)

ggaggtggcggatccggaggtggaggttctggtggaggtgggagt

(anti-PDL1 heavy chain variable domain)

gaggtgcagctggtgcagtccggaggaggactggtgcagcctggcggatccctgaggctgtcctgtgccgcttccggcttcaccttc agctcctactccatgaactgggtgaggcaggcccctggaaagggcctggagtgggtgtcctacatctccagctcctcctccaccatcc agtacgccgactccgtgaagggcaggttcaccatctccagggacaacgccaagaactccctgtacctgcagatgaacagcctgagg

gacgaggacaccgccgtgtactactgcgccaggggcgactattactacggcatggacgtgtggggccagggaaccaccgtgaccg
tgtcctcc

(Human IL-15R α sushi domain)

atcacgtgtcctcctcctatgtccgtggaacacgcagacatctgggtcaagagctacagcttgtactccagggagcggtacatttgtaac
tctggtttcaagcgtaaagccggcacgtccagcctgacggagtgcgtgttgaacaaggccacgaatgtcgcccactggacaaccccc
agtctcaaatgcattaga

(Human IgG1 CH2-CH3 (Fc) domain)

gagccgaaatcttgtgacaaaactcacacatgcccaccgtgcccagcacctgaactcctggggggaccgtcagtcttcctcttcccccc
caaaacccaaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtc
aagttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccgcgggaggagcagtacaacagcacgtaccgtg
tggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagccc
ccatcgagaaaaccatctccaaagccaaagggcagccccgagaaccacaggtgtacaccctgcccccatcccgggatgagctgac
caagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggagtgggagagcaatgggcagccgg
agaacaactacaagaccacgcctcccgtgctggactccgacggctccttcttcctctacagcaagctcaccgtggacaagagcaggt
ggcagcaggggaacgtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagcctctccctgtctcctgg
taaa

(Human TGFβRII)

atcccccccccacgtgcagaagtccgttaacaacgacatgatcgtgaccgacaacaacggcgccgtgaagttcccccagctgtgcaag
ttctgcgacgtgaggttctccacctgcgacaaccagaagtcctgcatgtccaactgctccatcacctccatctgcgagaagcctcagga
ggtgtgcgtggctgtgtggcggaagaacgacgagaacatcaccctggagaccgtgtgccacgaccccaagctgccctaccacgact
tcatcctggaggacgccgcctcccccaagtgcatcatgaaggagaagaagaagcccggcgagaccttctttatgtgctcctgctccag
cgacgagtgcaacgacaacatcatcttctccgaggagtacaacacctccaaccccgac

The amino acid sequence of the anti-PDL1/IL-15RαSu/Fc/ TGFβRII fusion protein (including signal peptide sequence) is as follows (SEQ ID NO: 12):

(Signal peptide)

MKWVTFISLLFLFSSAYS

(anti-PDL1 single chain)

(anti-PDL1 light chain variable domain)

NIQMTQSPSSVSASVGDRVTITCRASQDISRWLAWYQQKPGKAPKLLIYAASSLQSG
VPSRFSGSGSGTDFALTISSLQPEDFATYYCQQADSRFSITFGQGTRLEIKR

(Linker)

GGGGSGGGGSGGGGS

(anti-PDL1 heavy chain variable domain)

EVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYISSSSST IQYADSVKGRFTISRDNAKNSLYLQMNSLRDEDTAVYYCARGDYYYGMDVWGQG TTVTVSS

(Human IL-15R α sushi domain)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWT TPSLKCIR

(Human IgG1 CH2-CH3 (Fc) domain)

EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGK

(Human TGFβRII)

IPPHVQKSVNNDMIVTDNNGAVKFPQLCKFCDVRFSTCDNQKSCMSNCSITSICEKPQ

EV

CVAVWRKNDENITLETVCHDPKLPYHDFILEDAASPKCIMKEKKKPGETFFMCSCSS DECNDNIIFSEEYNTSNPD

C2B: anti-PDL1/IL-15RαSu/Fc/ TGFβRII with linker: The nucleic acid sequence of the anti-PDL1/IL-15RαSu/Fc/ TGFβRII construct with linker (including signal peptide sequence) is as follows (SEQ ID NO: 13):

(Signal peptide)

atgaagtgggtgaccttcatcagcctgctgttcctgttctccagcgcctactcc

anti-PDL1 single chain

(anti-PDL1 light chain variable domain)

aacatccagatgacccagtcccctagctccgtgtccgcctccgtgggagatcgggtgaccatcacctgtagggcctcccaggacatct ccaggtggctggcctggtaccagcagaagcccggcaaggcccccaagctgctgatctacgccgcctcctccctgcagtccggagtg cctagcaggttctccggctccggatccggcacagacttcgccctgaccatctcctccctgcagcccgaggacttcgccacctactactgccagcaggccgactccaggttctccatcaccttcggccagggcaccaggctggagatcaagagg

Linker)

ggaggtggcggatccggaggtggaggttctggtggaggtgggagt

(anti-PDL1 heavy chain variable domain)

gaggtgcagctggtgcagtccggaggaggactggtgcagcctggcggatccctgaggctgtcctgtgccgcttccggcttcaccttcagctcctactccatgaactgggtgaggcaggcccctggaaagggcctggagtgggtgtcctacatctccagctcctcctccaccatccagtacgccgactccgtgaagggcaggttcaccatctccagggacaacgccaagaactccctgtacctgcagatgaacagcctgagggacgaggacaccgccgtgtactactgcgccaggggcgactattactacggcatggacgtgtggggccagggaaccaccgtgaccgtgtcctcc

(Human IL-15R α sushi domain)

atcacgtgtcctcctcctatgtccgtggaacacgcagacatctgggtcaagagctacagcttgtactccagggagcggtacatttgtaactctggtttcaagcgtaaagccggcacgtccagcctgacggagtgcgtgttgaacaaggccacgaatgtcgcccactggacaacccccagtctcaaatgcattaga

(Human IgG1 CH2-CH3 (Fc) domain)

gagccgaaatcttgtgacaaaactcacacatgcccaccgtgcccagcacctgaactcctggggggaccgtcagtcttcctcttccccccaaaacccaaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagcccccatcgagaaaaccatctccaaagccaaagggcagccccgagaaccacaggtgtacaccctgcccccatcccgggatgagctgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaagaccacgcctcccgtgctggactccgacggctccttcttcctctacagcaagctcaccgtggacaagagcaggtggcagcaggggaacgtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagcctctccctgtctcctggtaaa

(Linker)

ggaggaggtggctccggaggcggtggctccggtggaggtggctccggaggtggcggttccggt

(Human TGFβRII)

atcccccccccacgtgcagaagtccgttaacaacgacatgatcgtgaccgacaacaacggcgccgtgaagttcccccagctgtgcaagttctgcgacgtgaggttctccacctgcgacaaccagaagtcctgcatgtccaactgctccatcacctccatctgcgagaagcctcaggaggtgtgcgtggctgtgtggcggaagaacgacgagaacatcaccctggagaccgtgtgccacgaccccaagctgccctaccacgact tcatcctggaggacgccgcctcccccaagtgcatcatgaaggagaagaagaagcccggcgagaccttctttatgtgctcctgctccag cgacgagtgcaacgacaacatcatcttctccgaggagtacaacacctccaaccccgac

The amino acid sequence of the anti-PDL1/IL-15RαSu/Fc/ TGFβRII with linker fusion protein (including signal peptide sequence) is as follows (SEQ ID NO: 14):

(Signal peptide)

MKWVTFISLLFLFSSAYS

(anti-PDL1 single chain)

(anti-PDL1 light chain variable domain)

NIQMTQSPSSVSASVGDRVTITCRASQDISRWLAWYQQKPGKAPKLLIYAASSLQSG VPSRFSGSGSGTDFALTISSLQPEDFATYYCQQADSRFSITFGQGTRLEIKR

(Linker)

GGGGSGGGGSGGGGS

(anti-PDL1 heavy chain variable domain)

EVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYISSSSST IQYADSVKGRFTISRDNAKNSLYLQMNSLRDEDTAVYYCARGDYYYGMDVWGQG TTVTVSS

(Human IL-15R α sushi domain)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWT TPSLKCIR

(Human IgG1 CH2-CH3 (Fc) domain)

EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGK

(Linker)

GGGGSGGGGSGGGGSGGGGSG

(Human TGFβRII)

IPPHVQKSVNNDMIVTDNNGAVKFPQLCKFCDVRFSTCDNQKSCMSNCSITSICEKPQEV

CVAVWRKNDENITLETVCHDPKLPYHDFILEDAASPKCIMKEKKKPGETFFMCSCSSDECND NIIFSEEYNTSNPD

Co-transfection and protein purification: The IL-15N72D and αPDL1/IL-15RαSu/Fc/ TGFβRII constructs were cloned into expression vectors as described previously (U.S. Patent No. 8,507,222, at Example 1), and the expression vectors were transfected into CHO cells. Co-expression of the two constructs in CHO cells allowed for formation and secretion of the soluble IL-15N72D: αPDL1/IL-15RαSu/Fc/ TGFβRII fusion protein complex (referred to as αPDL1/TxM/ TGFβRII), which can be purified by Protein A affinity and other chromatography methods and analyzed by SDS-PAGE and SEC methods to confirm purity and appropriate banding patterns (FIG. 22).

In some cases, the leader peptide is cleaved from the intact polypeptide to generate the mature form that may be soluble or secreted.

Other sequences of the invention include:

2x-TGFβRII-IL15(N72D) (SEQ ID NO: 15):

Atgaagtgggtgaccttcatcagcctgctgttcctgttctccagcgcctactccatcccccccatgtgcaaaagagcgtgaacaacgatatgatcgtgaccgacaacaacggcgccgtgaagtttccccagctctgcaagttctgcgatgtcaggttcagcacctgcgataatcagaagtcctgcatgtccaactgcagcatcacctccatctgcgagaagccccaagaagtgtgcgtggccgtgtggcggaaaaatgacgagaacatcaccctggagaccgtgtgtcacgaccccaagctcccttatcacgacttcattctggaggacgctgcctcccccaaatgcatcatgaaggagaagaagaagcccggagagaccttctttatgtgttcctgtagcagcgacgagtgtaacgacaacatcatcttcagcgaagagtacaacaccagcaaccctgatggaggtggcggatccggaggtggaggttctggtggaggtgggagtattcctccccacgtgcagaagagcgtgaataatgacatgatcgtgaccgataacaatggcgccgtgaaatttccccagctgtgcaaattctgcgatgtgaggttttccacctgcgacaaccagaagtcctgtatgagcaactgctccatcacctccatctgtgagaagcctcaggaggtgtgcgtggctgtctggcggaagaatgacgagaatatcaccctggaaaccgtctgccacgatcccaagctgccctaccacgatttcatcctggaagacgccgccagccctaagtgcatcatgaaagagaaaaagaagcctggcgagacctttttcatgtgctcctgcagcagcgacgaatgcaacgacaatatcatctttagcgaggaatacaataccagcaaccccgacaactgggtgaatgtaataagtgatttgaaaaaaattgaagatcttattcaatctatgcatattgatgctactttatatacggaaagtgatgttcaccccagttgcaaagtaacagcaatgaagtgctttctcttggagttacaagttatttcacttgagtccggagatgcaagtattcatgatacagtagaaaatctgatcatcctagcaaacgacagtttgtcttctaatgggaatgtaacaga

Date Reçue/Date Received 2021-09-16

atctggatgcaaagaatgtgaggaactggaggaaaaaaatattaaagaatttttgcagagttttgtacatattgtccaaatgttcatcaacacttcttaa

TGFβRII-IgG1-Fc (SEQ ID NO: 16):

atgaagtgggtgaccttcatcagcctgctgttcctgttctccagcgcctactccatcccccccatgtgcaaaagagcgtgaacaacgatatgatcgtgaccgacaacaacggcgccgtgaagtttccccagctctgcaagttctgcgatgtcaggttcagcacctgcgataatcagaagtcctgcatgtccaactgcacgatcacctccatctgcgagaagccccaagaagtgtgcgtggccgtgtggcggaaaaatgacgagaacatcaccctggagaccgtgtgtcacgaccccaagctcccttatcacgacttcattctggaggacgctgcctcccccaaatgcatcatgaaggagaagaagaagcccggagagaccttctttatgtgttcctgtagcagcgacgagtgtaacgacaacatcatcttcagcgaagagtacaacaccagcaaccctgatgagcccaaatcttgtgacaaaactcacacatgcccaccgtgcccagcacctgaactcctggggggaccgtcagtcttcctcttccccccaaaacccaaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagcccccatcgagaaaaccatctccaaagccaaagggcagccccgagaaccacaggtgtacaccctgcccccatcccgggatgagctgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaagaccacgcctcccgtgctggactccgacggctccttcttcctctacagcaagctcaccgtggacaagagcaggtggcagcaggggaacgtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagcctctccctgtctccgggtaaataa

TGFβRII-Dimer-IL15RaSu-IgG1-Fc (SEQ ID NO: 17):

atgaagtgggtgaccttcatcagcctgctgttcctgttctccagcgcctactccatcccccccatgtgcaaaagagcgtgaacaacgatatgatcgtgaccgacaacaacggcgccgtgaagtttccccagctctgcaagttctgcgatgtcaggttcagcacctgcgataatcagaagtcctgcatgtccaactgcacgatcacctccatctgcgagaagccccaagaagtgtgcgtggccgtgtggcggaaaaatgacgagaacatcaccctggagaccgtgtgtcacgaccccaagctcccttatcacgacttcattctggaggacgctgcctcccccaaatgcatcatgaaggagaagaagaagcccggagagaccttctttatgtgttcctgtagcagcgacgagtgtaacgacaacatcatcttcagcgaagagtacaacaccagcaaccctgatggaggtggcggatccggaggtggaggttctggtggaggtgggagtattcctccccacgtgcagaagagcgtgaataatgacatgatcgtgaccgataacaatggcgccgtgaaatttccccagctgtgcaaattctgcgatgtgaggttttccacctgcgacaaccagaagtcctgtatgagcaactgcacaatcacctccatctgtgagaagcctcaggaggtgtgcgtggctgtctggcggaagaatgacgagaatatcaccctggaaaccgtctgccacgatcccaagctgccctaccacgatttcatcctggaagacgccgccagccctaagtgcatcatgaaagagaaaaagaagcctggcgagacctttttcatgtgctcctgcagcagcgacgaatgcaacgacaatatcatctttagcgaggaatacaataccagcaaccccgacatcacgtgtcctcctcctatgtccgtggaacacgcagacatctgggtcaagagctacagcttgtactccagggagcggtacatttgtaactctggtttcaagcgtaaagccggcacgtccagcctgacggagtgcgtgttgaacaaggccacgaatgtcgcccactggacaacccccagtctcaaatgtattagagagcccaaatcttgtgacaaaactcacacatgcccaccgtgcccagcacctgaactcctggggggaccgtcagtcttcctcttccccccaaaacccaaggacaccctcatgatctcccggacccc tgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagcccccatcgagaaaaccatctccaaagccaaagggcagccccgagaaccacaggtgtacaccctgcccccatcccgggatgagctgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaagaccacgcctcccgtgctggactccgacggctccttcttcctctacagcaagctcaccgtggacaagagcaggtggcagcaggggaacgtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagcctctccctgtctccgggtaaataa

IL15 (N72D) (SEQ ID NO: 18):

Aactgggtgaatgtaataagtgatttgaaaaaaattgaagatcttatccagtccatgcacatcgacgccaccctgtacaccgagagcgacgtgcacccctcctgcaaggtgaccgccatgaagtgcttcctgctggagctgcaggtgatctccctggagtccggcgacgcctccatccacgacaccgtggagaacctgatcatcctggccaacgactccctgtcctccaacggcaacgtgaccgagtccggctgcaaggagtgcgaggagctggaggagaagaacatcaaggagttcctgcagtccttcgtgcacatcgtccaaatgttcatcaacacttct

αPD-L1/SuFc/TGF-β (SEQ ID NO: 19):

atggaatggagctgggtctttctcttcttcctgtcagtaaccaccggtgtccactccaacatccagatgacccagtctccatcttctgtgtctgcatctgtaggagacagagtcaccatcacttgtcgggcgagtcaggatattagccgctggttagcctggtatcagcagaaaccagggaaagcccctaaactcctgatctatgctgcatccagtttgcaaagtggggtcccatcgaggttcagcggcagtggatctgggacagatttcgctctcactatcagcagcctgcagcctgaagattttgcaacttactattgtcaacaggctgacagtcgtttctcgatcaccttcggccaagggacacgactggagattaaacgaggaggtggcggatccggaggtggaggttctggtggaggtgggagtgaggtgcagctggtgcagtctgggggaggcttggtacagcctggggggtccctgagactctcctgtgcagcctctggattcaccttcagtagctatagcatgaactgggtccgccaggctccagggaaggggctggagtgggtttcatacattagtagtagtagtagtaccatacagtacgcagactctgtgaagggccgattcaccatctccagagacaatgccaagaactcactgtatctgcaaatgaacagcctgagagacgaggacacggctgtgtattactgtgcgagaggggactactactacggtatggacgtctggggccaagggaccacggtcaccgtgagctcaatcacgtgtcctcctcctatgtccgtggaacacgcagacatctgggtcaagagctacagcttgtactccagggagcggtacatttgtaactctggtttcaagcgtaaagccggcacgtccagcctgacggagtgcgtgttgaacaaggccacgaatgtcgcccactggacaacccccagtctcaaatgcattagagagccgaaatcttgtgacaaaactcacacatgcccaccgtgcccagcacctgaactcctggggggaccgtcagtcttcctcttccccccaaaacccaaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagcccccatcgagaaaaccatctccaaagccaaagggcagccccgagaaccacaggtgtacaccctgcccccatcccgggatgagctgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaagaccacgcctcccgtgctggactccgacggctccttcttcctctacagcaagctcaccgtggacaagagcaggtggcagcaggggaacgtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagcctctccctgtctcc tggtaaaggaggaggtggctccggaggcggtggctccggtggaggtggctccggaggtggcggttccggtatcccccccccacgtg cagaagtccgttaacaacgacatgatcgtgaccgacaacaacggcgccgtgaagttcccccagctgtgcaagttctgcgacgtgagg ttctccacctgcgacaaccagaagtcctgcatgtccaactgcccaatcacctccatctgcgagaagcctcaggaggtgtgcgtggctgt gtggcggaagaacgacgagaacatcaccctggagaccgtgtgccacgaccccaagctgccctaccacgacttcatcctggaggac gccgcctcccccaagtgcatcatgaaggagaagaagaagcccggcgagaccttctttatgtgctcctgctccagcgacgagtgcaac gacaacatcatcttctccgaggagtacaacacctccaaccccgactga

In addition, the fusion proteins described above can also comprise the sequence of wild type IL-15 instead of the IL-15N72D variant. For example, the nucleic acid sequences above encoding the IL-15N72D domains could be substituted with nucleic acid sequences encoding wild type IL-15. Nucleic acid sequences of the invention could be native sequences or those optimized for expression in the host cells, i.e., codon optimized sequences.

The amino acid sequence of the wild type IL15 protein domain is as follows (SEQ ID NO: 20):

(Human IL-15)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDAS IHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

<u>N-810 A</u>

The amino acid sequence of the N-810A (αPD-L1 Light Chain Fv/Linker/αPD-L1 Heavy Chain Fv/Linker/IL15RαSuFc/Linker/TGFβRII) protein is as follows (SEQ ID NO: 21):

(IL-15 (N72D))

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDAS IHDTVENLIILANDSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

(αPD-L1 Light Chain Fv)

NIQMTQSPSSVSASVGDRVTITCRASQDISRWLAWYQQKPGKAPKLLIYAASSLQSG VPSRFSGSGSGTDFALTISSLQPEDFATYYCQQADSRFSITFGQGTRLEIKR

(Linker)

GGGGSGGGGSGGGGS

(αPD-L1 Heavy Chain Fv)

EVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYISSSSST
IQYADSVKGRFTISRDNAKNSLYLQMNSLRDEDTAVYYCARGDYYYGMDVWGQG
TTVTVSS

(IL15RαSuFc)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWT
TPSLKCIREPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN
HYTQKSLSLSPGK

(Linker)

GGGGSGGGGSGGGGSGGGGSG

(TGFβRII)

IPPHVQKSVNNDMIVTDNNGAVKFPQLCKFCDVRFSTCDNQKSCMQNCPITSICEKP
QEVCVAVWRKQDENITLETVCHDPKLPYHDFILEDAASPKCIMKEKKKPGETFFMCS
CSSDECNDNIIFSEEYQTSNPD.

