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(54) **SARS-COV-2 ANTIBODIES AND USES THEREOF**

(71) Applicant: **Icahn School of Medicine at Mount Sinai**, New York, NY (US)

(72) Inventors: **Thomas Moran**, New York, NY (US); **Thomas Kraus**, New York, NY (US); **Domenico Tortorella**, New York, NY (US); **J. Andrew Duty**, New York, NY (US)

(73) Assignee: **Icahn School of Medicine at Mount Sinai**, New York, NY (US)

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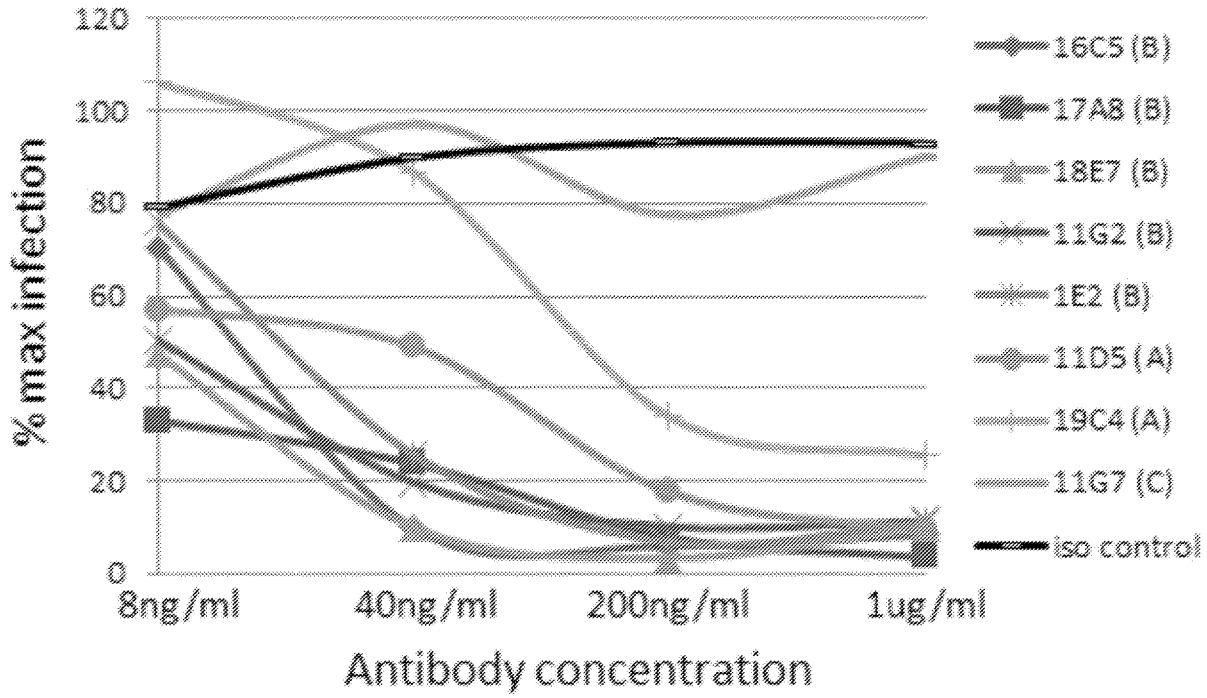
(57) **ABSTRACT**

Provided herein are antibodies that bind to SARS-CoV-2 spike protein or a fragment thereof (e.g., receptor binding domain (RBD)), host cells for producing such antibodies, and kits comprising such antibodies. Also provided herein are compositions comprising antibodies that bind to SARS-CoV-2 spike protein or a fragment thereof (e.g., receptor binding domain) and methods of using such antibodies to diagnose, prevent or treat a SARS-CoV-2 infection, or COVID-19.

Specification includes a Sequence Listing.



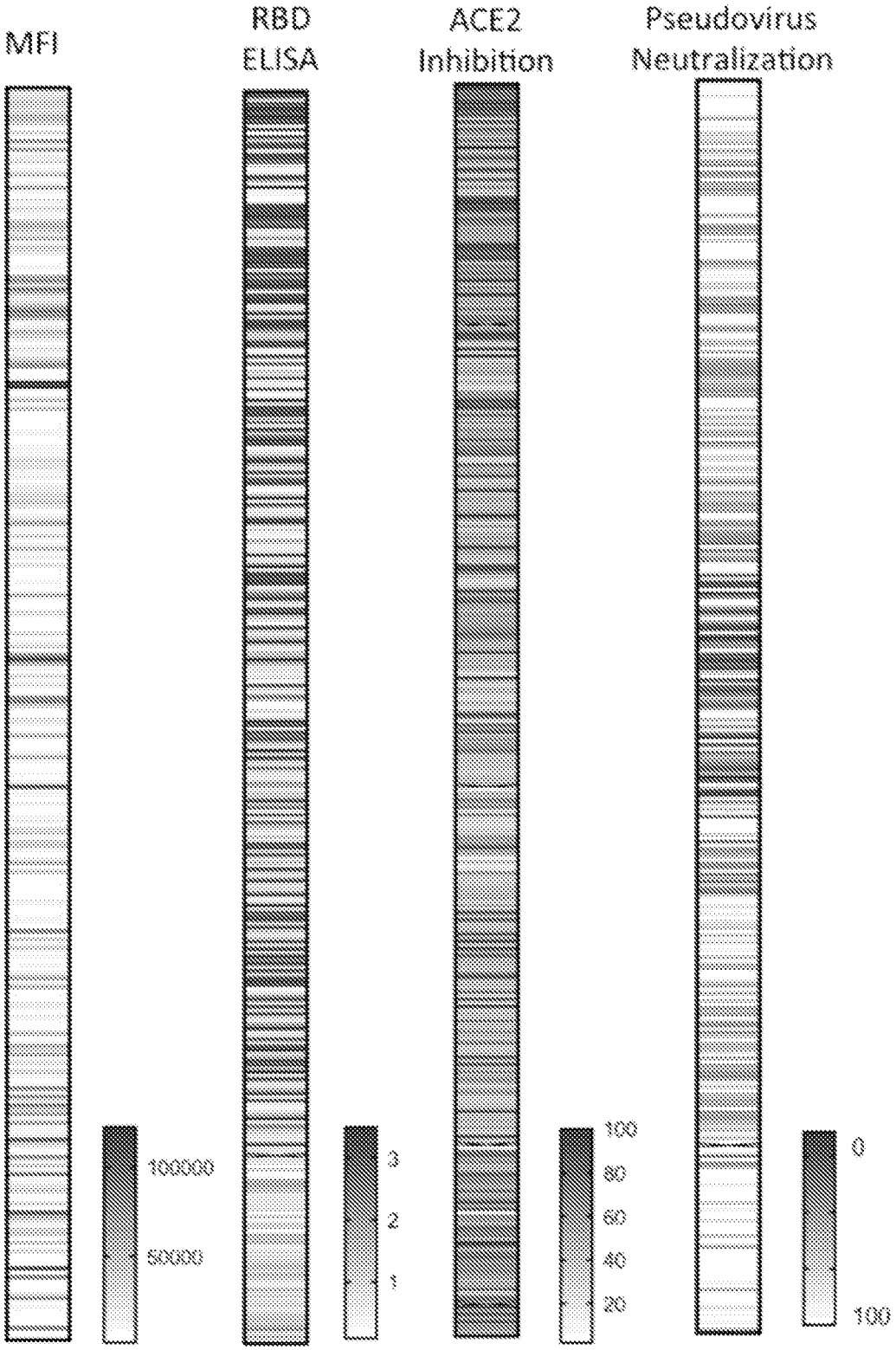

MFI
100000
50000
RBD ELISA
3
2
1
ACE2 Inhibition
100
80
60
40
20
Pseudovirus Neutralization
0
100

Fig. 1

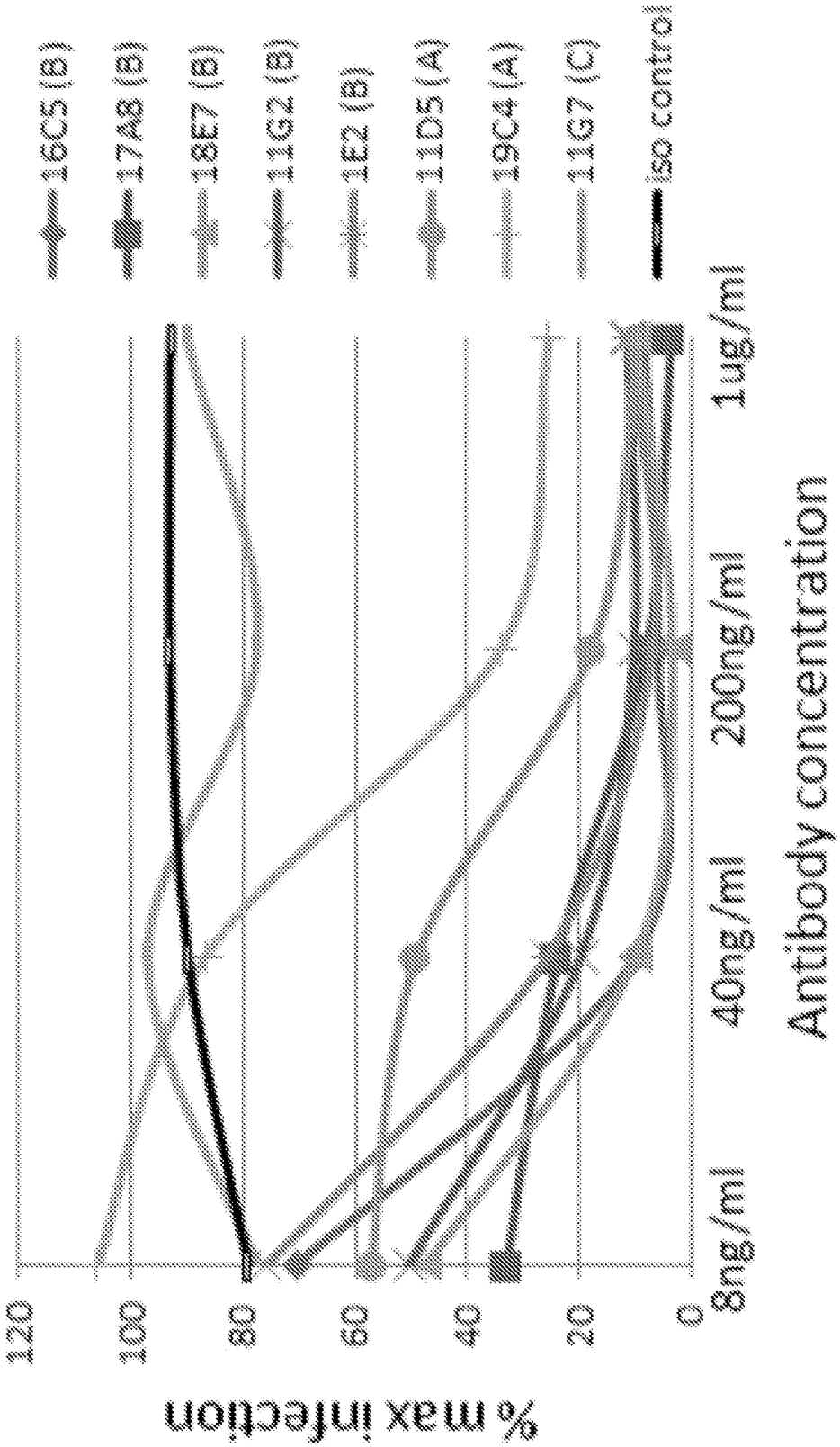

16C5 (B)
17A8 (B)
18E7 (B)
11G2 (B)
1E2 (B)
11D5 (A)
19C4 (A)
11G7 (C)
iso control
% max infection
120
100
80
60
40
20
0
8ng/ml
40ng/ml
200ng/ml
1ug/ml
Antibody concentration

Fig. 2

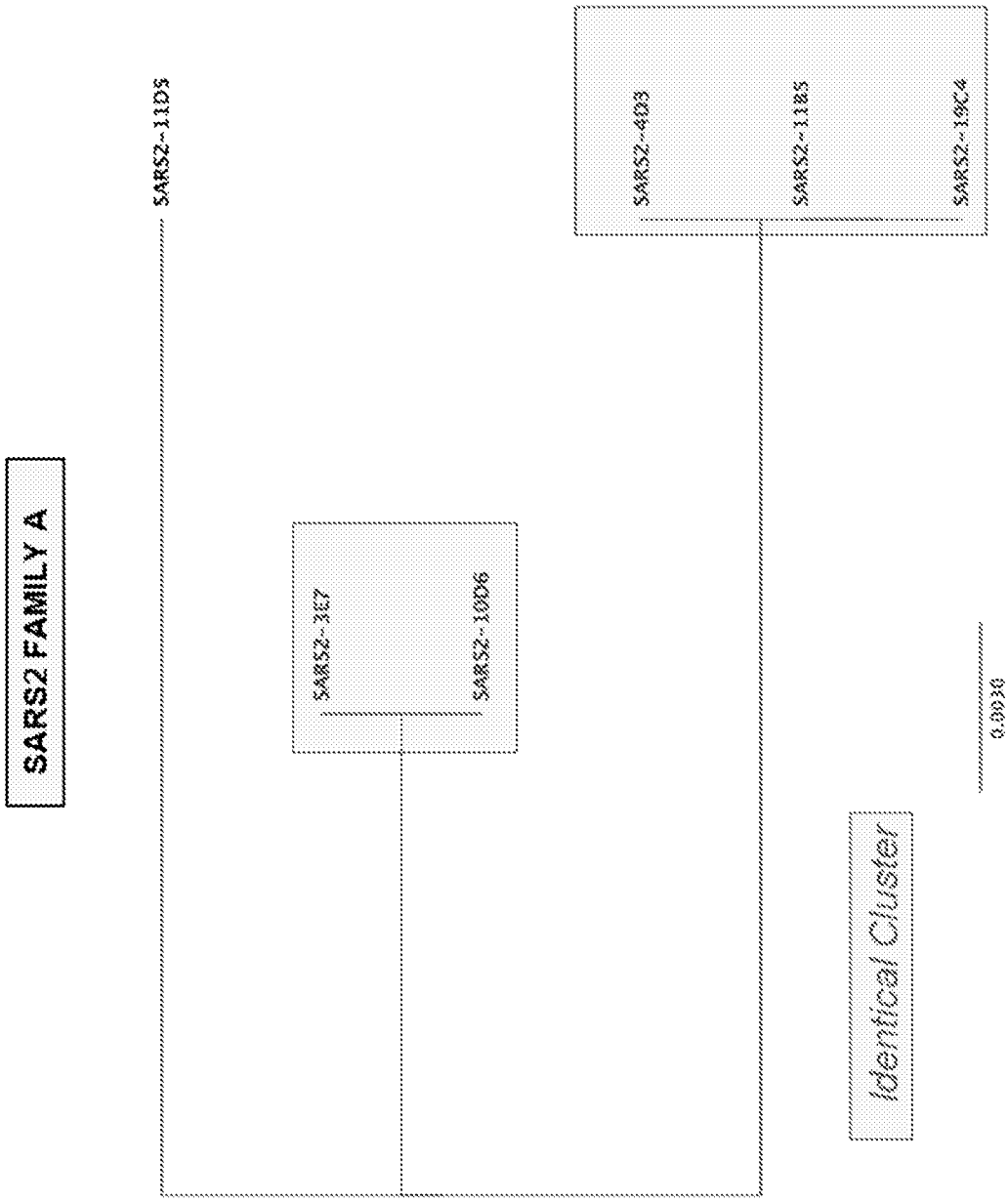
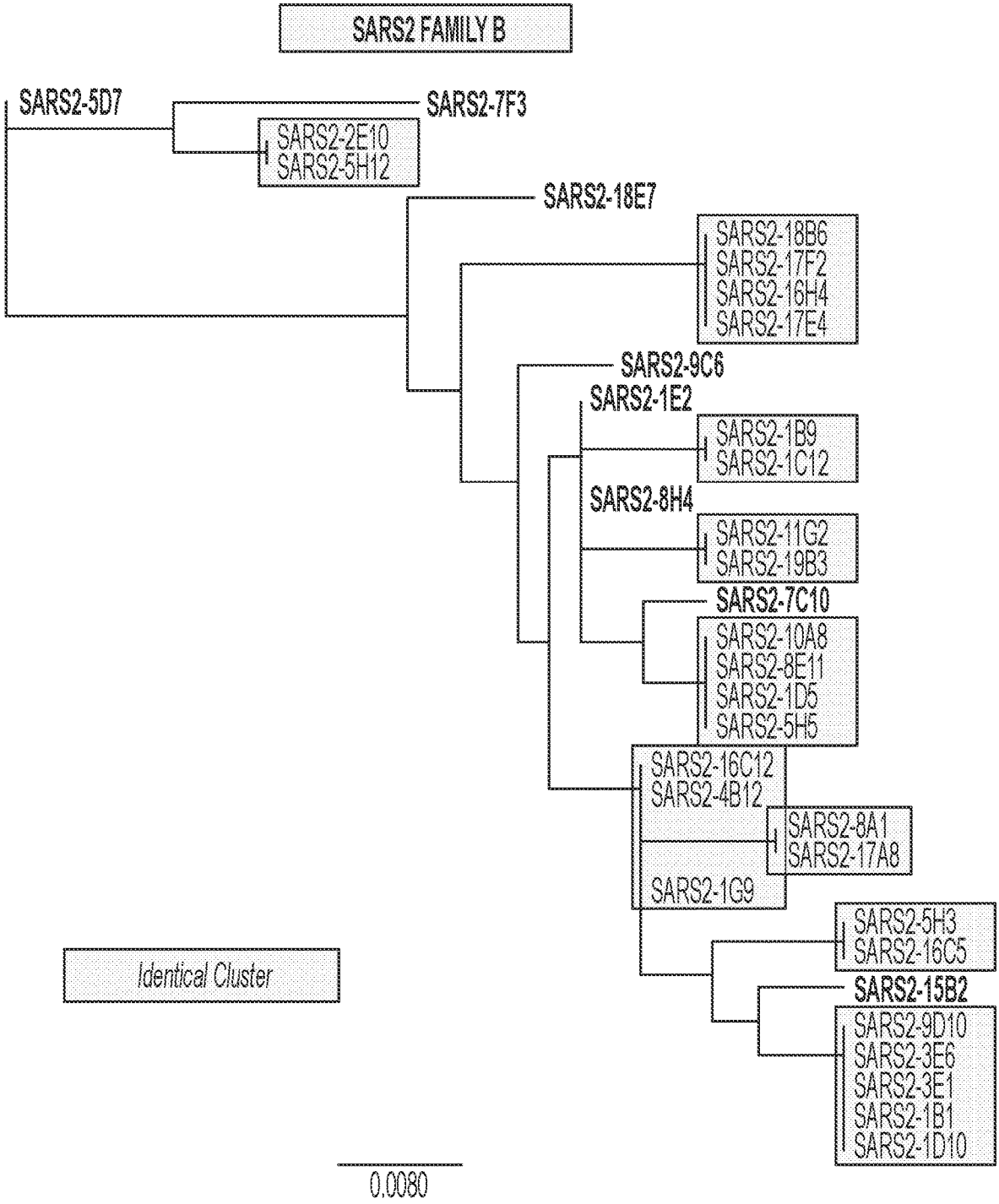