The amino acid of N-810A aglycosylated TGFβRII* (αPD-L1 Light Chain Fv/Linker/αPD-L1 Heavy Chain Fv/Linker/IL15RαSuFc/Linker/TGFβRII) (SEQ ID NO: 22) is as follows:

(IL-15 (N72D))

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDAS
IHDTVENLIILANDSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

(αPD-L1 Light Chain Fv)

NIQMTQSPSSVSASVGDRVTITCRASQDISRWLAWYQQKPGKAPKLLIYAASSLQSG
VPSRFSGSGSGTDFALTISSLQPEDFATYYCQQADSRFSITFGQGTRLEIKR

(Linker)

GGGGSGGGGSGGGGS

(αPD-L1 Heavy Chain Fv)

EVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYISSSSST IQYADSVKGRFTISRDNAKNSLYLQMNSLRDEDTAVYYCARGDYYYGMDVWGQG TTVTVSS

(*IL15RαSuFc*)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWT TPSLKCIREPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK

(*Linker*)

GGGGSGGGGSGGGGSGGGGSG

(*TGFβRII*)

IPPHVQKSVNNDMIVTDNNGAVKFPQLCKFCDVRFSTCDNQKSCMQNCPITSICEKP QEVCVAVWRKQDENITLETVCHDPKLPYHDFILEDAASPKCIMKEKKKPGETFFMCS CSSDECNDNIIFSEEYQTSNPD.

The amino acid of N-810A aglycosylated TGFβRII + Δfree cysteine* (αPD-L1 Light Chain Fv/Linker/αPD-L1 Heavy Chain Fv/Linker/IL15RαSuFc/Linker/TGFβRII) (SEQ ID NO: 23) is as follows:

((IL-15 (N72D))

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDAS IHDTVENLIILANDSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

(αPD-L1 Light Chain Fv)

NIQMTQSPSSVSASVGDRVTITCRASQDISRWLAWYQQKPGKAPKLLIYAASSLQSG VPSRFSGSGSGTDFALTISSLQPEDFATYYCQQADSRFSITFGQGTRLEIKR

(Linker)

GGGGSGGGGSGGGGS

(αPD-L1 Heavy Chain Fv)

EVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYISSSSST IQYADSVKGRFTISRDNAKNSLYLQMNSLRDEDTAVYYCARGDYYYGMDVWGQG TTVTVSS

(IL15RαSuFc)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWT TPSLKCIREPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK

(Linker)

GGGGSGGGGSGGGGSGGGGSG

(TGFβRII)

IPPHVQKSVNNDMIVTDNNGAVKFPQLCKFCDVRFSTCDNQKSCMQNCPITSICEKP QEVCVAVWRKQDENITLETVCHDPKLPYHDFILEDAASPKCIMKEKKKPGETFFMCS CSSDECNDNIIFSEEYQTSNPD.

The amino acid of N-810A Δ hinge** (αPD-L1 Light Chain Fv/Linker/αPD-L1 Heavy Chain Fv/Linker/IL15RαSuFc/Linker/TGFβRII) (SEQ ID NO: 24) is as follows:

((IL-15 (N72D))

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDAS IHDTVENLIILANDSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

(αPD-L1 Light Chain Fv)

NIQMTQSPSSVSASVGDRVTITCRASQDISRWLAWYQQKPGKAPKLLIYAASSLQSG VPSRFSGSGSGTDFALTISSLQPEDFATYYCQQADSRFSITFGQGTRLEIKR

(Linker)

GGGGSGGGGSGGGGS

(αPD-L1 Heavy Chain Fv)

EVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYISSSSSTIQYADSVKGRFTISRDNAKNSLYLQMNSLRDEDTAVYYCARGDYYYGMDVWGQGTTVTVSS

(IL15RαSuFc)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR~~EPKSC~~DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

(Linker)

GGGGSGGGGSGGGGSGGGGSG

(TGFβRII)

IPPHVQKSVNNDMIVTDNNGAVKFPQLCKFCDVRFSTCDNQKSCMNNCPITSICEKPQEVCVAVWRKNDENITLETVCHDPKLPYHDFILEDAASPKCIMKEKKKPGETFFMCSCSSDECNDNIIFSEEYNTSNPD.

The amino acid of N-810A + (IL15-K41Q, L45S, I67T, N79Y, E93A)* (αPD-L1 Light Chain Fv/Linker/αPD-L1 Heavy Chain Fv/Linker/IL15RαSuFc/Linker/TGFβRII) (SEQ ID NO: 25) is as follows:

(IL-15-K41Q, L45S, I67T, N79Y, E93A)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMQCFLSELQVISLESGDASIHDTVENLTILANDSLSSNGYVTESGCKECEELEAKNIKEFLQSFVHIVQMFINTS

(αPD-L1 Light Chain Fv)

NIQMTQSPSSVSASVGDRVTITCRASQDISRWLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFALTISSLQPEDFATYYCQQADSRFSITFGQGTRLEIKR

(Linker)

GGGGSGGGGSGGGGS

(αPD-L1 Heavy Chain Fv)

EVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYISSSSST IQYADSVKGRFTISRDNAKNSLYLQMNSLRDEDTAVYYCARGDYYYGMDVWGQG TTVTVSS

(IL15RαSuFc)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWT TPSLKCIREPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK

(Linker)

GGGGSGGGGSGGGGSGGGGSG

(TGFβRII)

IPPHVQKSVNNDMIVTDNNGAVKFPQLCKFCDVRFSTCDNQKSCMSNCPITSICEKPQ EVCVAVWRKNDENITLETVCHDPKLPYHDFILEDAASPKCIMKEKKKPGETFFMCSC SSDECNDNIIFSEEYNTSNPD.

The amino acid of N-810A + (IL15-L45S)* (αPD-L1 Light Chain Fv/Linker/αPD-L1 Heavy Chain Fv/Linker/IL15RαSuFc/Linker/TGFβRII) (SEQ ID NO: 26) is as follows:

(IL15-L45S)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLSELQVISLESGDAS IHDTVENLIILANDSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

(αPD-L1 Light Chain Fv)

NIQMTQSPSSVSASVGDRVTITCRASQDISRWLAWYQQKPGKAPKLLIYAASSLQSG VPS RFSGSGSGTDFALTISSLQPEDFATYYCQQADSRFSITFGQGTRLEIKR

(Linker)

GGGGSGGGGSGGGGS

(αPD-L1 Heavy Chain Fv)

EVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYISSSSST IQYADSVKGRFTISRDNAKNSLYLQMNSLRDEDTAVYYCARGDYYYGMDVWGQG TTVTVSS

(IL15RαSuFc)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWT TPSLKCIREPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK

(Linker)

GGGGSGGGGSGGGGSGGGGSG

(TGFβRII)

IPPHVQKSVNNDMIVTDNNGAVKFPQLCKFCDVRFSTCDNQKSCMSNCPITSICEKPQ EVCVAVWRKNDENITLETVCHDPKLPYHDFILEDAASPKCIMKEKKKPGETFFMCSC SSDECNDNIIFSEEYNTSNPD

<u>N-810D</u>

αPD-L1 Light Chain Fv/Linker/αPD-L1 Heavy Chain Fv/IL-15 (N72D) (SEQ ID NO: 27):

(αPD-L1 Light Chain Fv)

NIQMTQSPSSVSASVGDRVTITCRASQDISRWLAWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFALTISSLQPEDFATYYCQQADSRFSITFGQGTRLEIKR

(Linker)

GGGGSGGGGSGGGGS

(αPD-L1 Heavy Chain Fv)

EVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYIS SSSSTIQYADSVKGRFTISRDNAKNSLYLQMNSLRDEDTAVYYCARGDYYYGMDV WGQGTTVTVSS

((IL-15 (N72D))

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLE SGDASIHDTVENLIILANDSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFIN TS

IL15RαSuFc/Linker/TGFβRII (SEQ ID NO: 28):

(IL15RαSuFc)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWT TPSLKCIREPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK

(Linker)

GGGGSGGGGSGGGGSGGGGSG

(TGFβRII)

IPPHVQKSVNNDMIVTDNNGAVKFPQLCKFCDVRFSTCDNQKSCMSNCPITSICEKPQ EVCVAVWRKNDENITLETVCHDPKLPYHDFILEDAASPKCIMKEKKKPGETFFMCSC SSDECNDNIIFSEEYNTSNPD

N-810D aglycosylated TGFβRII*

αPD-L1 Light Chain Fv/Linker/αPD-L1 Heavy Chain Fv/IL-15 (N72D) (SEQ ID NO: 29) is as follows:

(αPD-L1 Light Chain Fv)

NIQMTQSPSSVSASVGDRVTITCRASQDISRWLAWYQQKPGKAPKLLIYAASSLQSG VPSRFSGSGSGTDFALTISSLQPEDFATYYCQQADSRFSITFGQGTRLEIKR

(Linker)

GGGGSGGGGSGGGGS

(αPD-L1 Heavy Chain Fv)

EVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYISSSSST IQYADSVKGRFTISRDNAKNSLYLQMNSLRDEDTAVYYCARGDYYYGMDVWGQG TTVTVSS

((IL-15 (N72D))

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDAS IHDTVENLIILANDSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

IL15RαSuFc/Linker/TGFβRII (SEQ ID NO: 30):

(IL15RαSuFc)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWT TPSLKCIREPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK

(Linker)

GGGGSGGGGSGGGGSGGGGSG

(TGFβRII)

IPPHVQKSVNNDMIVTDNNGAVKFPQLCKFCDVRFSTCDNQKSCMQNCPITSICEKP QEVCVAVWRKQDENITLETVCHDPKLPYHDFILEDAASPKCIMKEKKKPGETFFMCS CSSDECNDNIIFSEEYQTSNPD

<u>N-810E</u>

αPD-L1 Light Chain Fv/Linker/αPD-L1 Heavy Chain Fv/IL-15 (N72D) (SEQ ID NO: 31):

(αPD-L1 Light Chain Fv)

NIQMTQSPSSVSASVGDRVTITCRASQDISRWLAWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFALTISSLQPEDFATYYCQQADSRFSITFGQGTRLEIKR

(Linker)

GGGGSGGGGSGGGGS

(αPD-L1 Heavy Chain Fv)

EVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYIS SSSSTIQYADSVKGRFTISRDNAKNSLYLQMNSLRDEDTAVYYCARGDYYYGMDV WGQGTTVTVSS

((IL-15 (N72D))

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLE SGDASIHDTVENLIILANDSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFIN TS

TGFβRII/IL15RαSuFc (SEQ ID NO: 32):

(TGFβRII)

IPPHVQKSVNNDMIVTDNNGAVKFPQLCKFCDVRFSTCDNQKSCMSNCSITSI CEKPQEVCVAVWRKNDENITLETVCHDPKLPYHDFILEDAASPKCIMKEKKKPGETF FMCSCSSDECNDNIIFSEEYNTSNPD

(IL15RαSuFc)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWT TPSLKCIREPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK

<u>N-810E aglycosylated TGFβRII*</u>

αPD-L1 Light Chain Fv/Linker/αPD-L1 Heavy Chain Fv/IL-15 (N72D) (SEQ ID NO: 33)

(αPD-L1 Light Chain Fv)

NIQMTQSPSSVSASVGDRVTITCRASQDISRWLAWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFALTISSLQPEDFATYYCQQADSRFSITFGQGTRLEIKR

(Linker)

GGGGSGGGGSGGGGS

(αPD-L1 Heavy Chain Fv)

EVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYIS SSSSTIQYADSVKGRFTISRDNAKNSLYLQMNSLRDEDTAVYYCARGDYYYGMDV WGQGTTVTVSS

(IL-15 (N72D))

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLE SGDASIHDTVENLIILANDSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFIN TS

TGFβRII/IL15RαSuFc (SEQ ID NO: 34):

(TGFβRII)

IPPHVQKSVNNDMIVTDNNGAVKFPQLCKFCDVRFSTCDNQKSCMQNCPITSICEKP QEVCVAVWRKQDENITLETVCHDPKLPYHDFILEDAASPKCIMKEKKKPGETFFMCS CSSDECNDNIIFSEEYQTSNPD

(IL15RαSuFc)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWT TPSLKCIREPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK

*New point mutations are notated within sequence with underlined residue.

**Deletions are denoted with a strikethrough. Final sequence does not include these residues.

Note: All aglycosylated versions, mutated free cysteine and/or hinge deletion versions can also be combined with the IL15- K41Q, L45S, I67T, N79Y, E93A mutations.

Example 2. Biological Activities of Fusion Protein Complexes Comprising IL-15, anti-PDL1, and TGFβRII domains. A variety of methods were used to characterize the biological activities of the complexes of the invention (FIG. 9)

IL-15 immunostimulatory activity: The IL-15 immunostimulatory activity of the αPDL1/TxM/TGFβRII, TGFβRII/αPDL1/TXM and αPDL1/TGFβRII/TXM fusion protein complexes was assessed based on the proliferation of IL-15-dependent 32Dβ cells, a mouse hematopoietic cell line. Increasing levels of αPDL1/TxM/TGFβRII, TGFβRII/αPDL1/TXM or αPDL1/TGFβRII /TXM were added to 32Dβ cells (10^4 cell/well) in 200 μL RPMI:10% FBS media and cells were incubated for 3 days at 37°C. PrestoBlue cell viability reagent (20 μL/well) was added then. After 4 hours, absorbance was measured at 570 nm (with a 600 nm reference wavelength for normalization) to determine cell proliferation based on reduction of PrestoBlue, a resazurin-based solution, by metabolically active cells. The half maximal effective concentration (EC_{50}) of IL-15 bioactivity for αPDL1/TxM/TGFβRII, TGFβRII/αPDL1/TXM and αPDL1/TGFβRII/ TXM was then determined based on the relationship between absorbance and protein concentration. The bioactivity of ALT-803 was assessed as a positive control.

As shown in FIGS. 10, 13, 14A and 14B, the αPDL1/TxM/TGFβRII, TGFβRII/αPDL1/TXM and αPDL1/TGFβRII/TXM fusion protein complexes were capable of stimulating growth of 32Dβ cells, demonstrating that these proteins retain IL-15 immunostimulatory activity.

Binding to PD-L1: Flow cytometry-based assays were used to assess binding of αPDL1/TxM/TGFβRII, TGFβRII/αPDL1/TXM and αPDL1/TGFβRII/TXM to PD-L1 *in vitro*. Specifically, serial dilutions of αPDL1/TxM/TGFβRII, TGFβRII/αPDL1/TXM, αPDL1/ TGFβRII /TXM and anti-PD-L1 antibody controls were incubated with human H441 tumor cells expressing PD-L1 (2.5×10^5 cells) in the dark on ice for 2 hours. The cells were then washed, resuspended and stained with APC Anti-Human IgG Fc Antibody (clone HP6017) in the dark at 4°C for 30 minutes. After washing twice, cells were resuspended in 250 μl FACS buffer (1% BSA and 0.05% NaN_3 in phosphate buffered saline) and kept on ice until analyzed on BD FCSVerse flow cytometer with BD FD FCS Suite V1.0.6. The mean fluorescence intensity (MFI) was quantified for each concentration of protein.

As shown in FIGS. 12, 13, 15A and 15B. the αPDL1/TxM/TGFβRII, TGFβRII/αPDL1/TXM and αPDL1/TGFβRII/TXM fusion protein complexes were capable of binding PDL1 expressed on human tumor cells. Similarly, FIG. 22 shows the binding of the αPDL1/TxM/TGFβRII complex to PD-L1 by a surface plasmon resonance (SPR) assay.

Inhibition of TGFβ activity: TGFβ proteins bind to receptors on the cell surface, initiating a signaling cascade that leads to phosphorylation and activation of SMAD2 and SMAD3, which then form a complex with SMAD4. The SMAD complex then translocates to the nucleus and binds to the SMAD binding element (SBE) in the nucleus, leading to transcription and expression of TGF-β/ SMAD responsive genes. The ability of the αPDL1/TxM/TGFβRII, TGFβRII/αPDL1/TXM and αPDL1/TGFβRII/TXM fusion protein complexes to inhibit TGF-β-induced Smad2/3 signaling was assessed.

HEK293 carrying TGFβ/SMAD signaling pathway SEB reporter (BPS Bioscience, # 60653) were plated in a white clear-bottom 96-well microplate (Corning 3610) at a density of 5×10^4 cells per well in 100 μl of MEM medium, and incubated overnight at 37°C and 5%

CO_2. After 24 hours, wells were changed to 80 µl fresh assay medium and incubated at 37°C and 5% CO2 for 4hrs. Then 10 µl of serial dilutions of αPDL1/TxM/TGFβRII, TGFβRII/αPDL1/TXM, αPDL1/TGFβRII/TXM or TGFβRII-Fc control were added to each wall and incubated for 1 hour, following by addition of 10 µl recombinant human TGF-β1 or TGF-β3 (R&D Systems, 100 ng/mL) to each well to reach a total volume of 100 µl. After overnight incubation, 100 µl of ONE-Step™ Luciferase reagent (BPS Bioscience, #60690) was added and plates were incubated for at least 5 minutes at room temperature. Luminescence based on TGF-β-induced Smad2/3 signaling was measured using a GloMax Explorer plate reader (Promega). The half maximal inhibitory concentration (EC_{50}) of TGF-β-induced Smad2/3 signaling for αPDL1/TxM/TGFβRII, TGFβRII/αPDL1/TXM and αPDL1/TGFβRII/TXM was then determined based on the relationship between absorbance and protein concentration using Graphpad Prism7 software.

As shown in FIGS. 11, 13, 16A, 16B, 17A and 17B, the αPDL1/TxM/TGFβRII, TGFβRII/αPDL1/TXM and αPDL1/TGFβRII/TXM fusion protein complexes were capable of inhibiting TGF-β1-induced Smad2/3 signaling. Similarly, the TGFβRII/αPDL1/TXM and αPDL1/TGFβRII/TXM fusion protein complexes were also capable of inhibiting TGF-β3-induced Smad2/3 signaling (FIGS. 17A, 17B). Thus, these complexes act as TGF-β trap molecules and are expected to block the activities of TGF-β proteins. Notably, both the TGFβRII/αPDL1/TXM and αPDL1/TGFβRII/TXM fusion protein complexes showed greater inhibitory activity against TGF-β1 and TGF-β3 than the positive control TGFβRII-Fc protein.

Previously, it has been shown that proteins containing TGF-β trap domain had the ability to antagonize TGF-β 1-induced mesenchymalization in tumor cells (David, et al. 2017. OncoImmunology. 6:10, e1349589). The αPDL1/TxM/TGFβRII, TGFβRII/αPDL1/TXM and αPDL1/TGFβRII/TXM fusion protein complexes are anticipated to retain this biological activity. This can be assessed based on inhibition of TGF-β 1-mediated changes in tumor cell mesenchymal marker expression (i.e., vimentin, fibronectin), proliferation suppression, and chemotherapeutic resistance in vitro or in vivo as provided by David, et al..

Assessment of protein binding to TGFβ proteins: ELISA methods were used to assess the binding of TGFβRII/αPDL1/TXM and αPDL1/ TGFβRII /TXM fusion protein complexes to TGFβ1 and TGFβ3. Specifically, 96-well ELISA plates (Nunc Maxisorb Immunoplate) were coated with TGFβ1 and TGFβ3 in PBS with 10% CSF overnight at 4°C. The next day, plates were washed three times with wash buffer (PBS, 0.05% Tween-20) and blocked with 1% bovine serum albumin in PBS for 1 hour at room temperature. The plates were then incubated with serial dilutions TGFβRII/αPDL1/TXM, αPDL1/ TGFβRII /TXM or TGFβRII-Fc control for 1 hour at room temperature. Following wash steps, protein binding was detected using anti-hIgG-horseradish peroxidase (HRP) (Jackson Immuno Research, 1:4,000 dilution) at room temperature for 30 minutes. Follow substrate development, absorbance was then read at 405 nm using a BioTek plate reader.

As shown in FIGS. 18A, 18B, 19A, and 19B, both the TGFβRII/αPDL1/TXM and αPDL1/TGFβRII/TXM fusion protein complexes were capable of binding TGFβ1 and TGFβ3, consistent with the TXM proteins ability to block TGFβ1- and TGFβ3-meidated biological activity.