SARS2 FAMILY A
SARS2-1105
SARS2-403
SARS2-1185
SARS2-1064
SARS2-307
SARS2-1006
Identical Cluster
0.0038

Fig. 3A


SARS2 FAMILY B
SARS2-5D7
SARS2-7F3
SARS2-2E10
SARS2-5H12
SARS2-18E7
SARS2-18B6
SARS2-17F2
SARS2-16H4
SARS2-17E4
SARS2-9C6
SARS2-1E2
SARS2-1B9
SARS2-1C12
SARS2-8H4
SARS2-11G2
SARS2-19B3
SARS2-7C10
SARS2-10A8
SARS2-8E11
SARS2-1D5
SARS2-5H5
SARS2-16C12
SARS2-4B12
SARS2-8A1
SARS2-17A8
SARS2-1G9
SARS2-5H3
SARS2-16C5
SARS2-15B2
SARS2-9D10
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SARS2-3E1
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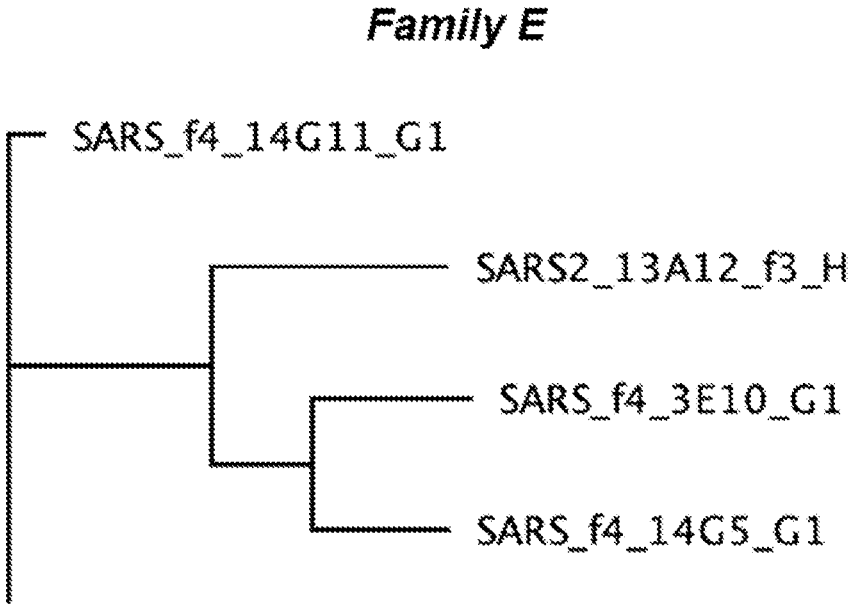
SARS2-1D10
Identical Cluster
0.0080

Fig. 3B



Single Member Families

Family C - 11G7 (f2)
Family D - 2C1 (f4)
Family F - 7D2 (f4)
Family H - 2G6 (f4)
Family I - 5B6 (f3)