Similarly, FIG. 23 shows the binding of the αPDL1/TxM/TGFβRII complex to TGFβ1, TGFβ2 and TGFβ3 by a surface plasmon resonance (SPR) assay.

Antibody-dependent cellular cytotoxicity against PD-L1-positive tumor cells: TGFβRII/αPDL1/TXM and αPDL1/TGFβRII/TXM proteins may be effective against tumor by inducing natural killer and CD8 T cell effector responses, blocking the immunosuppressive effects of TFG-β proteins or PD-1 checkpoint inhibitor and/or targeting immune responses against PD-L1 expressing tumor cells. To assess the ability of these proteins to mediate antibody-dependent cellular cytotoxicity against PD-L1-positive tumor cells, Celltrace labeled PD-L1-positive human H441 lung tumor cells ($2x10^5$ cells) were cultured in duplicate with NK effector cells at a 1:10 ratio at 37°C in the presence of different concentrations of TGFβRII/αPDL1/TXM, αPDL1/ TGFβRII /TXM, anti-PD-L1 antibody, non-targeting TXM (101074/TXM) or other controls. After 20hrs incubation, cells were harvested and resuspended in PI solution (2μg/ml) to label dead cells. The percentage of dead Celltrace-positive PI-positive H441 tumor cells were then measured by flow cytometry.

As shown in FIGS. 20 and 21, both the TGFβRII/αPDL1/TXM and αPDL1/TGFβRII/TXM fusion protein complexes were capable of mediating ADCC against PD-L1 expressing tumor cells. In fact, TGFβRII/αPDL1/TXM exhibited greater ADCC than equivalent molar concentrations of an anti-PD-L1 IgG1 antibody. Similar results were observed with PD-L1-positive human HCC4006 lung cancer cells, CaSki cervical cancer cells and MDA-MB-231 breast cancer cells. Additionally, the αPDL1/TXM/TGFβRII complex exhibited ADCC activity against PD-L1-positive human cancer cells (FIG. 22).

Inhibition of PD-L1 activity: In addition to assessment of PD-L1 binding activity and ADCC activity against PD-L1 positive tumor cells, we evaluated the ability to the

TGFβRII/αPDL1/TXM and αPDL1/TGFβRII/TXM complexes to inhibit the immunosuppressive (checkpoint) activity of PD-L1 on PD-1 positive effector cells. In a standardized assay, artificial antigen presenting cells (aAPCs) expressing human PD-L1 and an engineered cell surface protein designed to activate cognate TCRs in an antigen-independent manner are mixed with Jurkat T cells expressing human PD-1 and a luciferase reporter driven by an NFAT response element. When the two cell types are co-cultured, the PD-1/PD-L1 interaction inhibits TCR signaling and NFAT-RE-mediated luminescence. Addition of either an anti-PD-1 or anti-PD-L1 antibody domain that blocks the PD-1/PD-L1 interaction releases the inhibitory signal and results in TCR activation and NFAT-RE-mediated luminescence (FIG. 23). The activities of the TGFβRII/αPDL1/TXM and αPDL1/TGFβRII/TXM complexes were assessed in this assay using standard procedures (FIG. 24). Anti-PD-L1 antibody and PD-L1/TxM protein complexes (similar to TGFβRII/αPDL1/TXM and αPDL1/TGFβRII/TXM complexes but lacking the TGFβRII domains) served as positive controls.

As shown in FIGS. 25A and 25B, αPDL1/TGFβRII/TXM, TGFβRII/αPDL1/TXM and αPDL1/TXM/TGFβRII complexes were capable of inducing NFAT-RE-mediated luminescence in a dose dependent manner with similar activity as the anti-PD-L1 Ab control. These results verify that αPDL1/TGFβRII/TXM, TGFβRII/αPDL1/TXM and αPDL1/TXM/TGFβRII complexes retain immune checkpoint blockade activity.

N-810: FIGS. 26A and 26B demonstrate the human TGFβ specific blocking activity for N-810 (FIG. 26A) compared against the activity of the parental control molecule, αPDL1/TxM (FIG. 26B). A stable cellular luciferase-based reporter system (HEK-293T-luc2P/SBE) was used in order to assess the specific TGFβ-blocking activity. Cultured cells were stimulated for 20 hours with 0.0175 nM of recombinant human TGFβ1 in the presence or absence of the blocking reagent. Response to hTGFβ1 was expressed by Relative Luminescence Units (RLU) ± SD.

N-810 Sorrento-Fc: FIGS. 27A and 27B demonstrate specific hTGFβ1 blocking activity for N-810 Sorrento-Fc (Fig 27A) compared against the activity of the parental control molecule, αPDL1/TxM (FIG. 27B). A stable cellular luciferase-based reporter system (HEK-293T-luc2P/SBE) was used in order to assess the specific TGFβ-blocking activity. Cultured cells were stimulated for 20 hours with 0.0175 nM of recombinant human TGFβ1 in the presence or absence of the blocking reagent. Response to hTGFβ1 was expressed by Relative Luminescence Units (RLU) ± SD.

N-810 Δ C: FIGS. 28A and 28B demonstrate specific hTGFβ1 blocking activity for N-810 Δ C (FIG. 28A) compared against the activity of the parental control molecule, αPDL1/TxM (FIG. 28B). A stable cellular luciferase-based reporter system (HEK-293T-luc2P/SBE) was used in order to assess the specific TGFβ-blocking activity. Cultured cells were stimulated for 20 hours with 0.0175 nM of recombinant human TGFβ1 in the presence or absence of the blocking reagent. Response to hTGFβ1 was expressed by Relative Luminescence Units (RLU) ± SD.

N-810 D: FIGS. 29A and 29B are graphs demonstrating specific hTGFβ1 blocking activity forN-810D (FIG. 29A) compared against the activity of the parental control molecule (αPDL1/TxM, FIG. 29B). A stable cellular luciferase-based reporter system (HEK-293T-luc2P/SBE) was used in order to assess the specific TGFβ-blocking activity. Cultured cells were stimulated for 20 hours with 0.0175 nM of recombinant human TGFβ1 in the presence or absence of the blocking reagent. Response to hTGFβ1 was expressed by Relative Luminescence Units (RLU) ± SD.

Antibody-dependent cellular cytotoxicity (ADCC) of the TxM constructs: FIG. 30 is a graph demonstrating the antibody-dependent cellular cytotoxicity (ADCC) of the TxM constructs in mammary adenocarcinoma cells (MDA-MB-231). Antibody-Dependent Cellular Cytotoxicity (ADCC) was used in order to determine the specific αPD-L1 activity. Effector cells: haNK (NK-92 derivative).

TxM constructs: FIGS. 31A-31H are schematic representations showing the various constructs. FIG. 31A: N-810A. FIG. 31B: N-810A aglycosylated. FIG. 31C: N-810A aglycosylated, Δ free cysteine. FIG. 31D: N-810A Δ hinge. FIG. 31E: N-810A (IL15-K41Q, L45S, I67T, N79Y, E93A). The mutations in IL15 enhance the solubility and expression of the molecule. FIG. 31F: N-810A (IL15-L45S). The mutations in IL15 enhance solubility and expression of the molecule. FIG. 31G: N-810D. FIG. 31H: N-810E.

FIG. 32 and Table 1 demonstrate that IL15 mutations increase protein yield and decrease aggregation. N-810D variation also increases yield and decreases aggregation.

Protein	Post-harvest Titer (ug/mL)	Total Yield (mg)	High Molecular Weight % Post Pro-A
N-810A	55.9		20.4
N-810 (IL15-K41Q, L45S,I67T,N79Y,E93A)	156.3	6.7	18.1
N810A (IL15-L45S)	151.3	6.6	16.5
N810D	117.7		8.8

OTHER EMBODIMENTS

While the invention has been described in conjunction with the detailed description thereof, the foregoing description is intended to illustrate and not limit the scope of the invention, which is defined by the scope of the appended claims. Other aspects, advantages, and modifications are within the scope of the following claims.

The patent and scientific literature referred to herein establishes the knowledge that is available to those with skill in the art. While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that various changes in form and details may be made therein without departing from the scope of the invention encompassed by the appended claims.

Date Reçue/Date Received 2021-09-16

What is claimed is:

1. An isolated soluble fusion protein complex comprising at least a first soluble protein and a second soluble protein, wherein the first soluble protein has at least 85% sequence identity to the amino acid sequence of SEQ ID NO:2, and wherein the second soluble protein has at least 85% sequence identity to the amino acid sequence of SEQ ID NO:4, and

wherein an interleukin-15 (IL-15) domain of the first soluble protein binds to an IL-15 receptor alpha sushi-binding domain (IL-15RαSu) domain of the second soluble protein to form the soluble fusion protein complex.

2. The soluble fusion protein complex of claim 1, wherein the first soluble protein has at least 95% sequence identity to the amino acid sequence of SEQ ID NO:2.

3. The soluble fusion protein complex of claim 2, wherein the first soluble protein comprises SEQ ID NO:2.

4. The soluble fusion protein complex of any one of claims 1-3, wherein the second soluble protein has at least 95% sequence identity to the amino acid sequence of SEQ ID NO:4.

5. The soluble fusion protein complex of claim 4, wherein the second soluble protein comprises the amino acid sequence of SEQ ID NO:4.

6. The soluble fusion protein complex of any one of claims 1-5, wherein the first soluble protein comprises a transforming growth factor-beta receptor type 2 (TGFβRII) domain bound to transforming factor beta (TGFβ).

7. The soluble fusion protein complex of any one of claims 1-6, wherein the fusion protein complex is covalently linked to a second fusion protein complex by a disulfide bond linking an Fc domain of the soluble fusion protein complex to an Fc domain of the second soluble fusion protein complex.

Date Reçue/Date Received 2022-04-26

8. An isolated soluble fusion protein complex comprising at least a first soluble protein and a second soluble protein, wherein the first soluble protein has at least 85% sequence identity to the amino acid sequence of SEQ ID NO:6, wherein the second soluble protein has at least 85% sequence identity to the amino acid sequence of SEQ ID NO:8, and

wherein an interleukin-15 (IL-15) domain of the first fusion protein binds to an IL-15 receptor alpha sushi-binding domain (IL-15RαSu) domain of the second fusion protein to form the soluble fusion protein complex.

9. The soluble fusion protein complex of claim 8, wherein the first soluble protein has at least 95% sequence identity to the amino acid sequence of SEQ ID NO:6

10. The soluble fusion protein complex of claim 9, wherein the first soluble protein comprises the amino acid sequence of SEQ ID NO:6.

11. The soluble fusion protein complex of any one of claims 8-10, wherein the second soluble protein has at least 95% sequence identity to the amino acid sequence of SEQ ID NO:8.

12. The soluble fusion protein complex of claim 11, wherein the second soluble protein comprises the amino acid sequence of SEQ ID NO:8.

13. The soluble fusion protein complex of any one of claims 8-12, wherein the first soluble protein is bound to programmed death ligand 1 (PD-L1).

14. The soluble fusion protein complex of any one of claims 8-13, wherein the second soluble protein comprises a transforming growth factor-beta receptor type 2 (TGFβRII) bound to transforming growth factor beta (TGFβ).

15. The soluble fusion protein complex of any one of claims 8-14, wherein a first fusion protein complex is covalently linked to a second fusion protein complex by a disulfide

Date Reçue/Date Received 2022-04-26

bond linking an Fc domain of the first soluble fusion protein complex to an Fc domain of the second soluble fusion protein complex.

16. A nucleic acid comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 16, 17, 18 and 19.

17. The nucleic acid of claim 16, wherein the nucleic acid sequence further comprises a promoter, translation initiation signal, and leader sequence operably linked to the sequence selected from the group consisting of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 16, 17, 18 and 19.

18. An expression vector comprising the nucleic acid sequence of claim 16.

19. A pharmaceutical composition comprising the soluble fusion protein complex of any one of claims 1-15, the nucleic acid of claim 16 or 17, or the expression vector of claim 18; and an excipient.

20. A method of preparing immune cells for infusion in a subject for treatment of neoplasia in the subject comprising:

isolating and separating immune cells from a biological sample;

contacting the immune cells *in vitro* with the soluble fusion protein complex of any one of claims 1-15.

21. A use of the soluble fusion protein complex of any one of claims 1-15 or the pharmaceutical composition comprising the soluble fusion protein complex of claim 19, for treatment of neoplasia.

22. A use of the soluble fusion protein complex of any one of claims 1-15 for the manufacture of a medicament for treatment of neoplasia.

Date Reçue/Date Received 2022-04-26

23. The use of claim 21 or 22 wherein the neoplasia is glioblastoma, prostate cancer, hematological cancer, B-cell neoplasms, multiple myeloma, B-cell lymphoma, B cell non-Hodgkin lymphoma, Hodgkin's lymphoma, chronic lymphocytic leukemia, acute myeloid leukemia, cutaneous T-cell lymphoma, T-cell lymphoma, a solid tumor, urothelial/bladder carcinoma, melanoma, lung cancer, renal cell carcinoma, breast cancer, gastric and esophageal cancer, prostate cancer, pancreatic cancer, colorectal cancer, ovarian cancer, non-small cell lung carcinoma, or squamous cell head and neck carcinoma.

24. The use of any one of claims 21-23, in combination with one or more chemotherapeutic agents.

25. The soluble fusion protein complex of any one of claims 1-15, or the pharmaceutical composition comprising the soluble fusion protein complex of claim 19, for use in treatment of neoplasia.

26. The soluble fusion protein complex or composition for use of claim 25 wherein the neoplasia is glioblastoma, prostate cancer, hematological cancer, B-cell neoplasms, multiple myeloma, B-cell lymphoma, B cell non-Hodgkin lymphoma, Hodgkin's lymphoma, chronic lymphocytic leukemia, acute myeloid leukemia, cutaneous T-cell lymphoma, T-cell lymphoma, a solid tumor, urothelial/bladder carcinoma, melanoma, lung cancer, renal cell carcinoma, breast cancer, gastric and esophageal cancer, prostate cancer, pancreatic cancer, colorectal cancer, ovarian cancer, non-small cell lung carcinoma, or squamous cell head and neck carcinoma.

27. The soluble fusion protein complex or composition for use of claim 25 or 26, in combination with one or more chemotherapeutic agents.

28. A method of inhibiting transforming growth factor beta (TGFβ) activity *in vitro*, comprising contacting a cell *in vitro* with the soluble fusion protein complex of any one of claims 1-15, the nucleic acid of claim 16 or 17, the expression vector of claim 18 or the

Date Reçue/Date Received 2022-04-26

pharmaceutical composition of claim 19, thereby inhibiting transforming growth factor beta (TGFβ) activity *in vitro*.

29. A use of the soluble fusion protein complex of any one of claims 1-15, the nucleic acid of claim 16 or 17, the expression vector of claim 18 or the pharmaceutical composition of claim 19, for inhibiting transforming growth factor beta (TGFβ) activity.

30. A use of the soluble fusion protein complex of any one of claims 1-15, the nucleic acid of claim 16 or 17, or the expression vector of claim 18, for the manufacture of a medicament for inhibiting transforming growth factor beta (TGFβ) activity.

31. The soluble fusion protein complex of any one of claims 1-15, the nucleic acid of claim 16 or 17, the expression vector of claim 18 or the pharmaceutical composition of claim 19, for use in inhibiting transforming growth factor beta (TGFβ) activity.

32. A use of the soluble fusion protein complex of any one of claims 1-15, the nucleic acid of claim 16 or 17, the expression vector of claim 18 or the pharmaceutical composition of claim 19, for decreasing the amount of transforming growth factor beta (TGFβ) *in vivo*.

33. A use of the soluble fusion protein complex of any one of claims 1-15, the nucleic acid of claim 16 or 17, or the expression vector of claim 18, for the manufacture of a medicament for decreasing the amount of transforming growth factor beta (TGFβ) *in vivo*.

34. The soluble fusion protein complex of any one of claims 1-15, the nucleic acid of claim 16 or 17, the expression vector of claim 18 or the pharmaceutical composition of claim 19, for use in decreasing the amount of transforming growth factor beta (TGFβ) *in vivo*.

35. A use of the soluble fusion protein complex of claims 1-15, the nucleic acid of claim 16 or 17, the expression vector of claim 18 or the pharmaceutical composition of claim 19, for inducing antibody-dependent cell-mediated cytotoxicity in a subject in need thereof.

Date Reçue/Date Received 2022-04-26

36. A use of the soluble fusion protein complex of claims 1-15, the nucleic acid of claim 16 or 17, or the expression vector of claim 18, for the manufacture of a medicament for inducing antibody-dependent cell-mediated cytotoxicity in a subject in need thereof.

37. The soluble fusion protein complex of claims 1-15, the nucleic acid of claim 16 or 17, the expression vector of claim 18 or the pharmaceutical composition of claim 19, for use in inducing antibody-dependent cell-mediated cytotoxicity in a subject in need thereof.

38. A use of the soluble fusion protein complex of any one of claims 1-15, the nucleic acid of claim 16 or 17, the expression vector of claim 18 or the pharmaceutical composition of claim 19, for inhibiting transforming growth factor beta (TGFβ) mediated phosphorylation and activation of SMAD polypeptides *in vivo*.

39. A use of the soluble fusion protein complex of any one of claims 1-15, the nucleic acid of claim 16 or 17, or the expression vector of claim 18, for the manufacture of a medicament for inhibiting transforming growth factor beta (TGFβ) mediated phosphorylation and activation of SMAD polypeptides *in vivo*.

40. The soluble fusion protein complex of any one of claims 1-15, the nucleic acid of claim 16 or 17, the expression vector of claim 18 or the pharmaceutical composition of claim 19, for use in inhibiting transforming growth factor beta (TGFβ) mediated phosphorylation and activation of SMAD polypeptides *in vivo*.