Fig. 3C

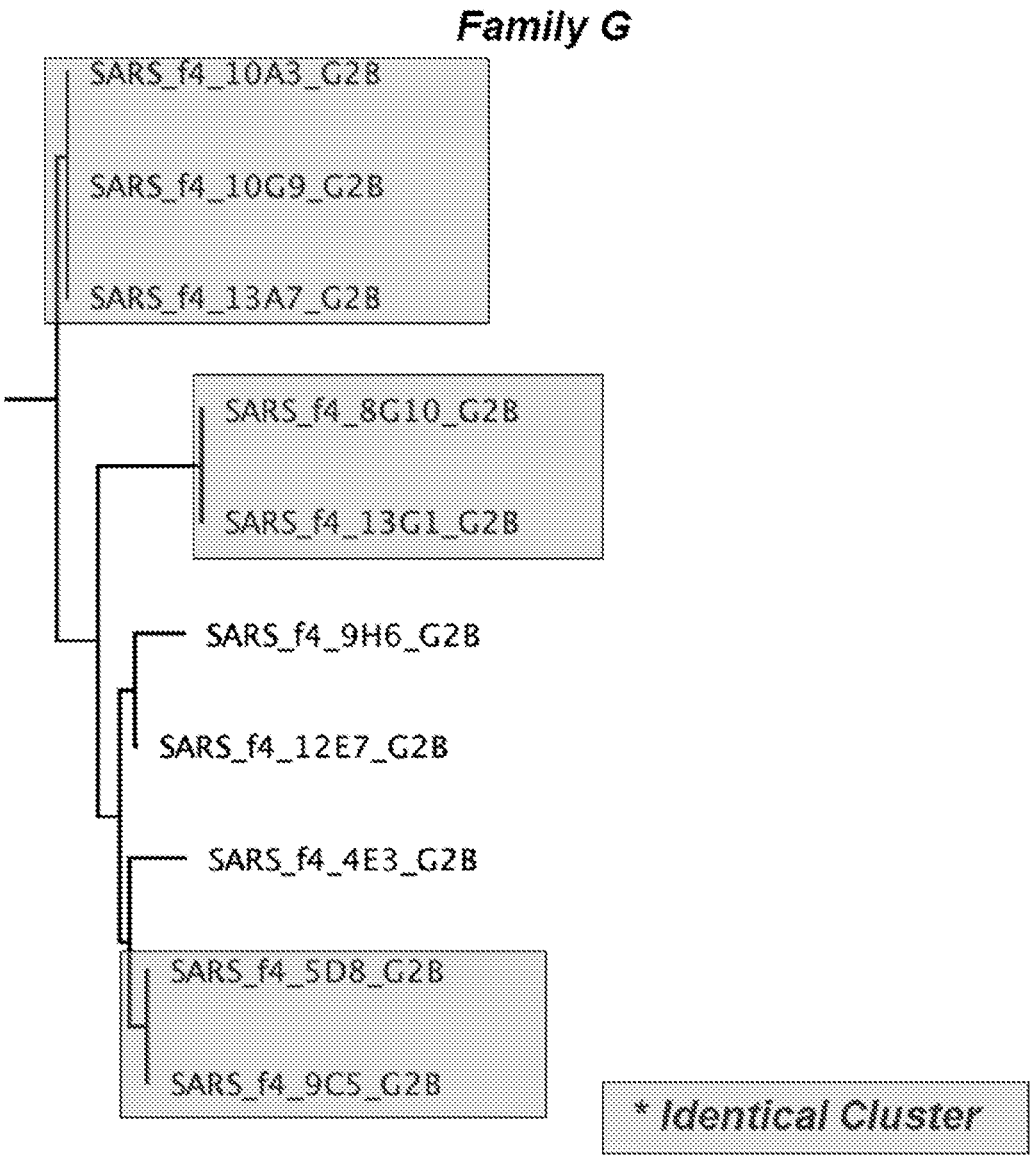

Family G
SARS_f4_10A3_G2B
SARS_f4_10G9_G2B
SARS_f4_13A7_G2B
SARS_f4_8G10_G2B
SARS_f4_13G1_G2B
SARS_f4_9H6_G2B
SARS_f4_12E7_G2B
SARS_f4_4E3_G2B
SARS_f4_5D8_G2B
SARS_f4_9C5_G2B
* Identical Cluster

Fig. 3D

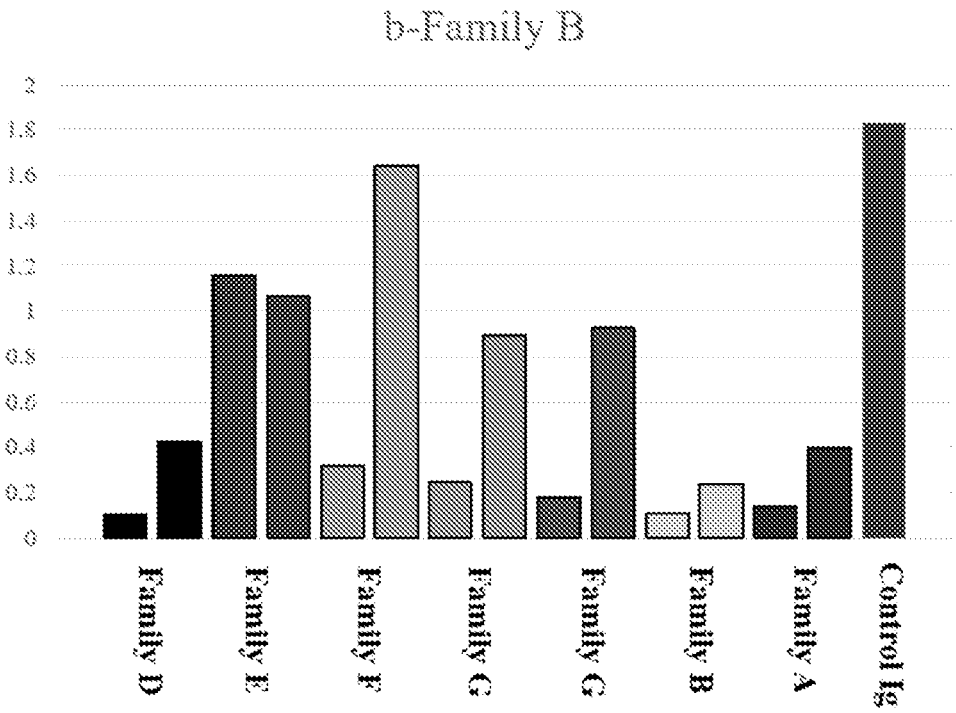

b-Family B
2
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
Family D
Family E
Family F
Family G
Family G
Family B
Family A
Control Ig

Fig. 4A

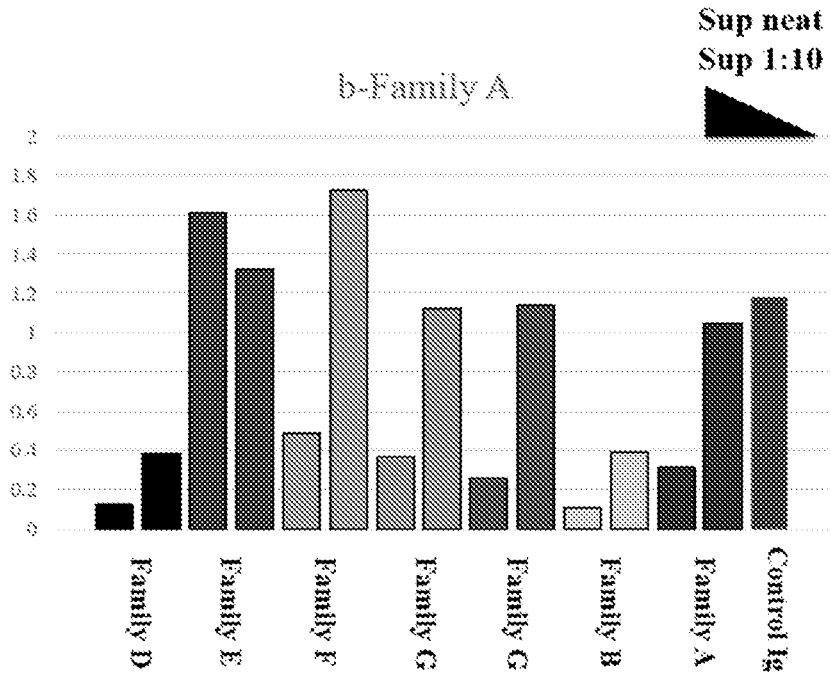

Sup neat
Sup 1:10
b-Family A
2
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
Family D
Family E
Family F
Family G
Family G
Family B
Family A
Control Ig

Fig. 4B

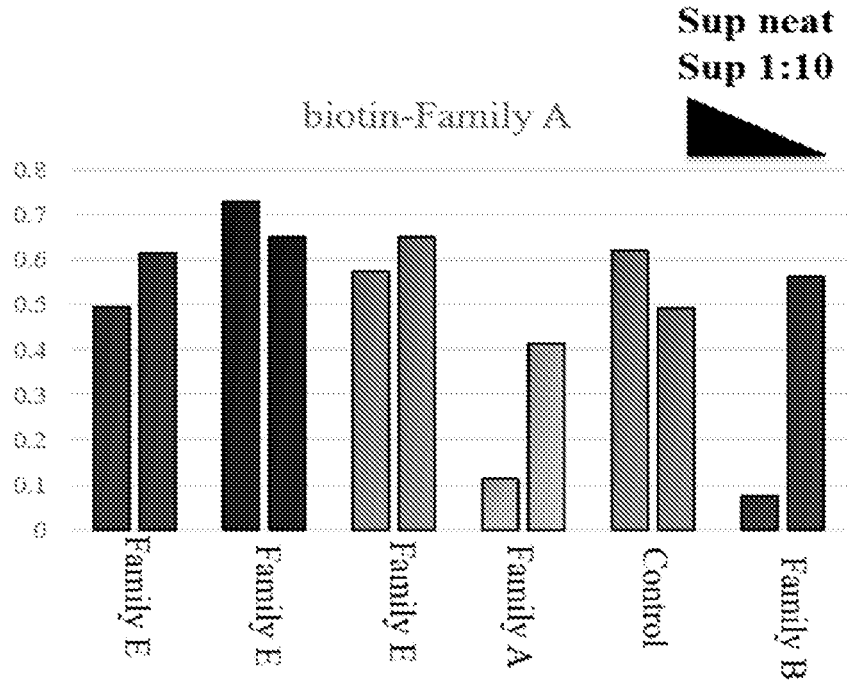

Sup neat
Sup 1:10
biotin-Family A
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
Family E
Family E
Family E
Family A
Control
Family B

Fig. 4C

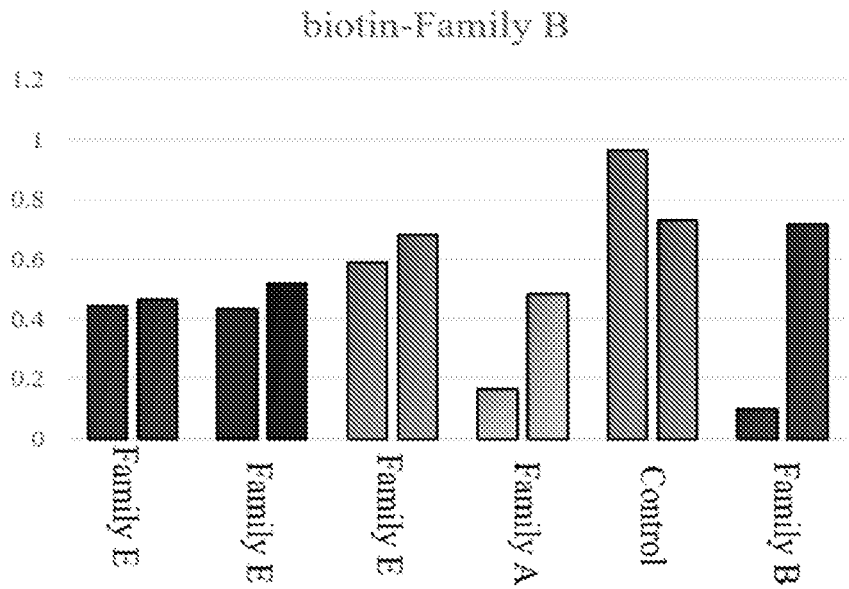

biotin-Family B
1.2
1
0.8
0.6
0.4
0.2
0
Family E
Family E
Family E
Family A
Control
Family B

Fig. 4D

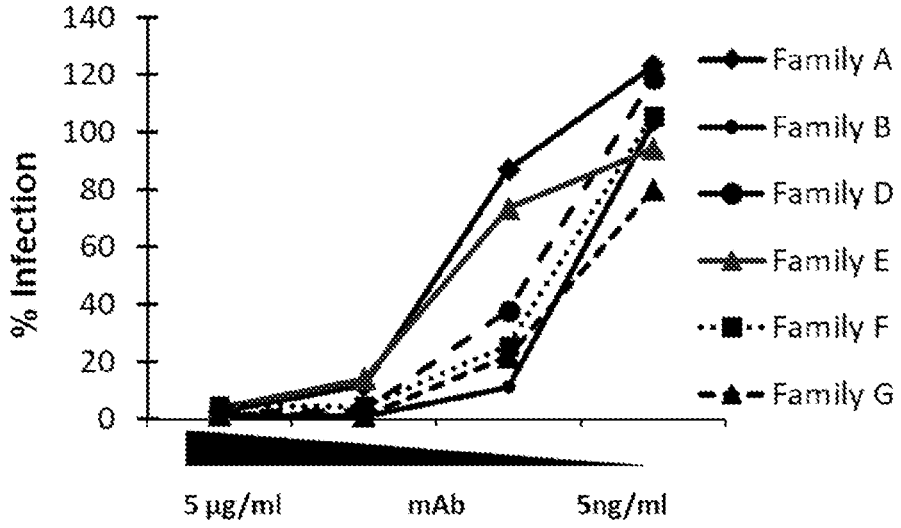

140
120
100
80
60
40
20
0
% Infection
Family A
Family B
Family D
Family E
Family F
Family G
5 µg/ml
mAb
5ng/ml

Fig. 5A

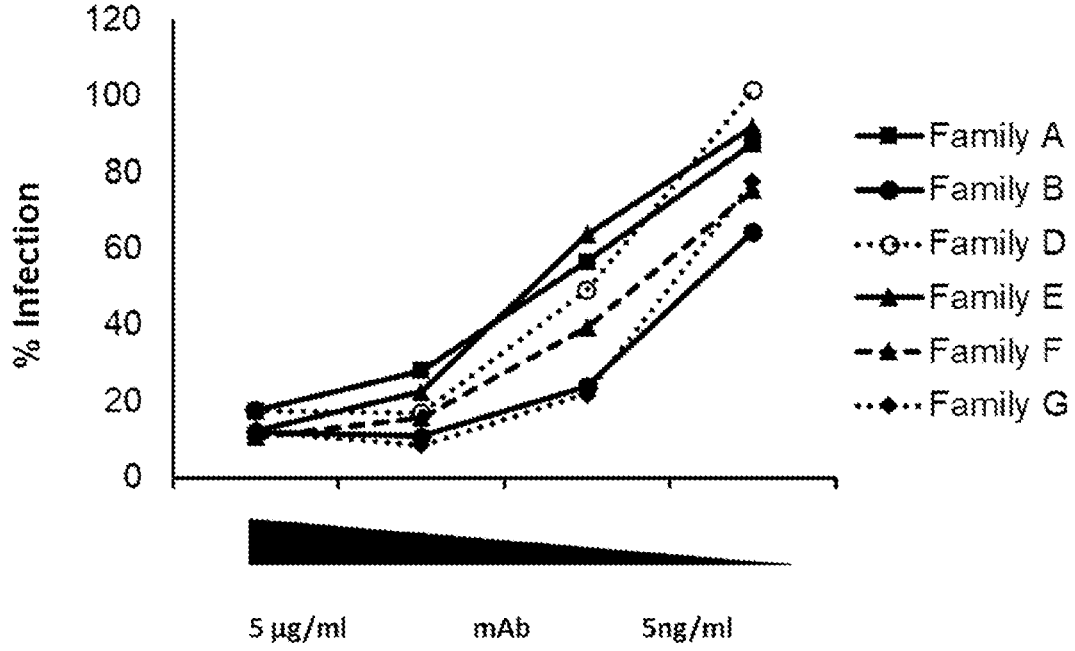

120
100
80
60
40
20
0
% Infection
Family A
Family B
Family D
Family E
Family F
Family G
5 µg/ml
mAb
5ng/ml