Date Reçue/Date Received 2022-04-26

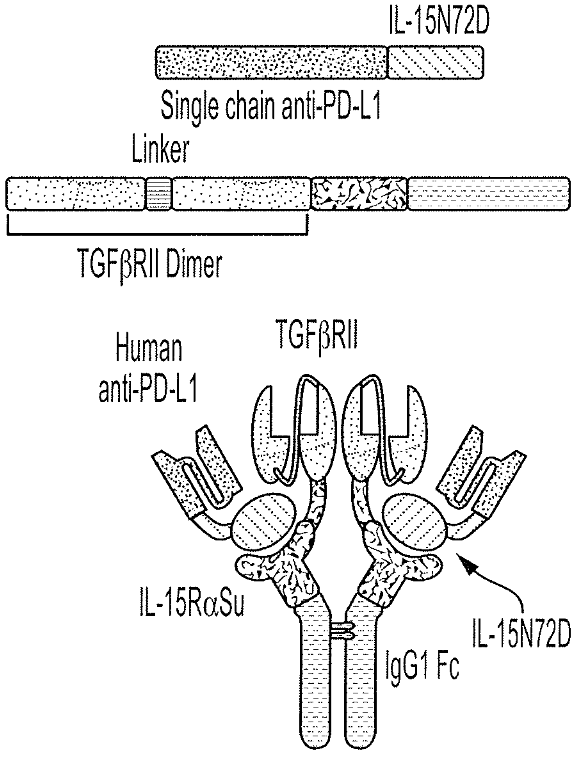

IL-15N72D
Single chain anti-PD-L1
Linker
TGFβRII Dimer
Human
anti-PD-L1
TGFβRII
IL-15RαSu
IL-15N72D
IgG1 Fc

FIG. 1

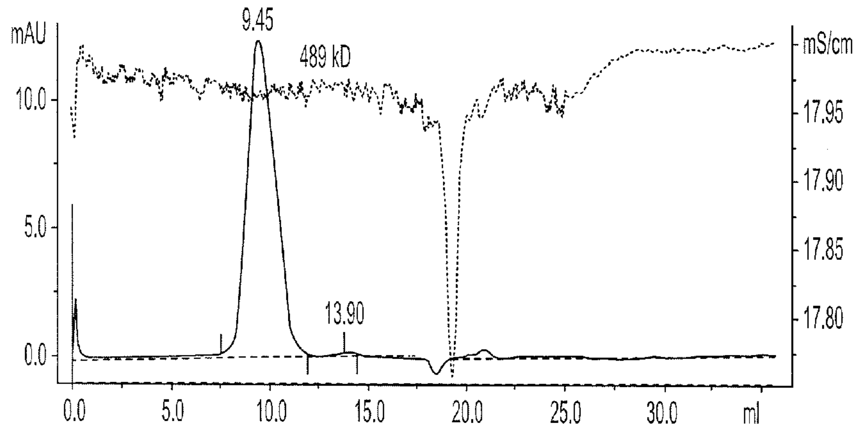

mAU
9.45
489 kD
mS/cm
10.0
17.95
17.90
5.0
17.85
13.90
17.80
0.0
0.0
5.0
10.0
15.0
20.0
25.0
30.0
ml

FIG. 2

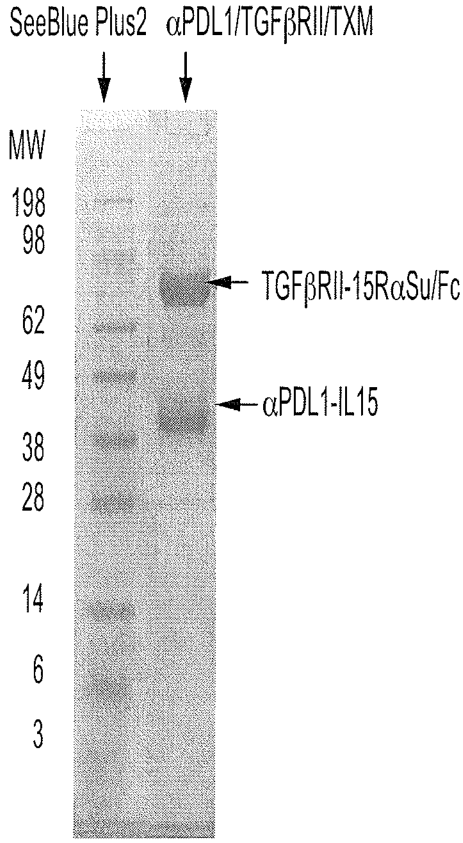

SeeBlue Plus2
αPDL1/TGFβRII/TXM
MW
198
98
62
49
38
28
14
6
3
TGFβRII-15RαSu/Fc
αPDL1-IL15

FIG. 3

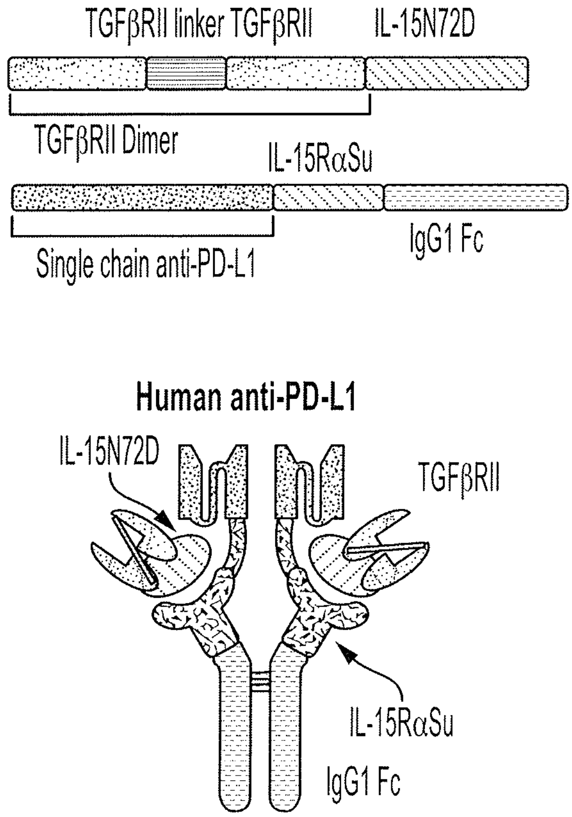

TGFβRII linker TGFβRII
IL-15N72D
TGFβRII Dimer
IL-15RαSu
Single chain anti-PD-L1
IgG1 Fc
Human anti-PD-L1
IL-15N72D
TGFβRII
IL-15RαSu
IgG1 Fc

FIG. 4

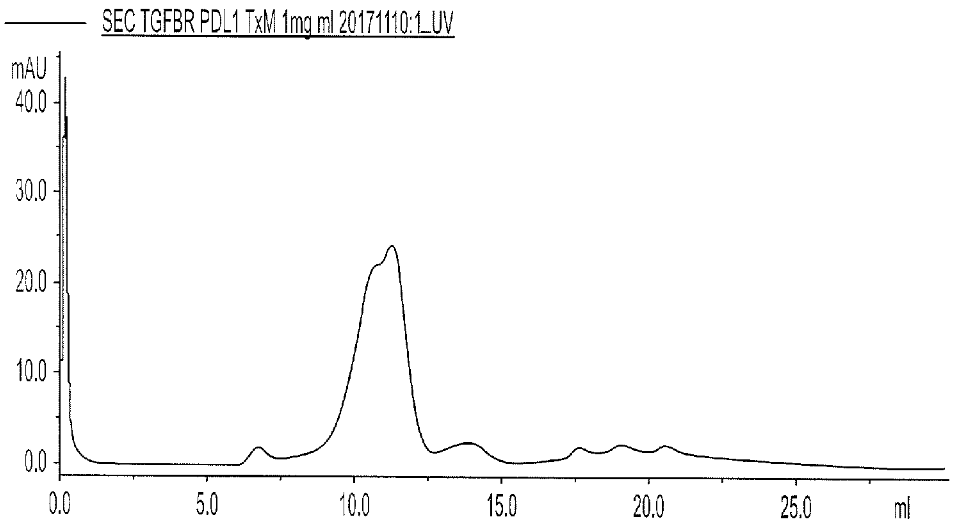

SEC TGFBR PDL1 TxM 1mg ml 20171110:1_UV
mAU
40.0
30.0
20.0
10.0
0.0
0.0
5.0
10.0
15.0
20.0
25.0
ml

FIG. 5

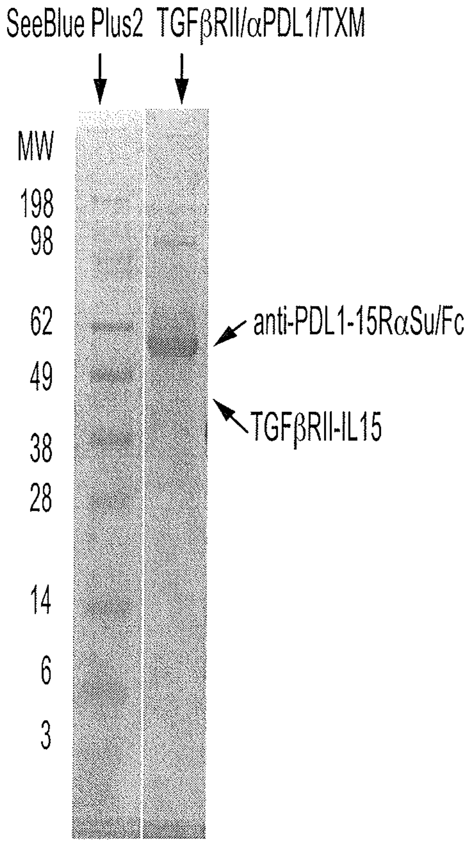

SeeBlue Plus2
TGFβRII/αPDL1/TXM
MW
198
98
62
49
38
28
14
6
3
anti-PDL1-15RαSu/Fc
TGFβRII-IL15

FIG. 6

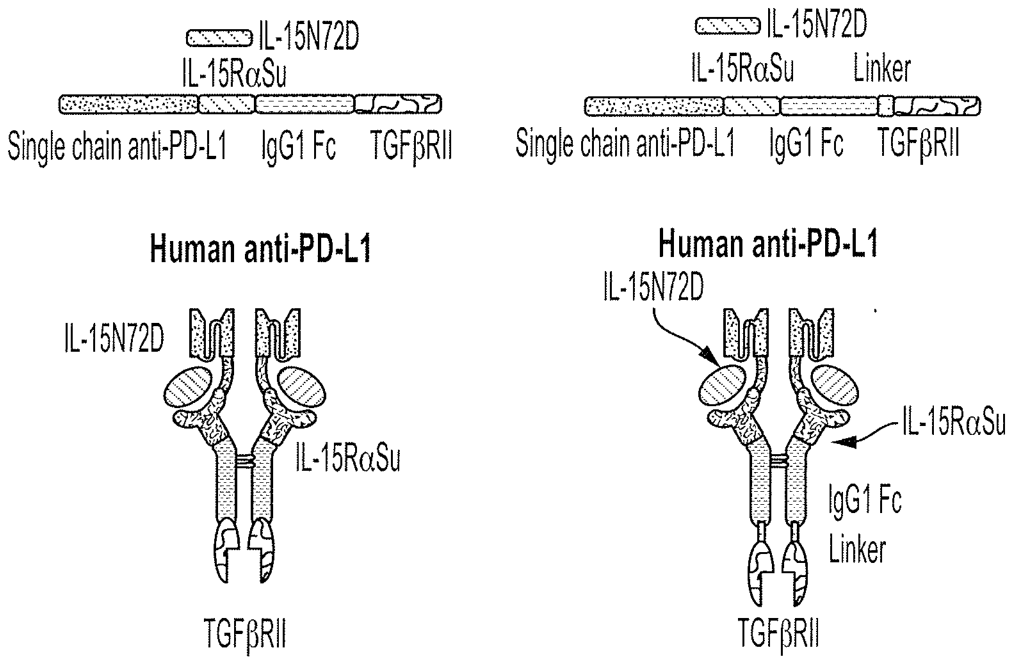
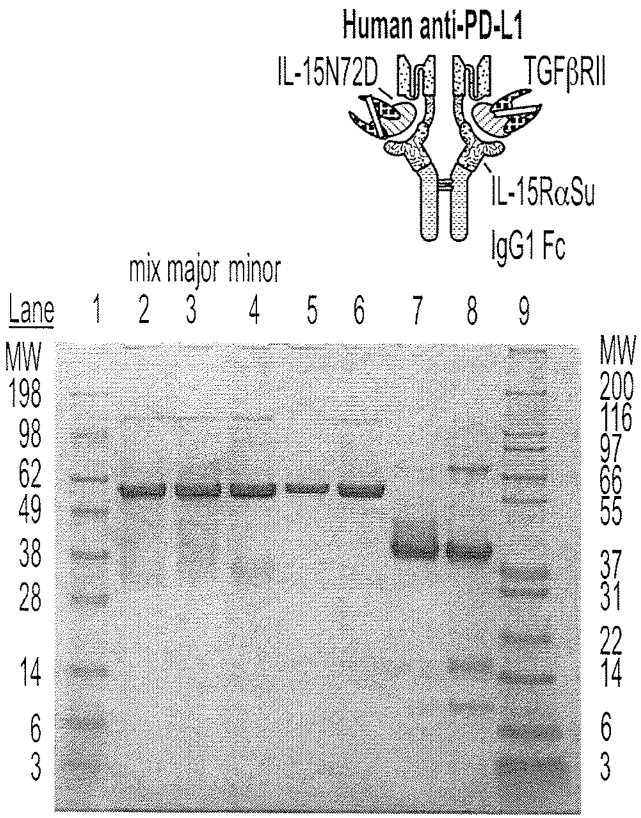
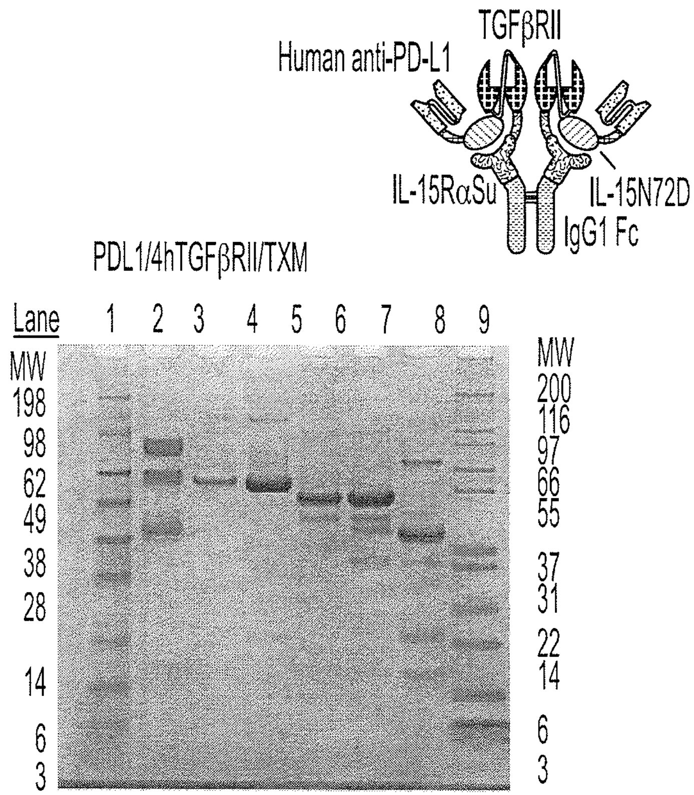

IL-15N72D
IL-15RαSu
Single chain anti-PD-L1
IgG1 Fc
TGFβRII
IL-15N72D
IL-15RαSu
Linker
Single chain anti-PD-L1
IgG1 Fc
TGFβRII
Human anti-PD-L1
IL-15N72D
IL-15RαSu
TGFβRII
Human anti-PD-L1
IL-15N72D
IL-15RαSu
IgG1 Fc
Linker
TGFβRII

FIG. 7





αPDL-1/IL15, MW 38.43; TGFbRII/SuFc, MW 65.12

FIG. 8

Early Protein Characterization

Component	Cell Line	Assay
IL15	32Dβ	Proliferation assay
TGFβRII	TGF/SMAD Signaling Pathway SBE Reporter - HEK293 Cell	Blocking Assay
anti-PDL1	H441	Binding Assay (Fc)
		Blocking Assay (Fc)

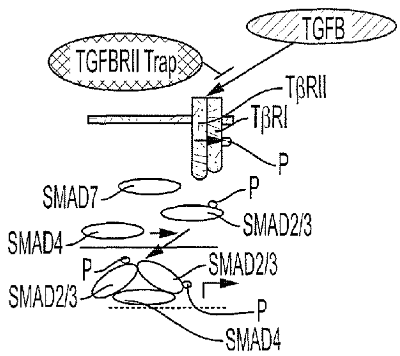


FIG. 9

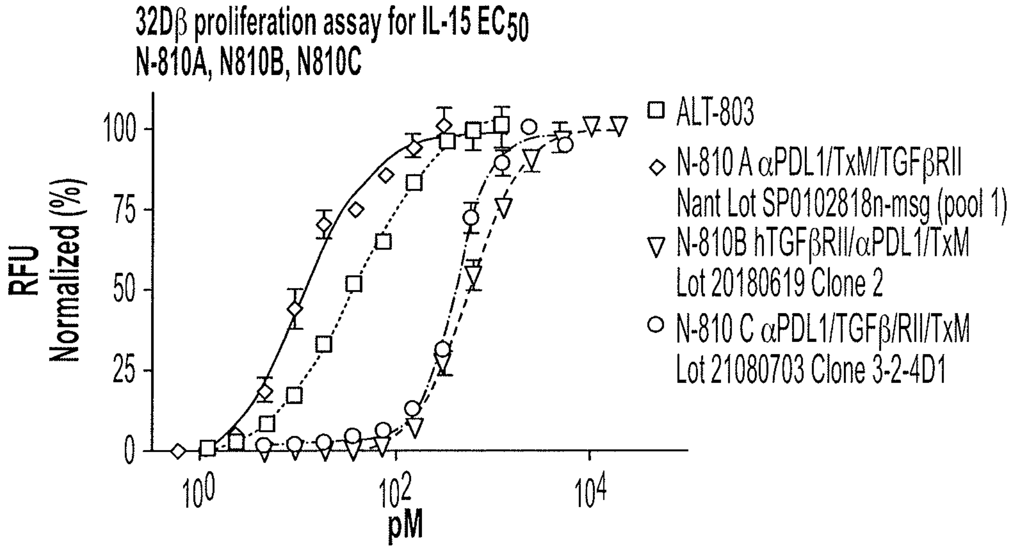


FIG. 10

	ALT-803	**N-810 A** αPDL1/TxM/TGFβ Nant Lot SP0102818n-msg (pool 1)	**N-810B** hTGFβRII/αPDL1/TxM Lot 20180619 Clone 2	**N-810C** αPDL1/TGFβ/RII/TxM Lot 21080703 Clone 3-2-4D1
EC50	39.26	10.71	557.9	411.7
HillSlope	0.9823	1.238	1.606	2.428
R square	0.9749	0.9842	0.9854	0.9948
Fold difference from ALT-803		0.3	14	10

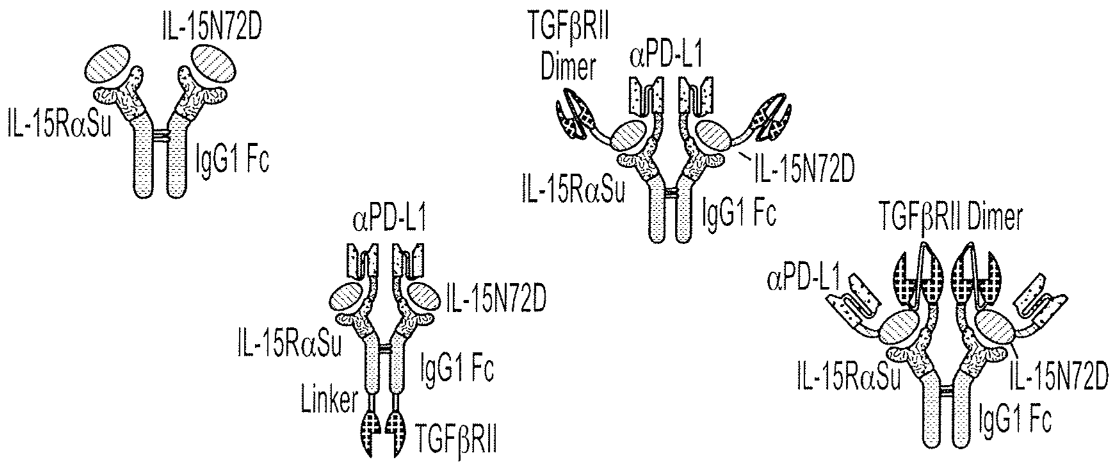
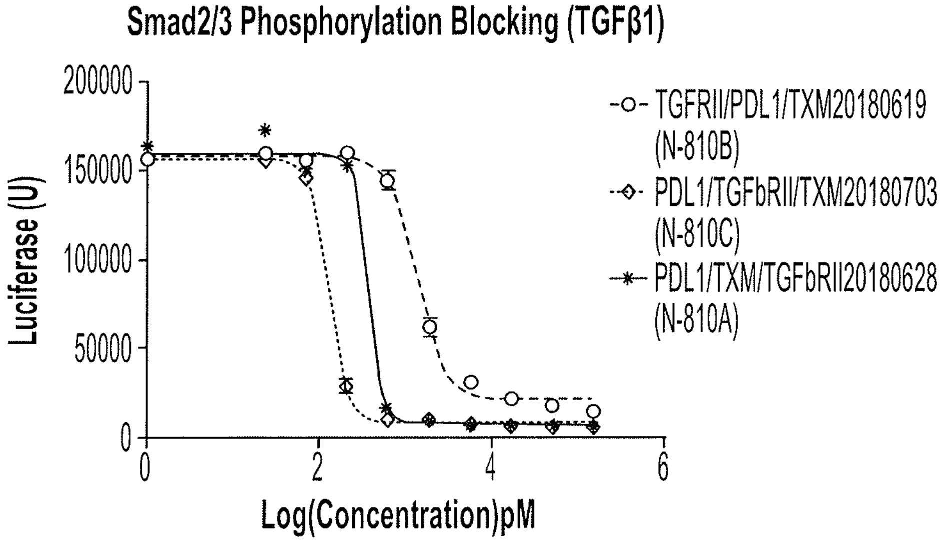


FIG. 10 CONT.