Fig. 5B

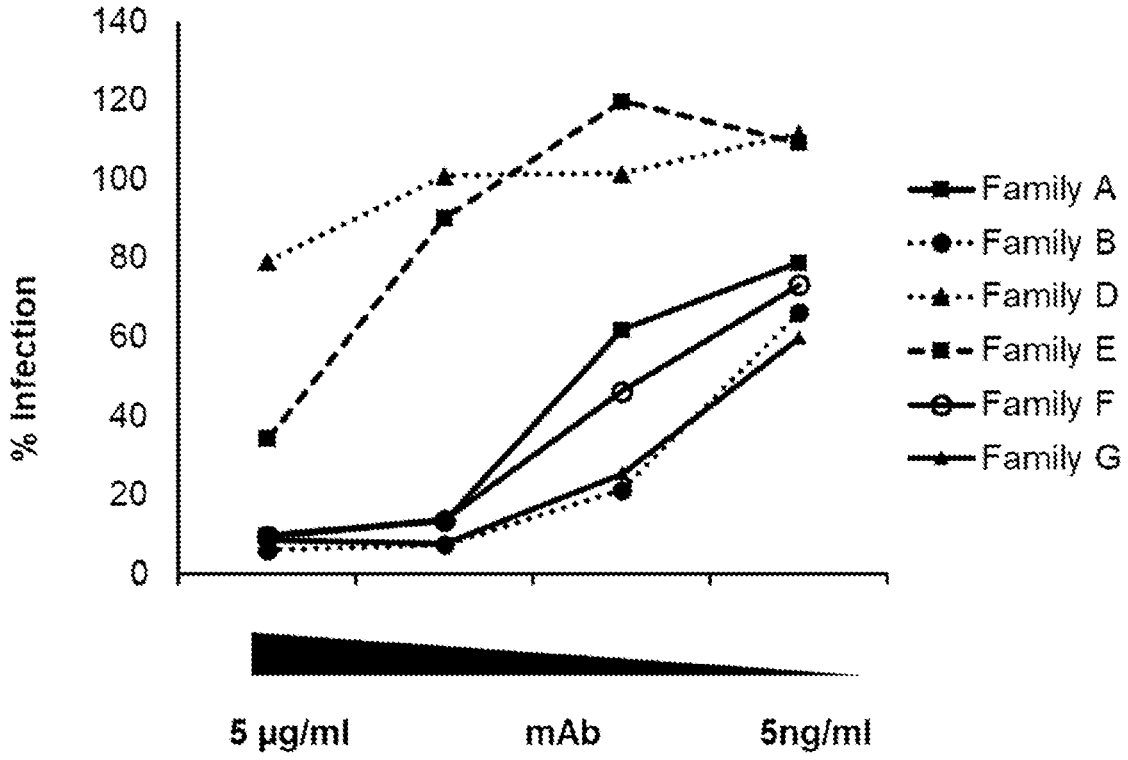

140
120
100
80
60
40
20
0
% Infection
Family A
Family B
Family D
Family E
Family F
Family G
5 µg/ml
mAb
5ng/ml

Fig. 5C

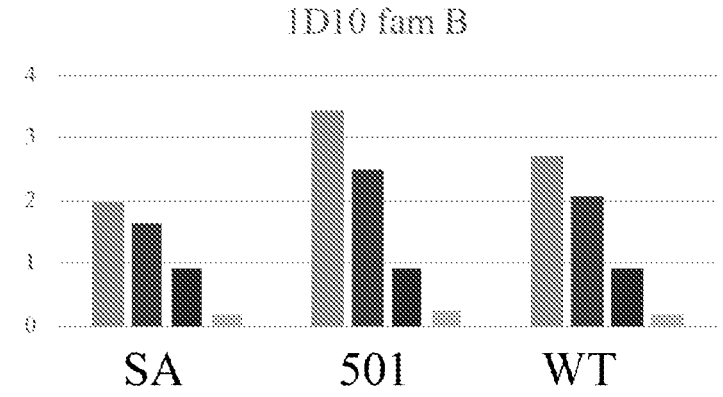


Fig. 6A

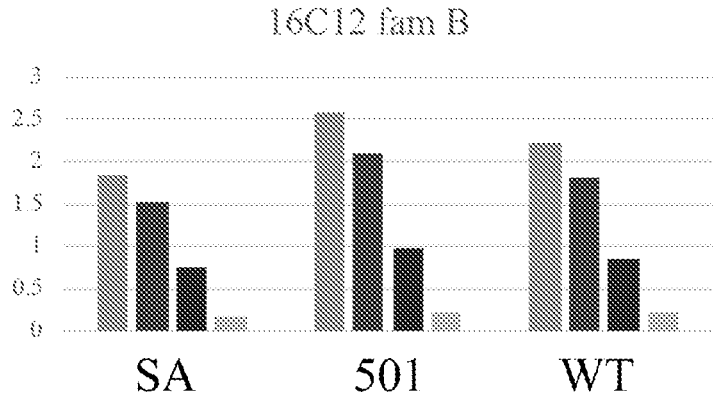


Fig. 6B

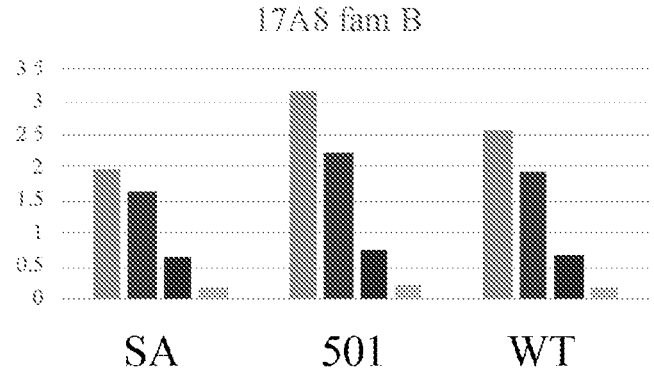


Fig. 6C

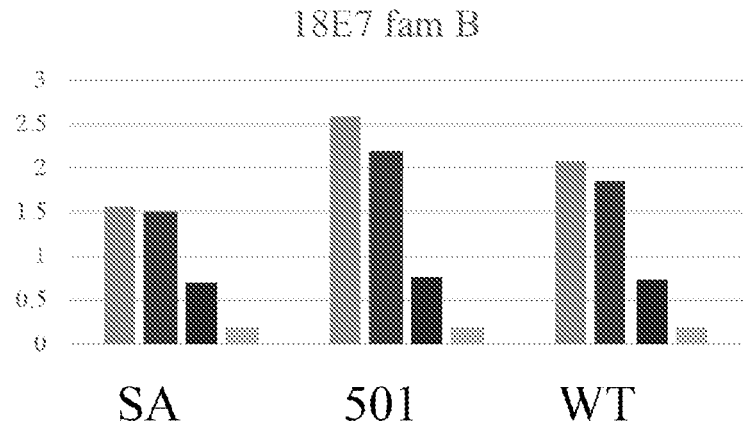


Fig. 6D

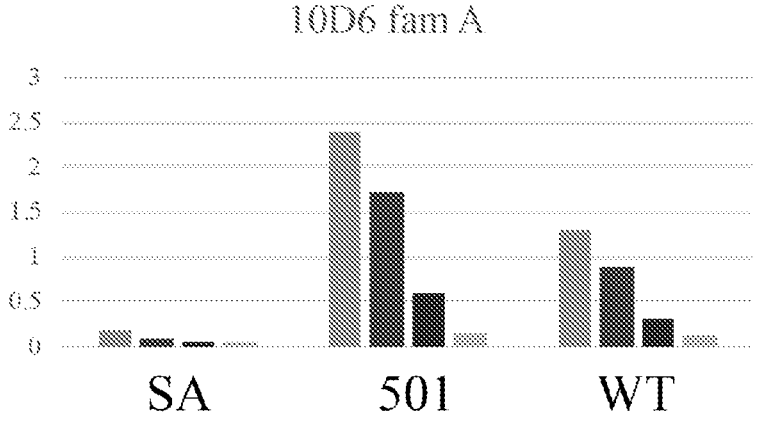


Fig. 6E

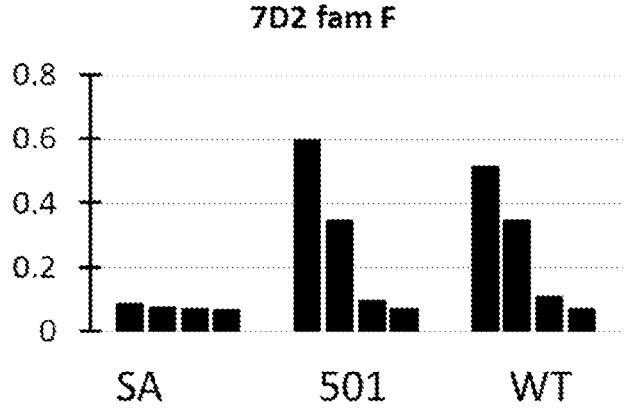


Fig. 6F

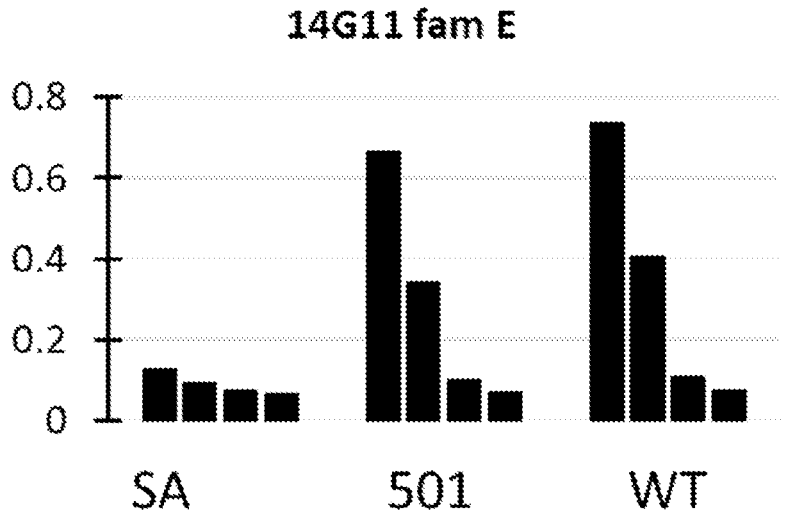


Fig. 6G

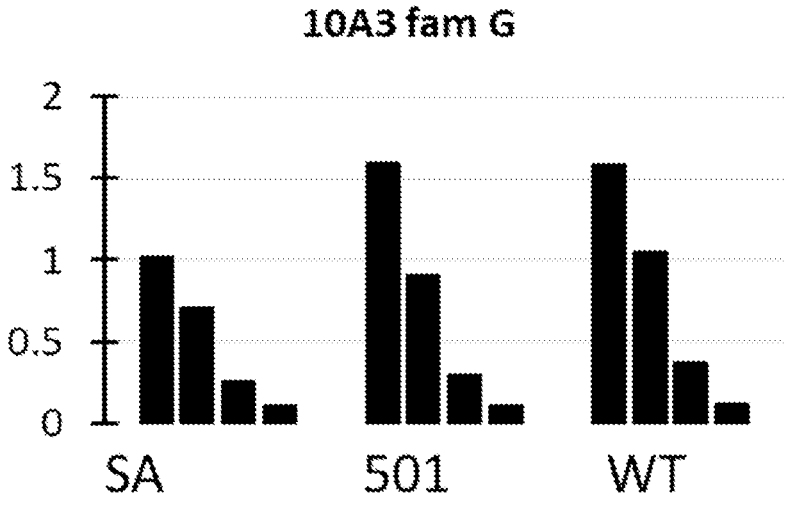


Fig. 6H

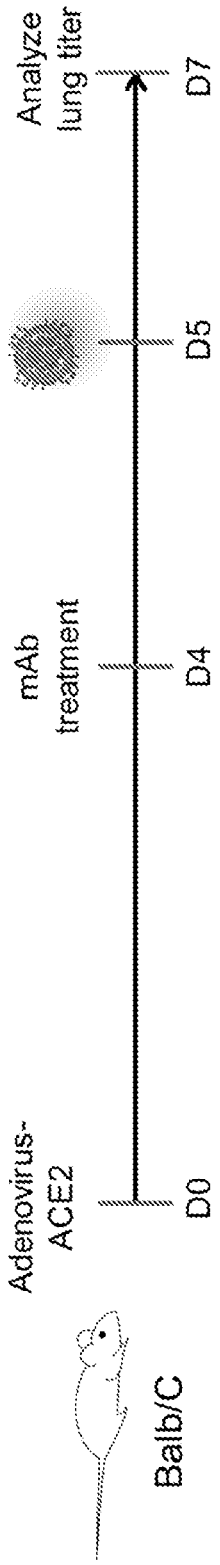

Balb/C
Adenovirus-ACE2
D0
mAb treatment
D4
D5
Analyze lung titer
D7

Fig. 7A

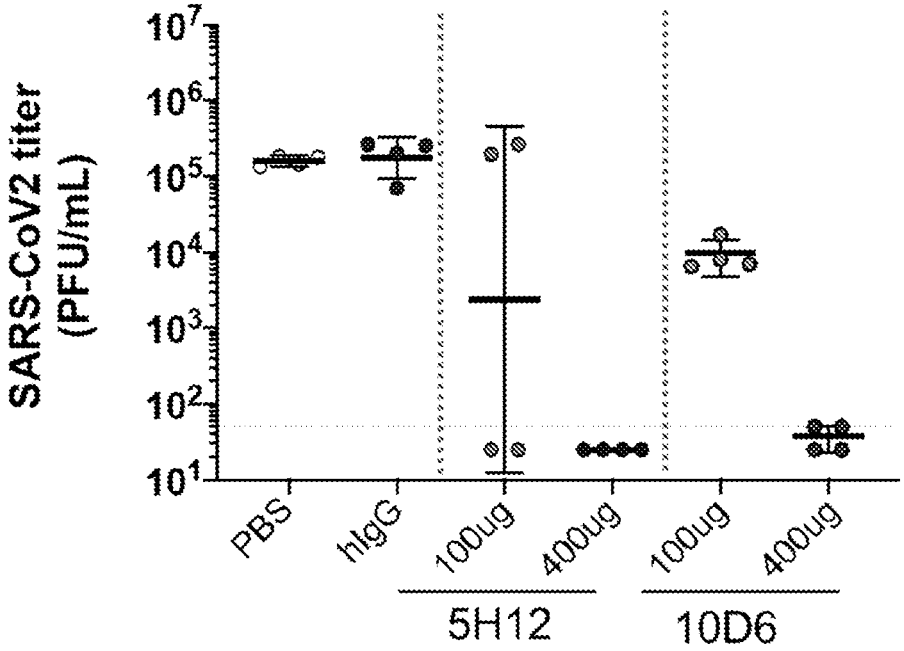

SARS-CoV2 titer
(PFU/mL)
10^7
10^6
10^5
10^4
10^3
10^2
10^1
PBS
hIgG
100ug
400ug
100ug
400ug
5H12
10D6

Fig. 7B

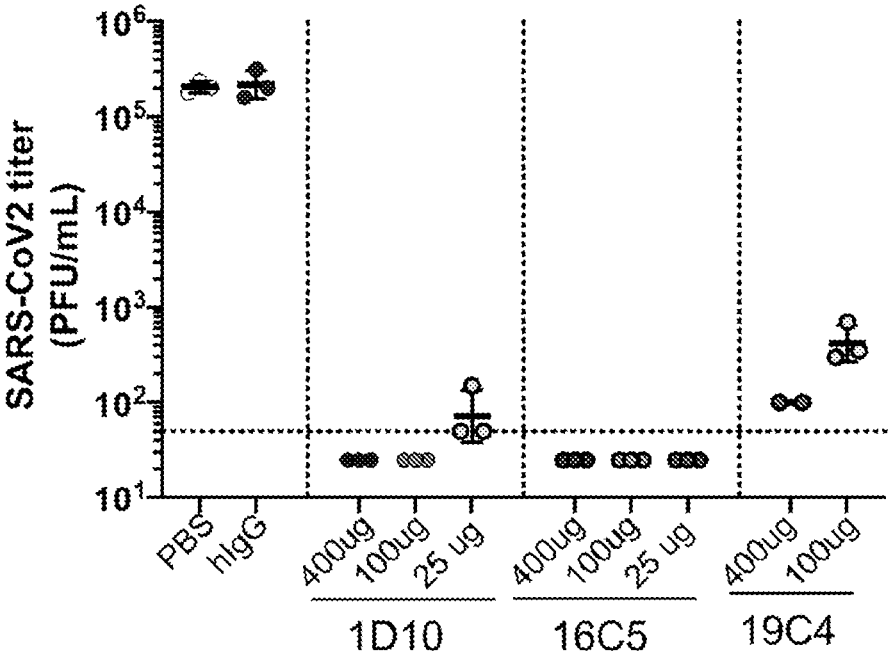

SARS-CoV2 titer
(PFU/mL)
10^6
10^5
10^4
10^3
10^2
10^1
PBS
hIgG
400ug
100ug
25 ug
400ug
100ug
25 ug
400ug
100ug
1D10
16C5
19C4

Fig. 7C

SARS-COV-2 ANTIBODIES AND USES THEREOF

1. CROSS REFERENCE TO RELATED APPLICATION

[0001] This application claims priority under 35 U.S.C. § 119(e) to U.S. Provisional Patent Application No. 63/105,190, filed Oct. 23, 2020 and U.S. Provisional Application No. 63/151,570 filed Feb. 19, 2021, the disclosures of which are incorporated herein by reference in their entireties.

2. SEQUENCE LISTING

[0002] The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on Oct. 22, 2021, is named 084284_00238_SL.txt and is 194,120 bytes in size.

3. BACKGROUND

[0003] Coronavirus disease 2019 (COVID-19) is a contagious disease caused by severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2). The disease has spread world-wide, with symptoms ranging from mild to severe illness. There is an urgent need to develop therapeutics to treat COVID-19 and diagnostics to detect SARS-CoV-2).