	TGFbRII/PDL1/TXM 20180619(N-810B)	PDL1/TGFbRII/TXM 20180703(N-810C)	PDL1/TXM/TGFbRII201 80628(N-810A)
HillSlope	-2.59	-3.967	-6.507
IC50	921.9	87.49	266.1
R square	0.995	0.9992	0.9976

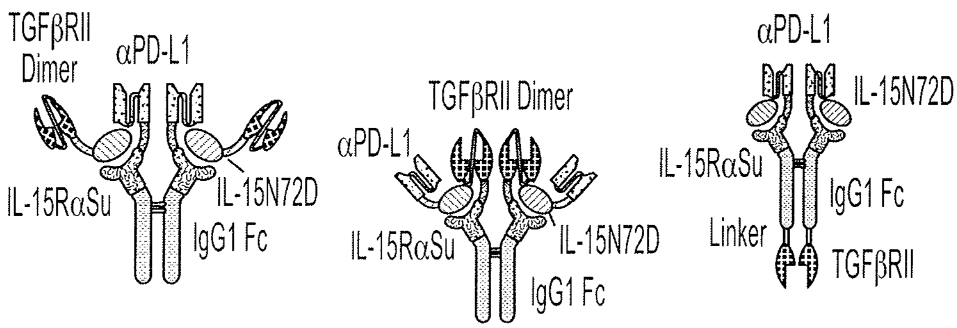
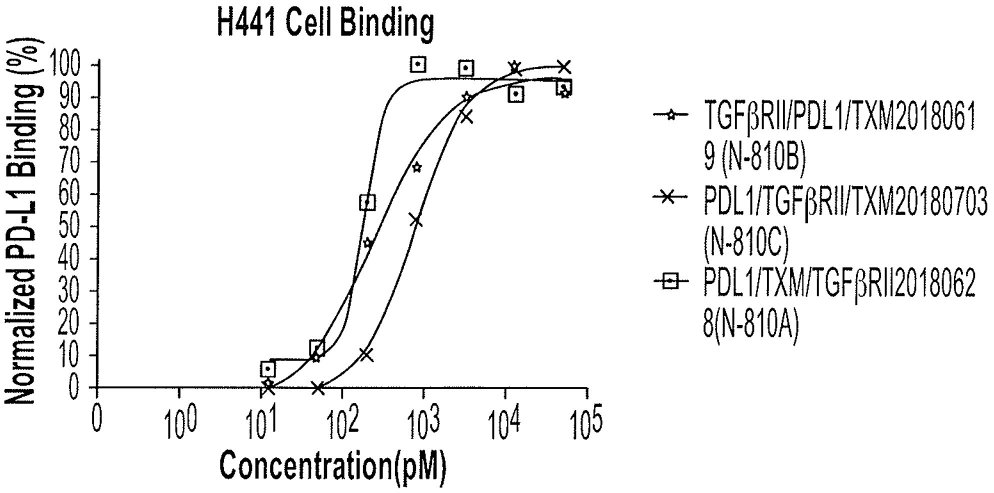


FIG. 11



	TGFbRII/PDL1/TXM 20180619(N-810B)	PDL1/TGFbRII/TXM 20180703(N-810C)	PDL1/TXM/TGFbRII 20180628(N-810A)
HillSlope	0.9819	1.342	3.504
EC50	233.3	750.7	182.3
R square	0.9899	0.9985	0.9926

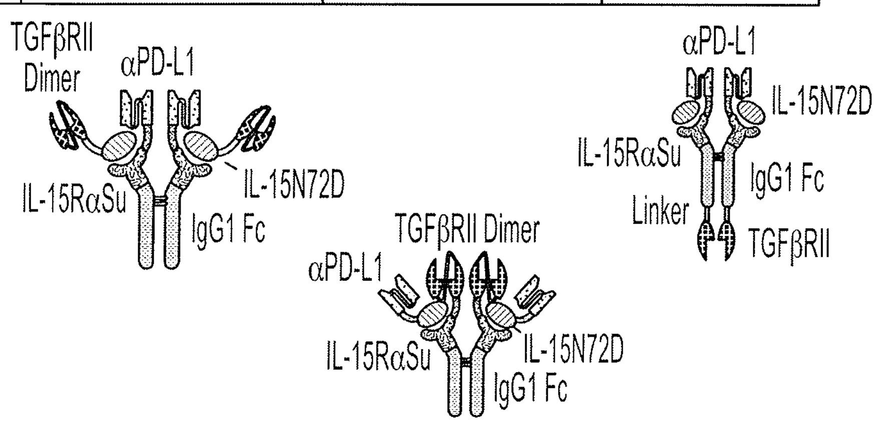


FIG. 12

	TGFβRII/αPDL1/TXM	αPDL1/TGFβRII/TXM
Protein expression	70mg/L	4mg/L
TGFβ Activity Blocking Assay IC50	2.47nM	0.55nM
IL-15 Activity Assay EC50	0.259nM	0.195nM
PDL1 Binding Assay EC50	0.20nM	0.26nM

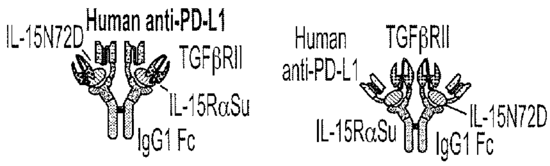


FIG. 13

TGFβRII/αPDL1/TXM

32Dβ Cell Proliferation

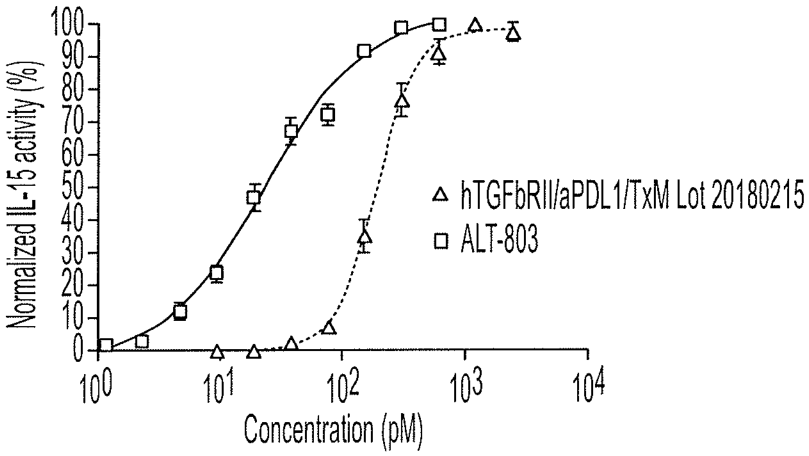


FIG. 14A

αPDL1/TGFβRII/TXM

32Dβ Cell Proliferation

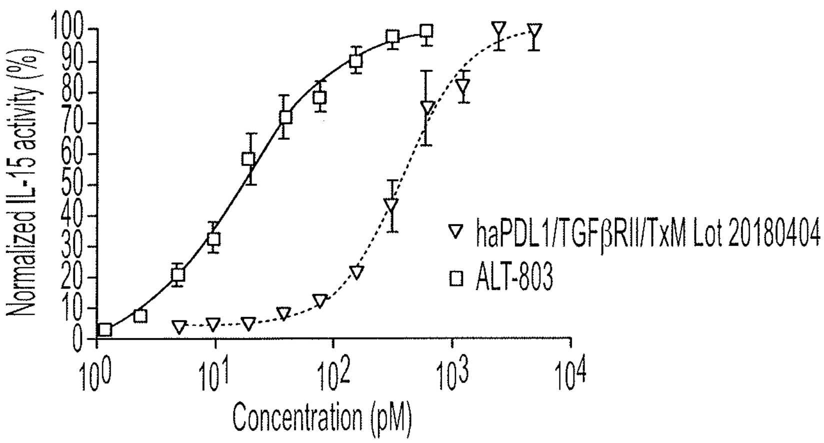


FIG. 14B

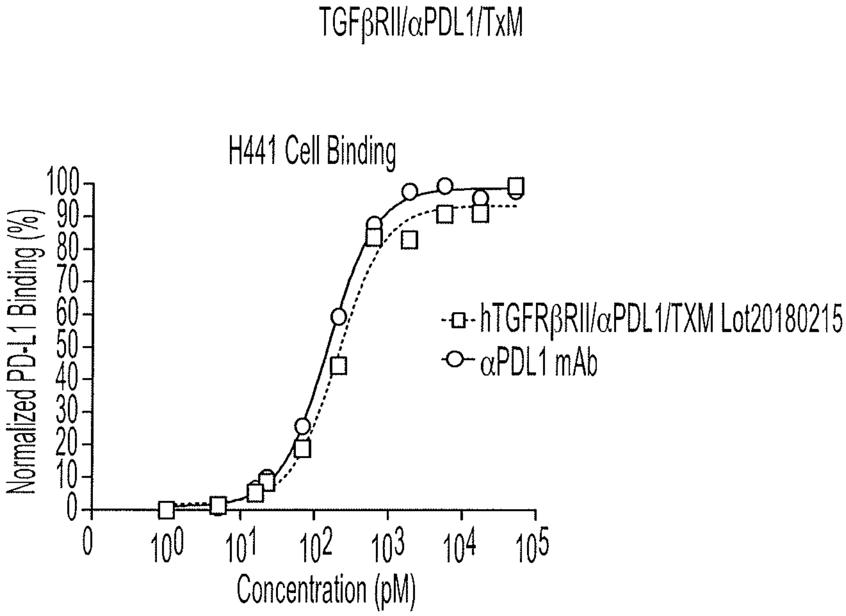


FIG. 15A

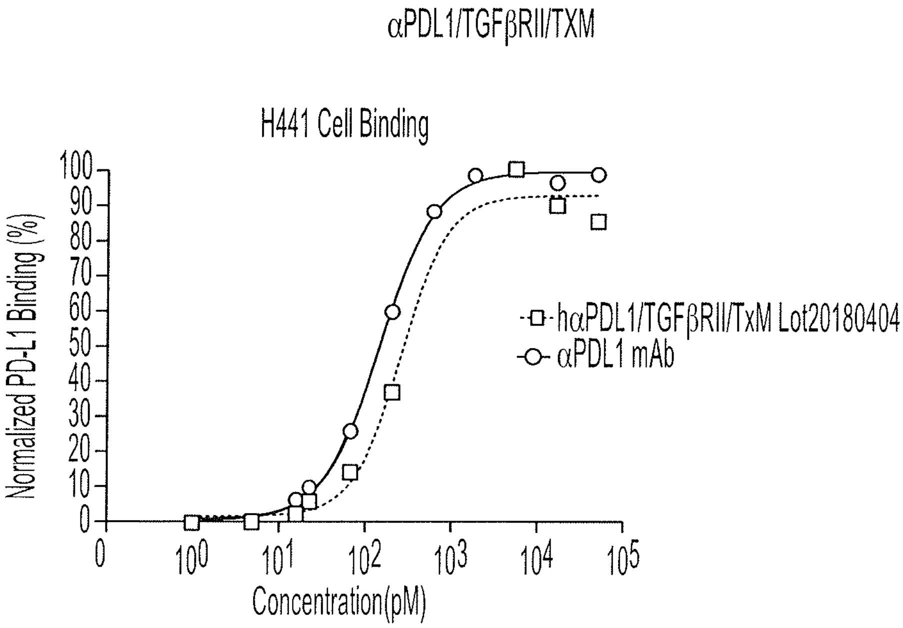


FIG. 15B

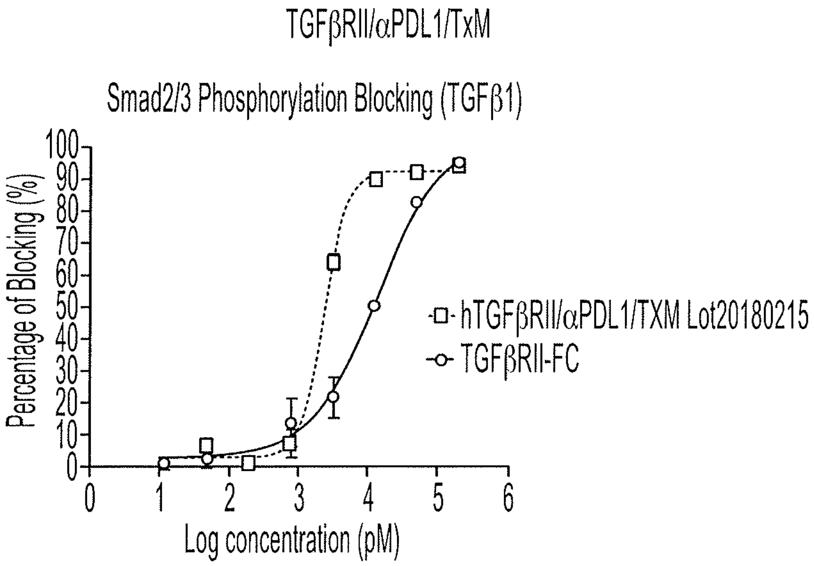


FIG. 16A

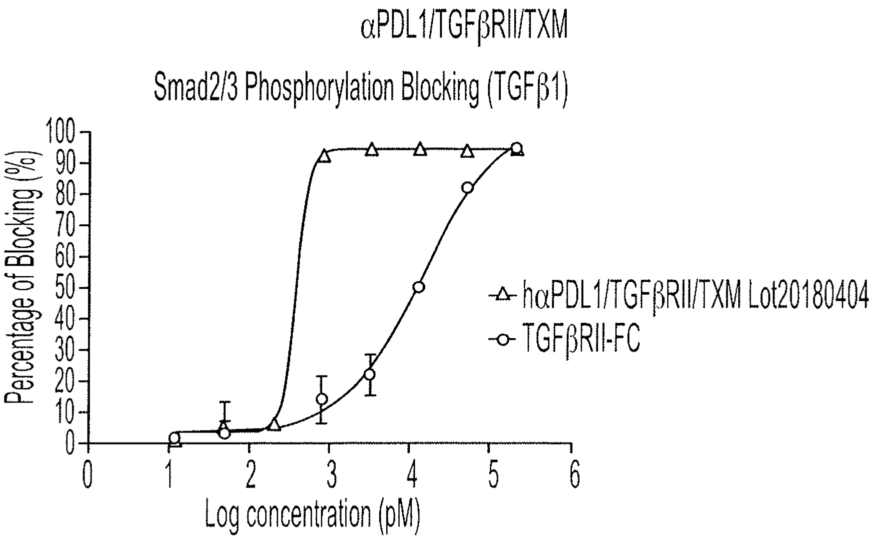


FIG. 16B

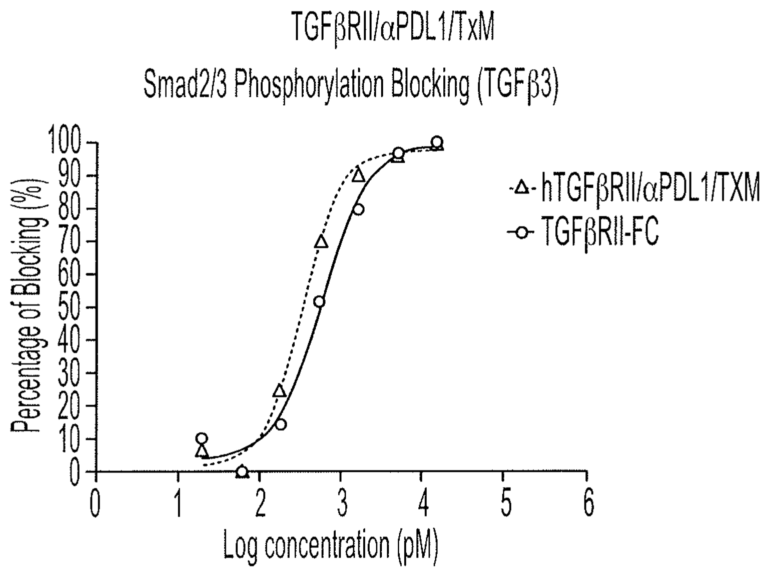


FIG. 17A

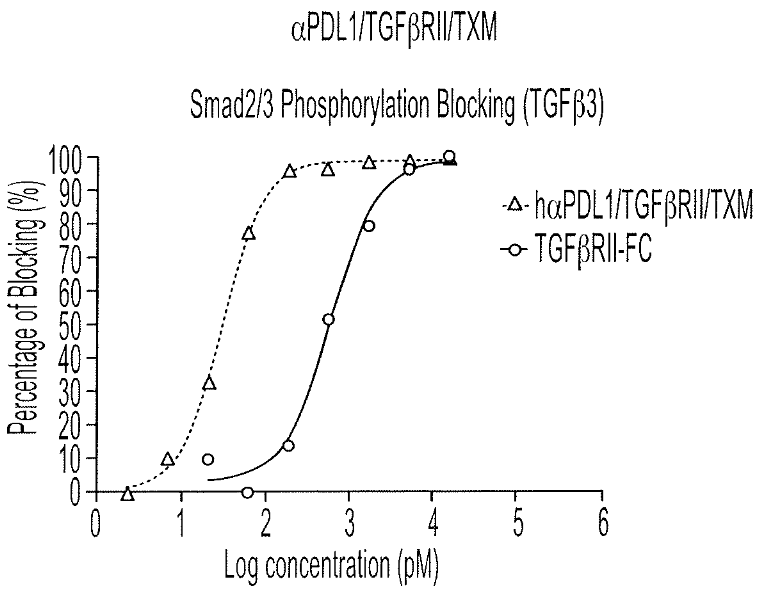


FIG. 17B

TGFβRII/αPDL1/TxM

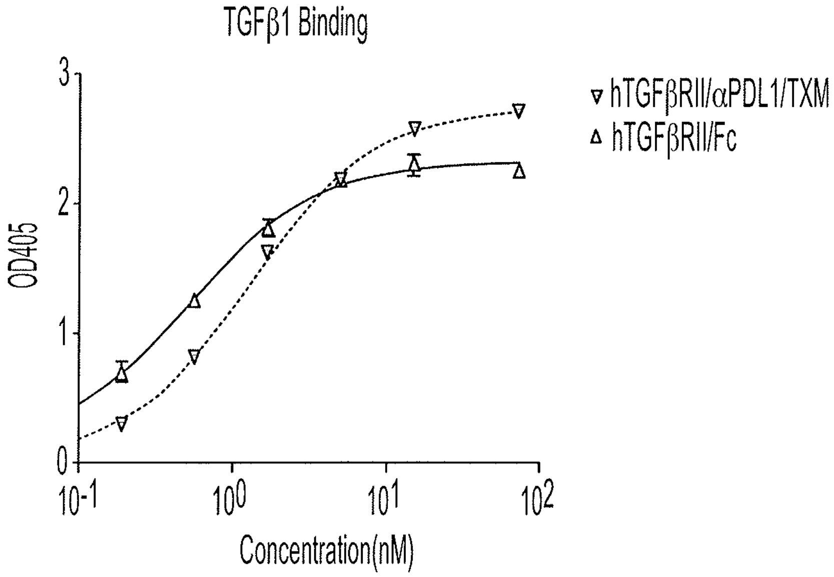


FIG. 18A

αPDL1/TGFβRII/TxM

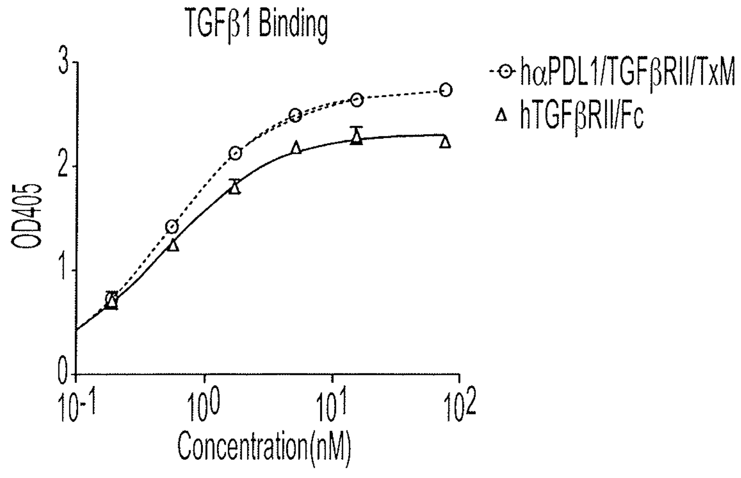


FIG. 18B

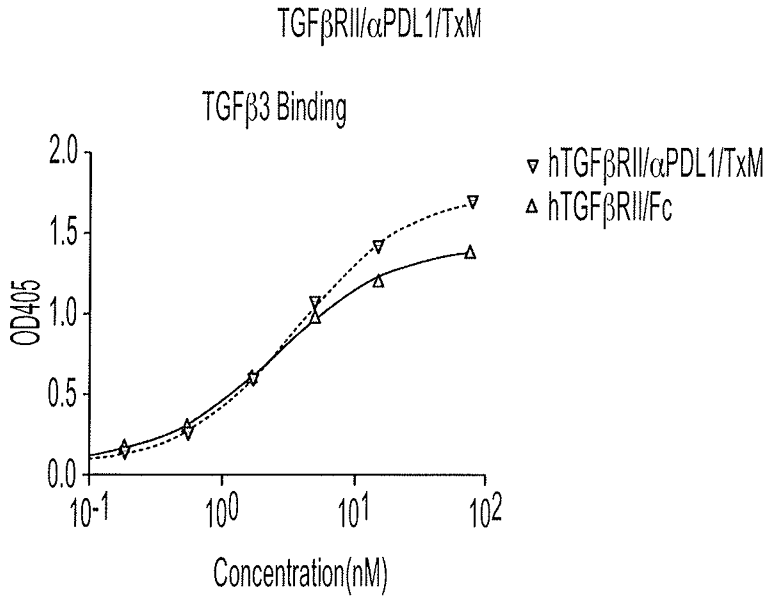


FIG. 19A

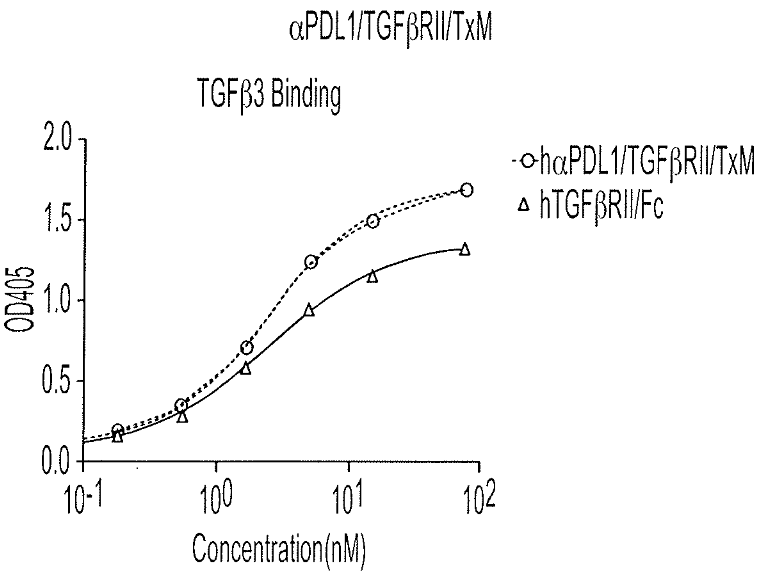


FIG. 19B

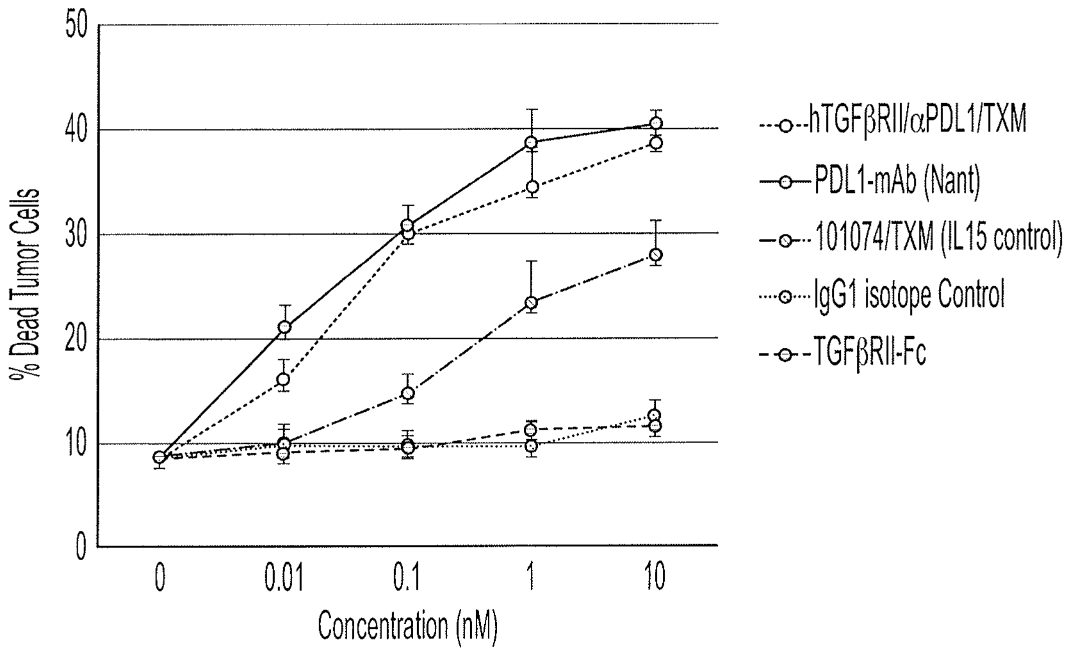

50
40
30
20
10
0
% Dead Tumor Cells
0
0.01
0.1
1
10
Concentration (nM)
hTGFβRII/αPDL1/TXM
PDL1-mAb (Nant)
101074/TXM (IL15 control)
IgG1 isotope Control
TGFβRII-Fc

FIG. 20

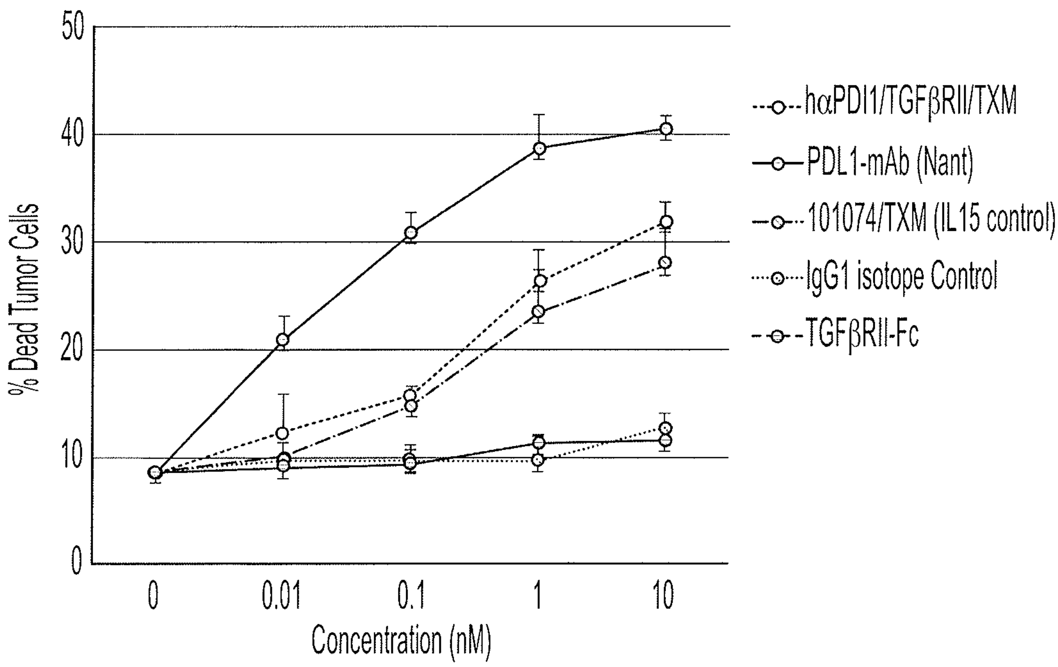

50
40
30
20
10
0
% Dead Tumor Cells
0
0.01
0.1
1
10
Concentration (nM)
hαPDI1/TGFβRII/TXM
PDL1-mAb (Nant)
101074/TXM (IL15 control)
IgG1 isotope Control
TGFβRII-Fc

FIG. 21

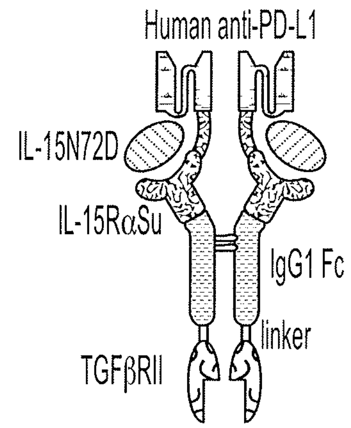


FIG. 22A

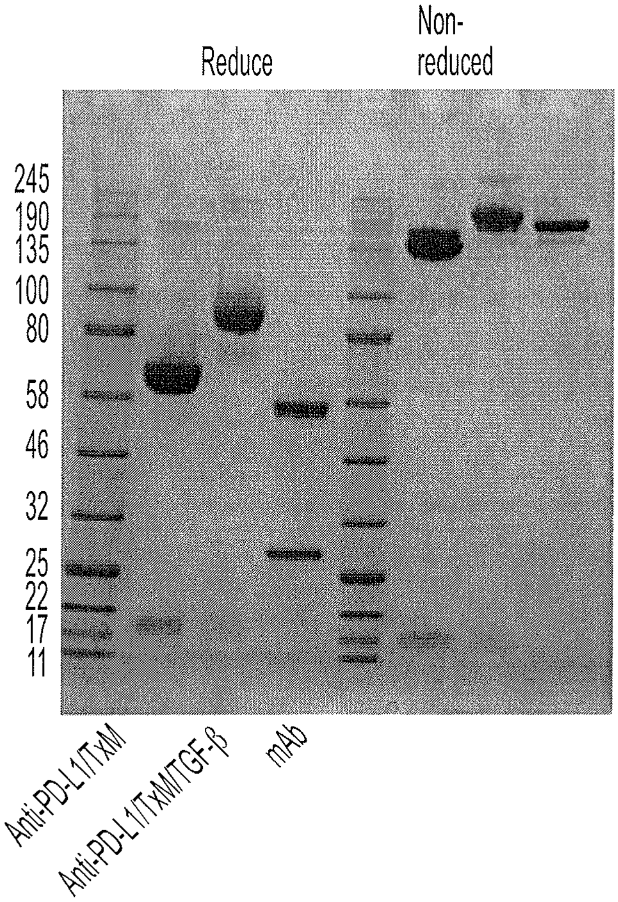


FIG. 22B

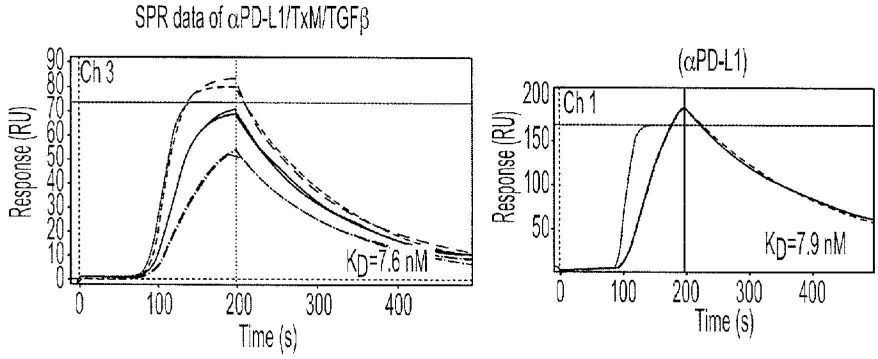


FIG. 22C

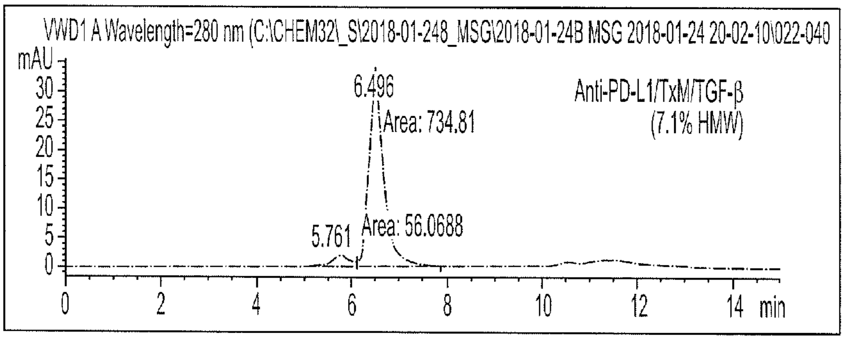


FIG. 22D

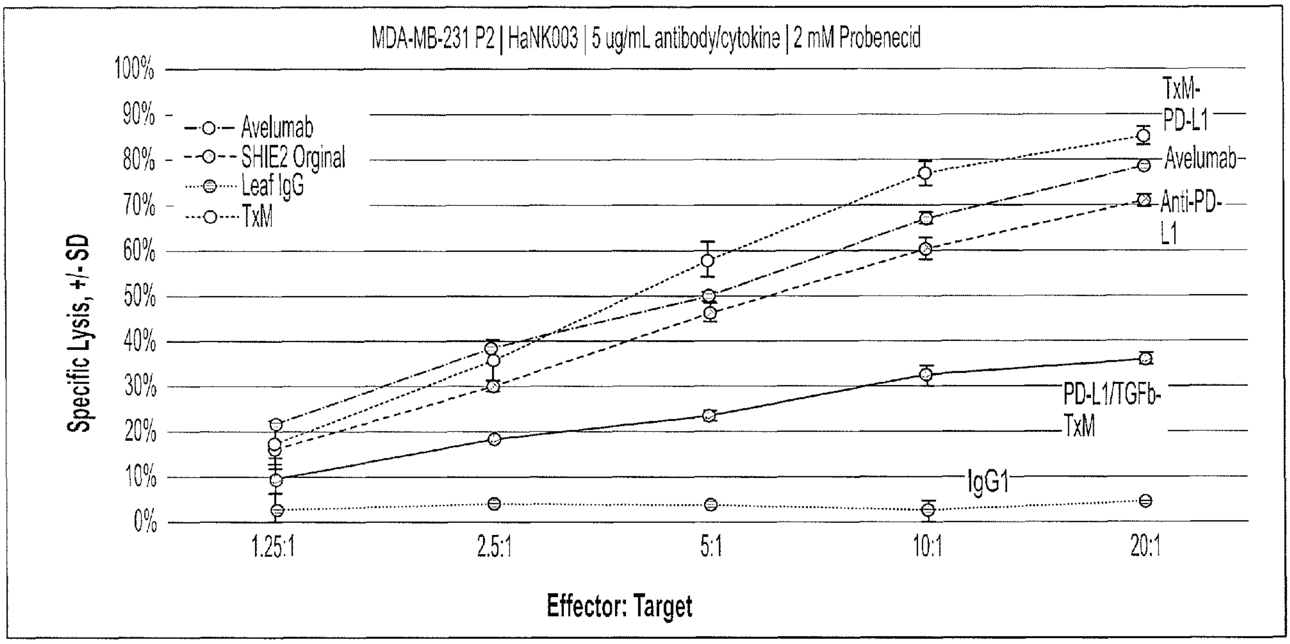

MDA-MB-231 P2 | HaNK003 | 5 ug/mL antibody/cytokine | 2 mM Probenecid
100%
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
Avelumab
SHIE2 Orginal
Leaf IgG
TxM
Specific Lysis, +/- SD
TxM-PD-L1
Avelumab
Anti-PD-L1
PD-L1/TGFb-TxM
IgG1
1.25:1
2.5:1
5:1
10:1
20:1
Effector: Target

FIG. 22E

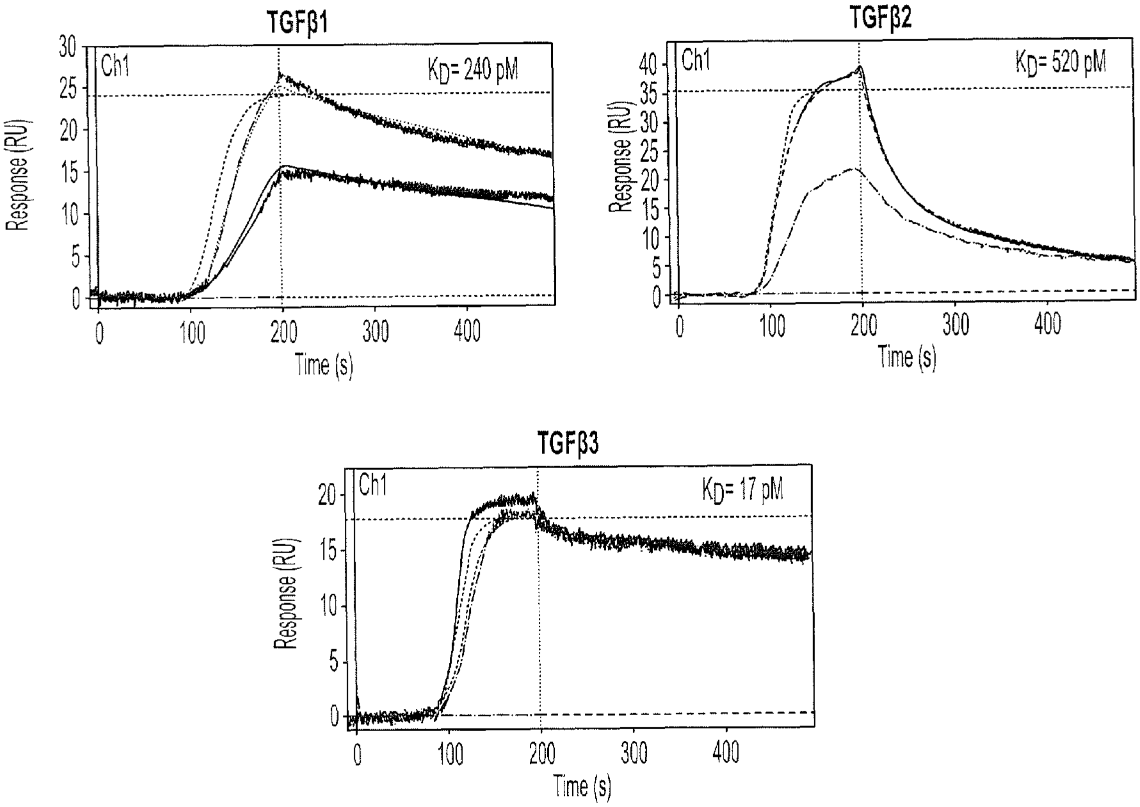

TGFβ1
Ch1
KD= 240 pM
Response (RU)
Time (s)
TGFβ2
Ch1
KD= 520 pM
Response (RU)
Time (s)
TGFβ3
Ch1
KD= 17 pM
Response (RU)
Time (s)

FIG. 23

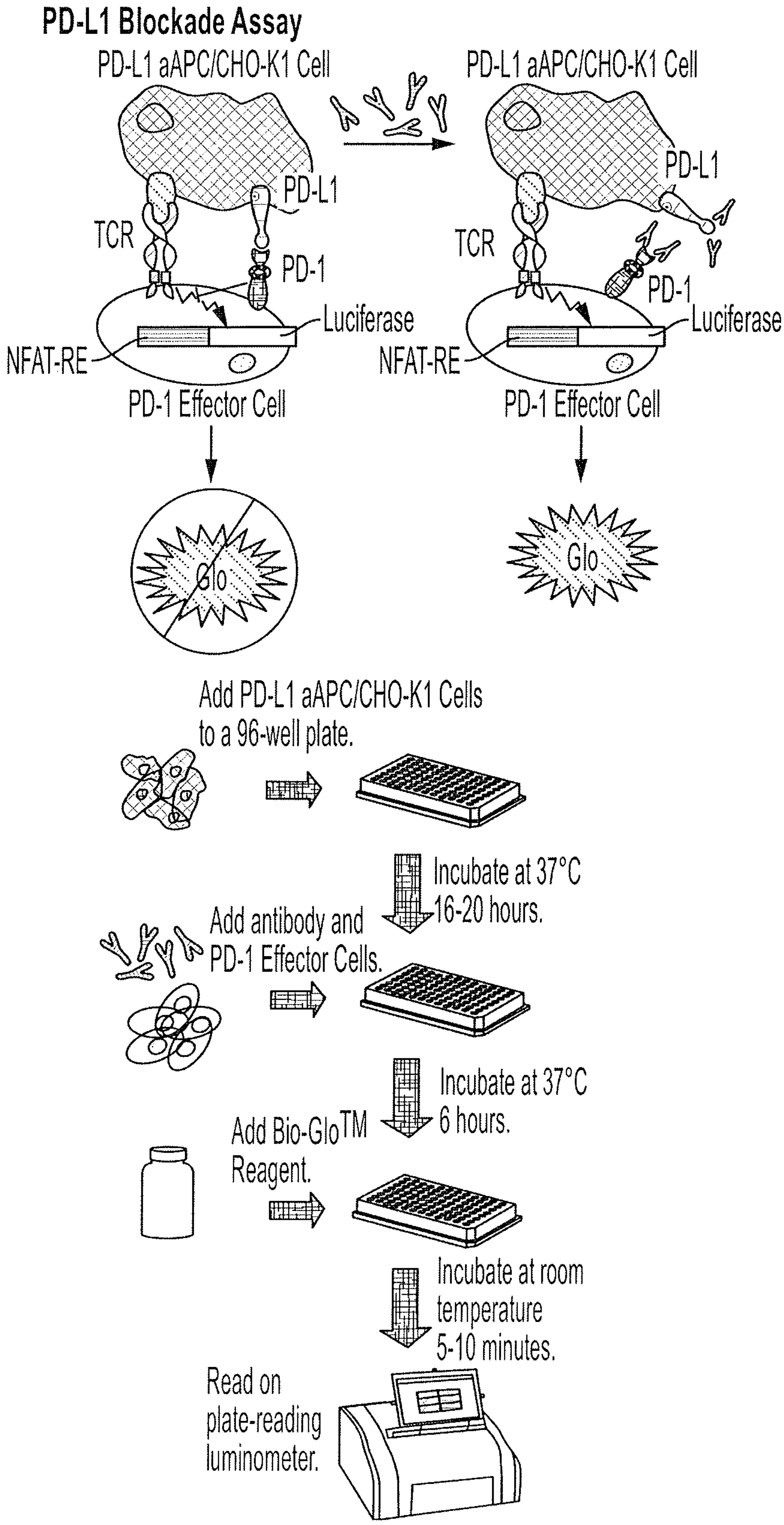

PD-L1 Blockade Assay
PD-L1 aAPC/CHO-K1 Cell
PD-L1 aAPC/CHO-K1 Cell
PD-L1
TCR
PD-1
Luciferase
NFAT-RE
PD-1 Effector Cell
PD-L1
TCR
PD-1
Luciferase
NFAT-RE
PD-1 Effector Cell
Glo
Glo
Add PD-L1 aAPC/CHO-K1 Cells to a 96-well plate.
Incubate at 37°C 16-20 hours.
Add antibody and PD-1 Effector Cells.
Incubate at 37°C 6 hours.
Add Bio-GloTM Reagent.
Incubate at room temperature 5-10 minutes.
Read on plate-reading luminometer.

FIG. 24

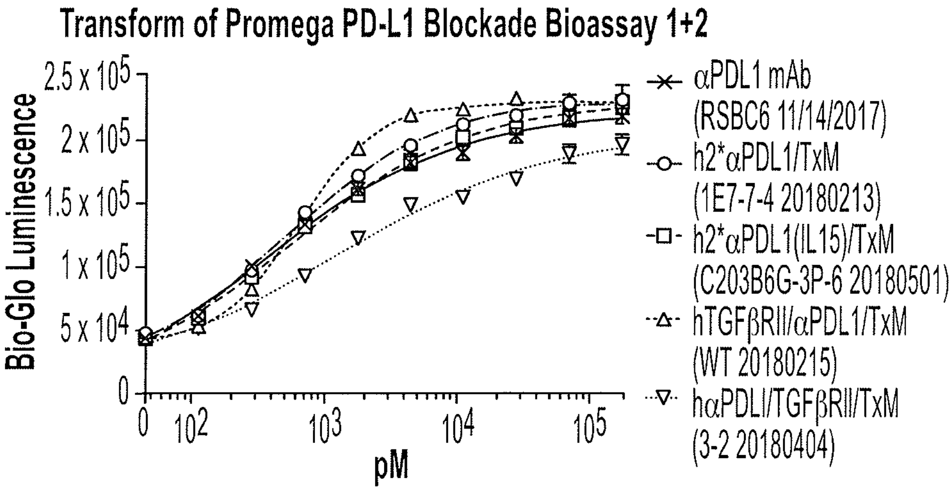


FIG. 25A

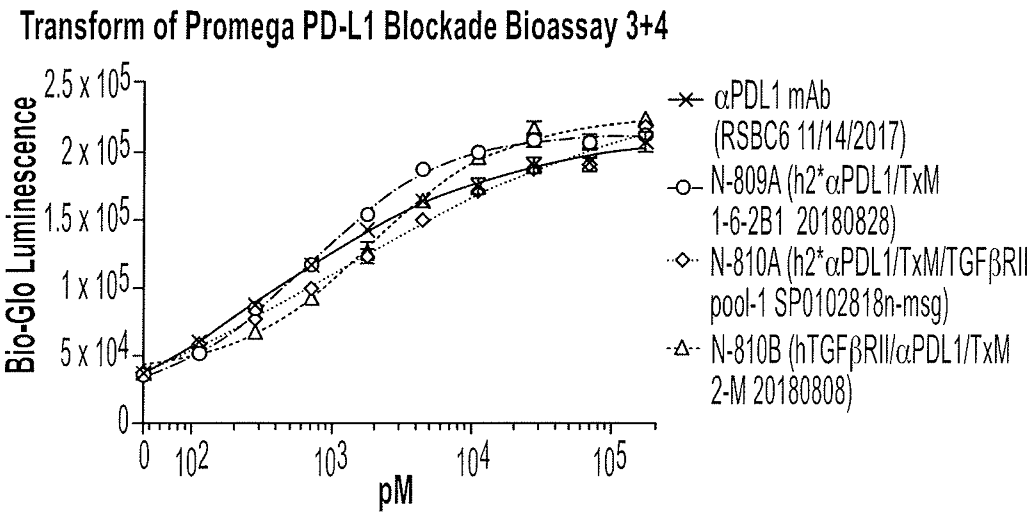


FIG. 25B

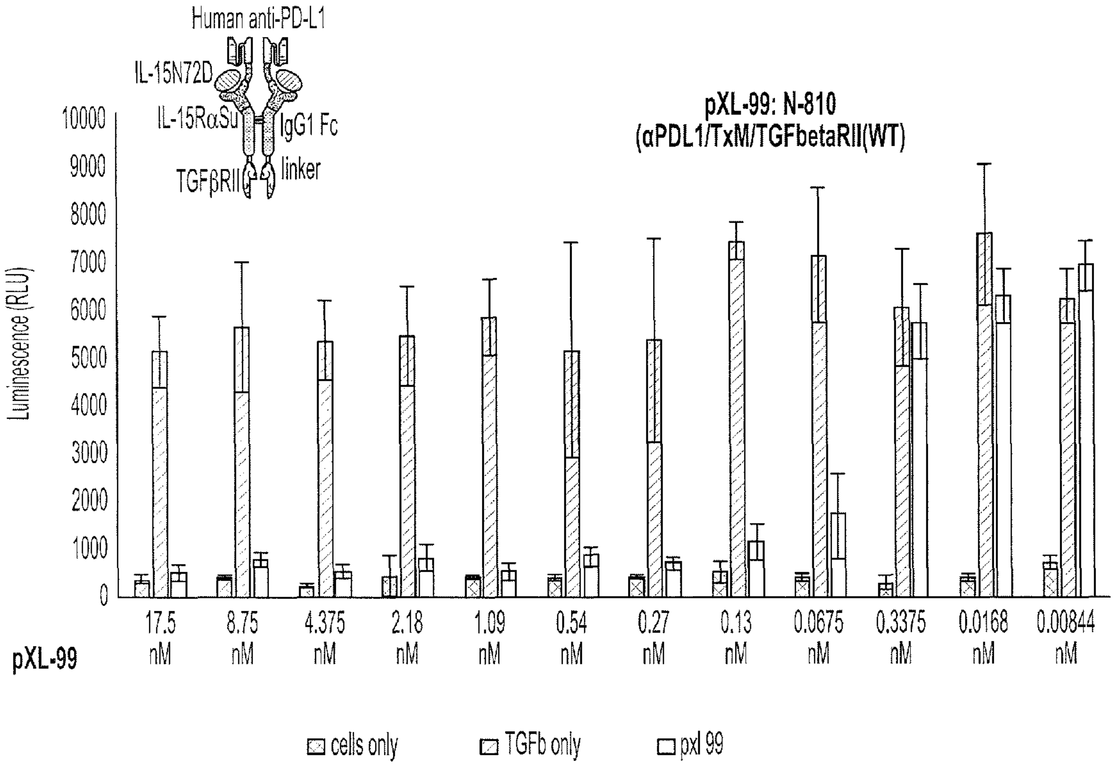

Human anti-PD-L1
IL-15N72D
IL-15RαSu
IgG1 Fc
TGFβRII
linker
pXL-99: N-810
(αPDL1/TxM/TGFbetaRII(WT)
Luminescence (RLU)
10000
9000
8000
7000
6000
5000
4000
3000
2000
1000
0
pXL-99
17.5 nM
8.75 nM
4.375 nM
2.18 nM
1.09 nM
0.54 nM
0.27 nM
0.13 nM
0.0675 nM
0.3375 nM
0.0168 nM
0.00844 nM
cells only
TGFb only
pxl 99

FIG. 26A

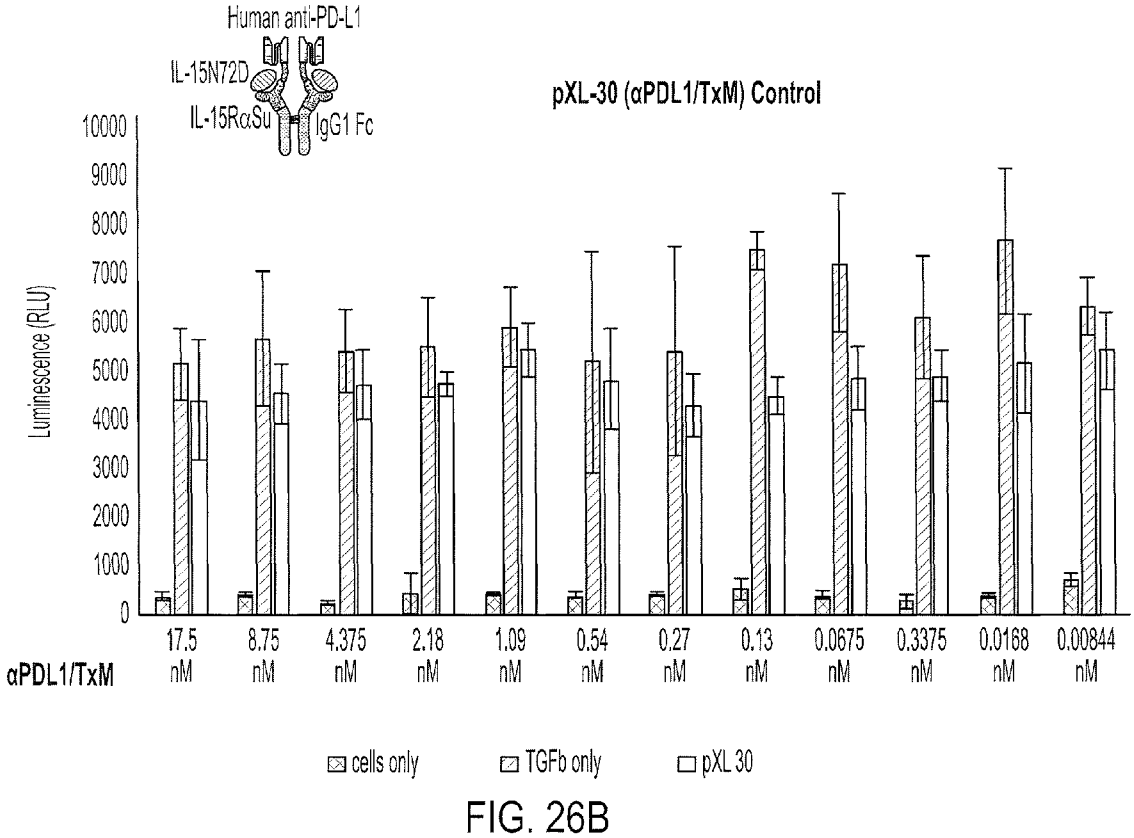

Human anti-PD-L1
IL-15N72D
IL-15RαSu
IgG1 Fc
pXL-30 (αPDL1/TxM) Control
Luminescence (RLU)
10000
9000
8000
7000
6000
5000
4000
3000
2000
1000
0
17.5 nM
8.75 nM
4.375 nM
2.18 nM
1.09 nM
0.54 nM
0.27 nM
0.13 nM
0.0675 nM
0.3375 nM
0.0168 nM
0.00844 nM
αPDL1/TxM
cells only
TGFb only
pXL 30

FIG. 26B

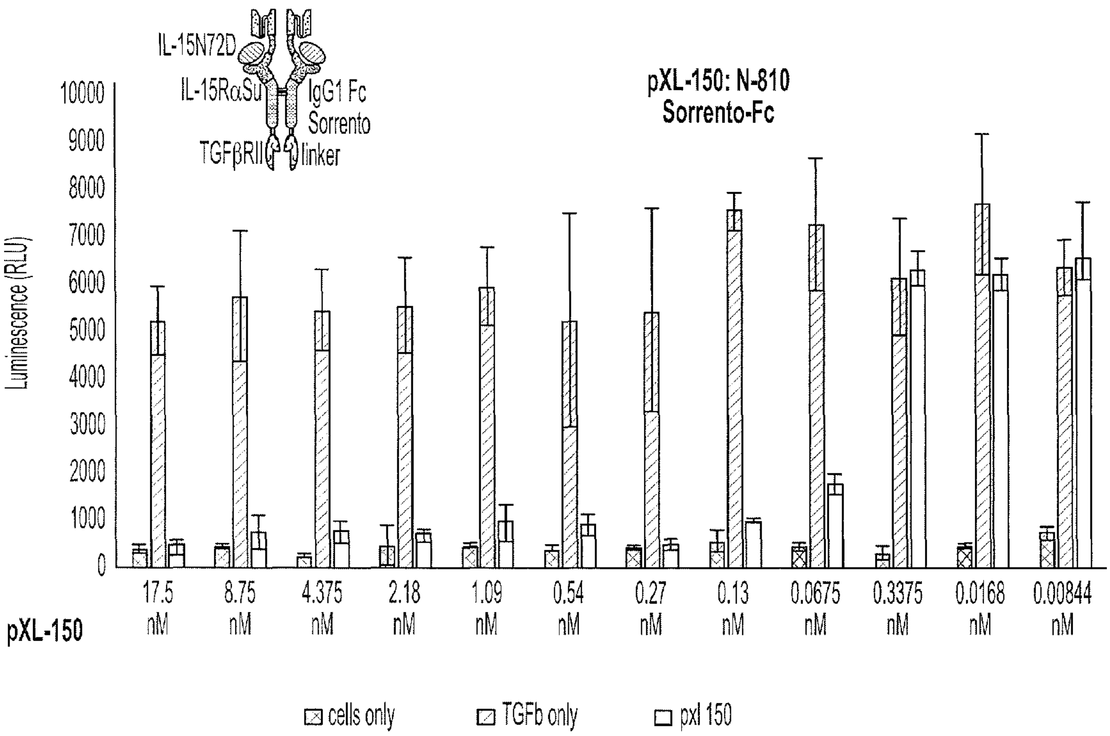

IL-15N72D
IL-15RαSu
IgG1 Fc
Sorrento
TGFβRII
linker
pXL-150: N-810
Sorrento-Fc
Luminescence (RLU)
10000
9000
8000
7000
6000
5000
4000
3000
2000
1000
0
17.5 nM
8.75 nM
4.375 nM
2.18 nM
1.09 nM
0.54 nM
0.27 nM
0.13 nM
0.0675 nM
0.3375 nM
0.0168 nM
0.00844 nM
pXL-150
cells only
TGFb only
pxl 150

FIG. 27A

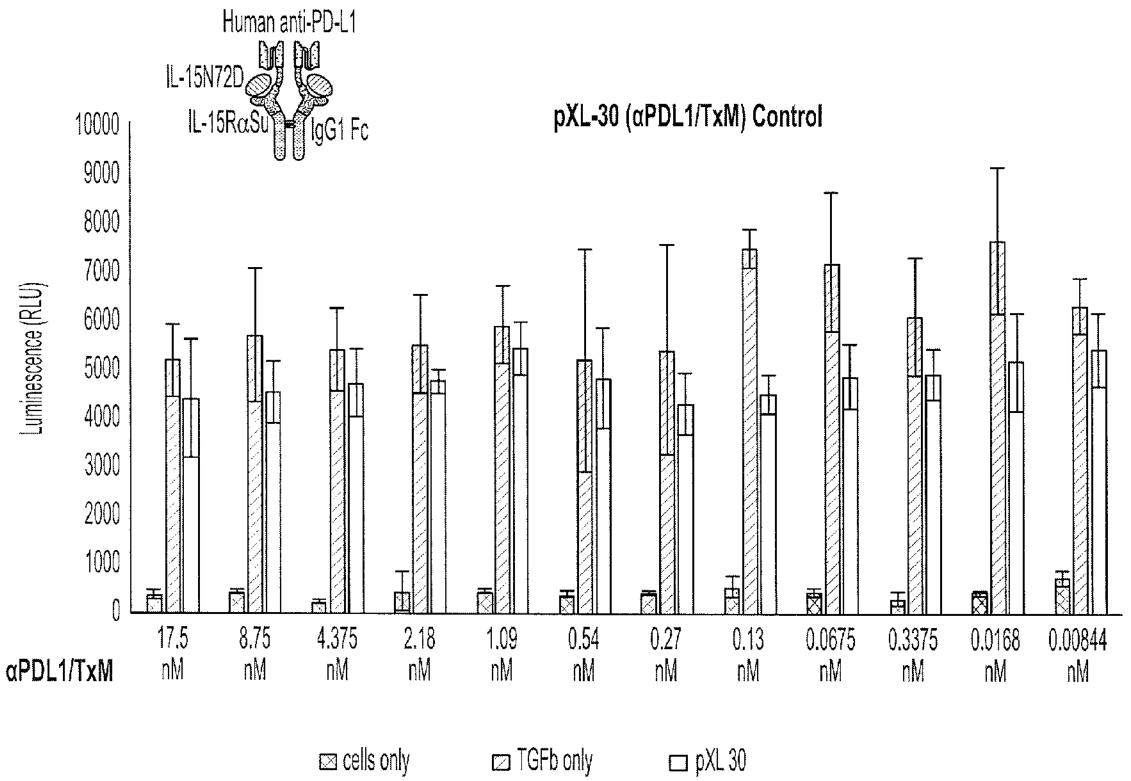

Human anti-PD-L1
IL-15N72D
IL-15RαSu
IgG1 Fc
pXL-30 (αPDL1/TxM) Control
Luminescence (RLU)
10000
9000
8000
7000
6000
5000
4000
3000
2000
1000
0
αPDL1/TxM
17.5 nM
8.75 nM
4.375 nM
2.18 nM
1.09 nM
0.54 nM
0.27 nM
0.13 nM
0.0675 nM
0.3375 nM
0.0168 nM
0.00844 nM
cells only
TGFb only
pXL 30

FIG. 27B

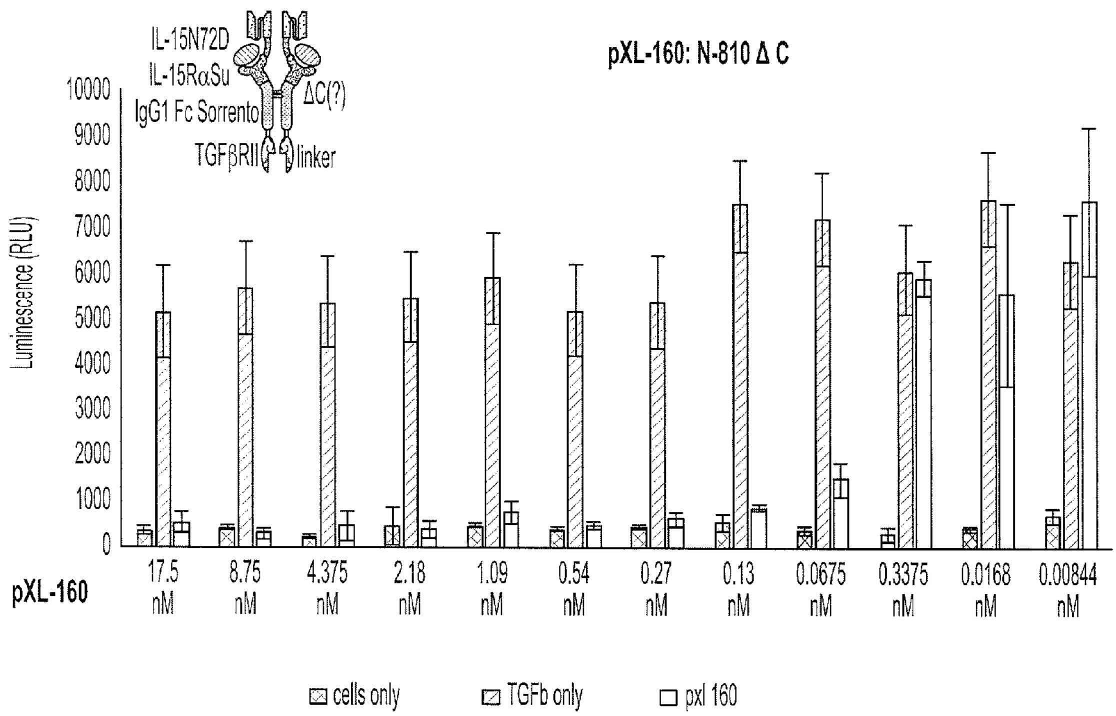

IL-15N72D
IL-15RαSu
IgG1 Fc Sorrento
TGFβRII
ΔC(?)
linker
pXL-160: N-810 Δ C
Luminescence (RLU)
10000
9000
8000
7000
6000
5000
4000
3000
2000
1000
0
pXL-160
17.5 nM
8.75 nM
4.375 nM
2.18 nM
1.09 nM
0.54 nM
0.27 nM
0.13 nM
0.0675 nM
0.3375 nM
0.0168 nM
0.00844 nM
cells only
TGFb only
pxl 160

FIG. 28A

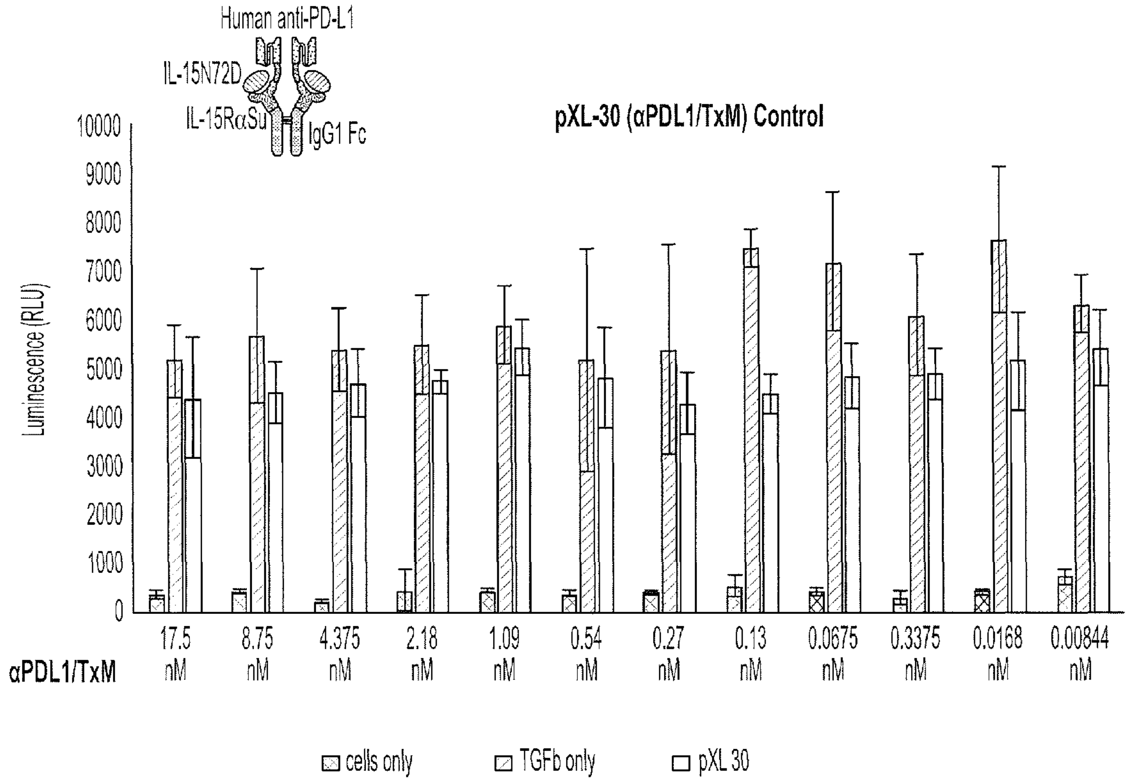

Human anti-PD-L1
IL-15N72D
IL-15RαSu
IgG1 Fc
pXL-30 (αPDL1/TxM) Control
Luminescence (RLU)
10000
9000
8000
7000
6000
5000
4000
3000
2000
1000
0
αPDL1/TxM
17.5 nM
8.75 nM
4.375 nM
2.18 nM
1.09 nM
0.54 nM
0.27 nM
0.13 nM
0.0675 nM
0.3375 nM
0.0168 nM
0.00844 nM
cells only
TGFb only
pXL 30

FIG. 28B

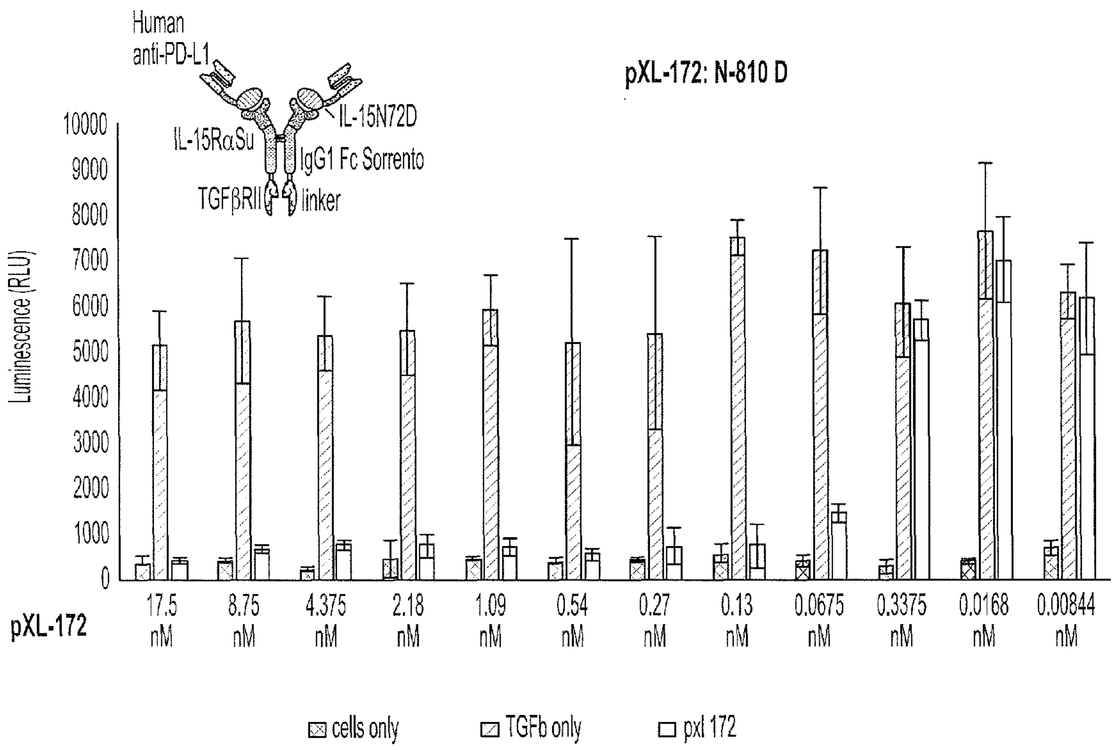

Human
anti-PD-L1
IL-15N72D
IL-15RαSu
IgG1 Fc Sorrento
TGFβRII
linker
pXL-172: N-810 D
Luminescence (RLU)
10000
9000
8000
7000
6000
5000
4000
3000
2000
1000
0
pXL-172
17.5 nM
8.75 nM
4.375 nM
2.18 nM
1.09 nM
0.54 nM
0.27 nM
0.13 nM
0.0675 nM
0.3375 nM
0.0168 nM
0.00844 nM
cells only
TGFb only
pxl 172

FIG. 29A

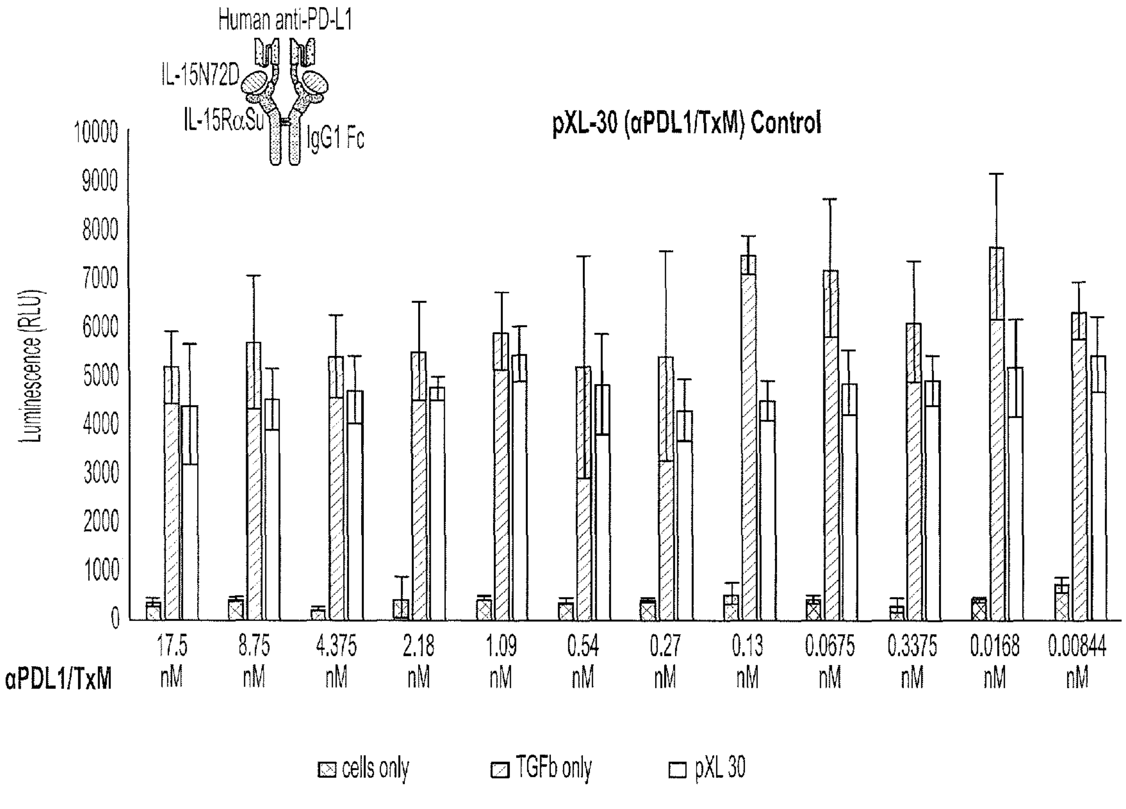

Human anti-PD-L1
IL-15N72D
IL-15RαSu
IgG1 Fc
pXL-30 (αPDL1/TxM) Control
Luminescence (RLU)
10000
9000
8000
7000
6000
5000
4000
3000
2000
1000
0
αPDL1/TxM
17.5 nM
8.75 nM
4.375 nM
2.18 nM
1.09 nM
0.54 nM
0.27 nM
0.13 nM
0.0675 nM
0.3375 nM
0.0168 nM
0.00844 nM
cells only
TGFb only
pXL 30

FIG. 29B

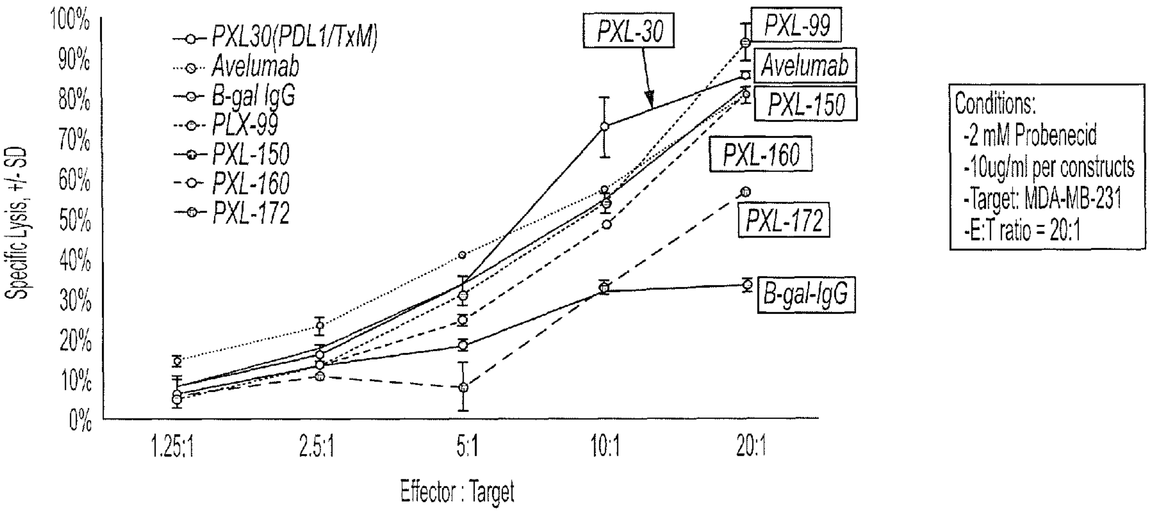

100%
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
Specific Lysis, +/- SD
PXL30(PDL1/TxM)
Avelumab
B-gal IgG
PLX-99
PXL-150
PXL-160
PXL-172
PXL-30
PXL-99
Avelumab
PXL-150
PXL-160
PXL-172
B-gal-IgG
1.25:1
2.5:1
5:1
10:1
20:1
Effector : Target
Conditions:
-2 mM Probenecid
-10ug/ml per constructs
-Target: MDA-MB-231
-E:T ratio = 20:1

FIG. 30

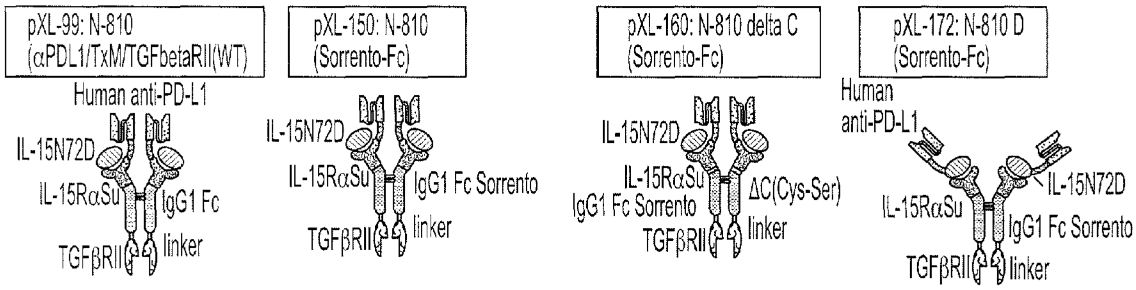


FIG. 30 CONTINUED

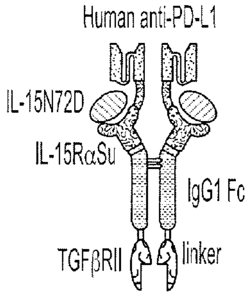


FIG. 31A

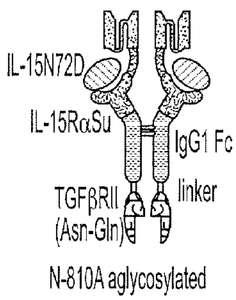


FIG. 31B

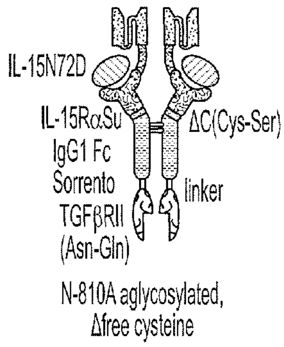
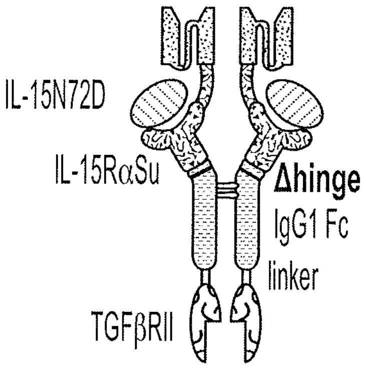
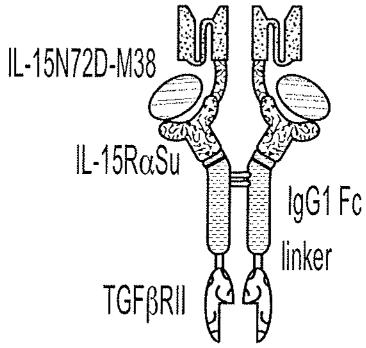


FIG. 31C



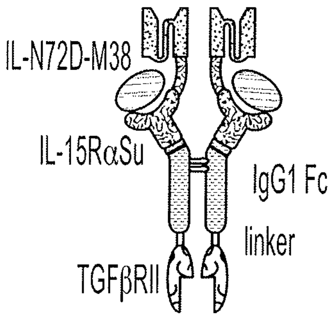
N-810A Δhinge

FIG. 31D



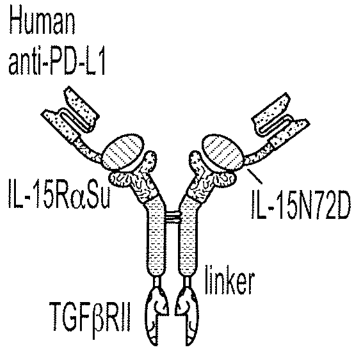
N-810A (IL15-K41Q, L45S,I67T,N79Y,E93A)
-Mutations in IL15 to enhance solubility and expression

FIG. 31E



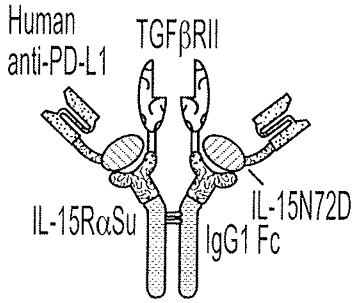
N-810A (IL15-L45S)
-Mutations in IL15 to enhance solubility and expression

FIG. 31F



N-810 D

FIG. 31G

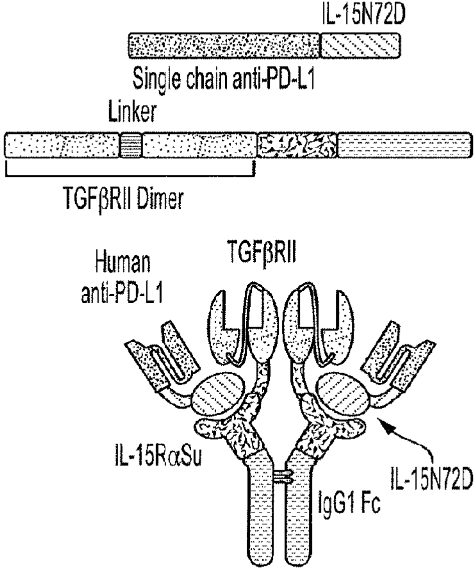


N-810 E

FIG. 31H

Protein	Post-harvest Titer (ug/mL)	Total Yield (mg)	High Molecular Weight % Post Pro-A
N-810A	55.9		20.4
N-810 (IL15-K41Q, L45S, I67T,N79Y,E93A)	156.3	6.7	18.1
N810A (IL15-L45S)	151.3	6.6	16.5
N810D	117.7		8.8

FIG. 32


IL-15N72D
Single chain anti-PD-L1
Linker
TGFβRII Dimer
Human
anti-PD-L1
TGFβRII
IL-15RαSu
IL-15N72D
IgG1 Fc