4. SUMMARY

[0004] In one aspect, provided herein is an antibody that binds to the spike protein of severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) or a fragment thereof (e.g., receptor binding domain (RBD)) and compositions comprising such an antibody. In one embodiment, an antibody described herein comprises the amino acid sequences of the variable heavy chain region and variable light chain region of antibody 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 or 26 (see Tables 1 and 2).

[0005] In one embodiment, an antibody provided herein comprises the amino acid sequences of the variable heavy chain region (Table 1) and the variable light chain region (Table 2) of the antibody SARS2-1C12_f3. In another embodiment, an antibody provided herein comprises the amino acid sequences of the variable heavy chain region (Table 1) and the variable light chain region (Table 2) of the antibody SARS2-1D5_f3. In one embodiment, an antibody provided herein comprises the amino acid sequences of the variable heavy chain region (Table 1) and the variable light chain region (Table 2) of the antibody SARS2-1D10_f3. In one embodiment, an antibody provided herein comprises the amino acid sequences of the variable heavy chain region (Table 1) and the variable light chain region (Table 2) of the antibody SARS2-1E2_f3. In one embodiment, an antibody provided herein comprises the amino acid sequences of the variable heavy chain region (Table 1) and the variable light chain region (Table 2) of the antibody SARS2-1G9_f3. In one embodiment, an antibody provided herein comprises the amino acid sequences of the variable heavy chain region (Table 1) and the variable light chain region (Table 2) of the antibody SARS2-5D7_f3. In one embodiment, an antibody provided herein comprises the amino acid sequences of the variable heavy chain region (Table 1) and the variable light chain region (Table 2) of the antibody SARS2-5H12_f3. In one embodiment, an antibody provided herein comprises the amino acid sequences of the variable heavy chain region (Table 1) and the variable light chain region (Table 2) of the antibody SARS2-7C10_f3. In one embodiment, an antibody provided herein comprises the amino acid sequences of the variable heavy chain region (Table 1) and the variable light chain region (Table 2) of the antibody SARS2-8H4_f3. In one embodiment, an antibody provided herein comprises the amino acid sequences of the variable heavy chain region (Table 1) and the variable light chain region (Table 2) of the antibody SARS2-9C6_f3. In one embodiment, an antibody provided herein comprises the amino acid sequences of the variable heavy chain region (Table 1) and the variable light chain region (Table 2) of the antibody SARS2-10D6_f3. In one embodiment, an antibody provided herein comprises the amino acid sequences of the variable heavy chain region (Table 1) and the variable light chain region (Table 2) of the antibody SARS2-11D5_f3. In one embodiment, an antibody provided herein comprises the amino acid sequences of the variable heavy chain region (Table 1) and the variable light chain region (Table 2) of the antibody SARS2-11G2_S. Ina specific embodiment, an antibody provided herein comprises the amino acid sequences of the variable heavy chain region (Table 1) and the variable light chain region (Table 2) of the antibody SARS2-11G7_f2. In one embodiment, an antibody provided herein comprises the amino acid sequences of the variable heavy chain region (Table 1) and the variable light chain region (Table 2) of the antibody SARS2-16C5_f3. In one embodiment, an antibody provided herein comprises the amino acid sequences of the variable heavy chain region (Table 1) and the variable light chain region (Table 2) of the antibody SARS2-16C12_f3. In one embodiment, an antibody provided herein comprises the amino acid sequences of the variable heavy chain region (Table 1) and the variable light chain region (Table 2) of the antibody SARS2-17A8_f3. In one embodiment, an antibody provided herein comprises the amino acid sequences of the variable heavy chain region (Table 1) and the variable light chain region (Table 2) of the antibody SARS2-17F2_f3. In one embodiment, an antibody provided herein comprises the amino acid sequences of the variable heavy chain region (Table 1) and the variable light chain region (Table 2) of the antibody SARS2-18E7_f3. In one embodiment, an antibody provided herein comprises the amino acid sequences of the variable heavy chain region (Table 1) and the variable light chain region (Table 2) of the antibody SARS2-19C4_f3. In one embodiment, an antibody provided herein comprises the amino acid sequences of the variable heavy chain region (Table 1) and the variable light chain region (Table 2) of the antibody SARS2_2C1_f4. In one embodiment, an antibody provided herein comprises the amino acid sequences of the variable heavy chain region (Table 1) and the variable light chain region (Table 2) of the antibody SARS2_4E3_f4. In one embodiment, an antibody provided herein comprises the amino acid sequences of the variable heavy chain region (Table 1) and the variable light chain region (Table 2) of the antibody SARS2_7D2_f4. In one embodiment, an antibody provided herein comprises the amino acid sequences of the variable heavy chain region (Table 1) and the variable light chain region (Table 2) of the antibody SASR2_9C5_f4. In one embodiment, an antibody provided herein comprises the amino acid sequences of the variable heavy chain region (Table 1) and the variable light chain region (Table 2) of the antibody SASR2_10A3_f4. In one embodiment, an antibody provided herein comprises the amino acid sequences of the

variable heavy chain region (Table 1) and the variable light chain region (Table 2) of the antibody SASR2_14G5_f4. In one embodiment, an antibody provided herein comprises the amino acid sequences of the variable heavy chain region (Table 1) and the variable light chain region (Table 2) of the antibody SASR2_13A12_f3. In one embodiment, an antibody provided herein comprises the amino acid sequences of the variable heavy chain region (Table 1) and the variable light chain region (Table 2) of the antibody SASR2_5B6_f3. In one embodiment, an antibody provided herein comprises the amino acid sequences of the variable heavy chain region (Table 1) and the variable light chain region (Table 2) of the antibody SASR2_2G6_f4.

[0006] In one embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region comprising the variable heavy chain region complementarity determining regions (CDRs) of antibody number 1 in Table 1; or (b) a variable light chain region comprising the variable light chain region CDRs of antibody number 1 in Table 2. In one embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region comprising the variable heavy chain region complementarity determining regions (CDRs) of antibody number 2 in Table 1; or (b) a variable light chain region comprising the variable light chain region CDRs of antibody number 2 in Table 2. In one embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region comprising the variable heavy chain region complementarity determining regions (CDRs) of antibody number 3 in Table 1; or (b) a variable light chain region comprising the variable light chain region CDRs of antibody number 3 in Table 2. In one embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region comprising the variable heavy chain region complementarity determining regions (CDRs) of antibody number 4 in Table 1; or (b) a variable light chain region comprising the variable light chain region CDRs of antibody number 4 in Table 2. In one embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region comprising the variable heavy chain region complementarity determining regions (CDRs) of antibody number 5 in Table 1; or (b) a variable light chain region comprising the variable light chain region CDRs of antibody number 5 in Table 2. In one embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region comprising the variable heavy chain region complementarity determining regions (CDRs) of antibody number 6 in Table 1; or (b) a variable light chain region comprising the variable light chain region CDRs of antibody number 6 in Table 2. In one embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region comprising the variable heavy chain region complementarity determining regions (CDRs) of antibody number 7 in Table 1; or (b) a variable light chain region comprising the variable light chain region CDRs of antibody number 7 in Table 2. In one embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region comprising the variable heavy chain region complementarity determining regions (CDRs) of antibody number 8 in Table 1; or (b) a variable light chain region comprising the variable light chain region CDRs of antibody number 8 in Table 2. In one embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region comprising the variable heavy chain region complementarity determining regions (CDRs) of antibody number 9 in Table 1; or (b) a variable light chain region comprising the variable light chain region CDRs of antibody number 9 in Table 2. In one embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region comprising the variable heavy chain region complementarity determining regions (CDRs) of antibody number 10 in Table 1; or (b) a variable light chain region comprising the variable light chain region CDRs of antibody number 10 in Table 2. In one embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region comprising the variable heavy chain region complementarity determining regions (CDRs) of antibody number 11 in Table 1; or (b) a variable light chain region comprising the variable light chain region CDRs of antibody number 11 in Table 2. In one embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region comprising the variable heavy chain region complementarity determining regions (CDRs) of antibody number 12 in Table 1; or (b) a variable light chain region comprising the variable light chain region CDRs of antibody number 12 in Table 2. In one embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region comprising the variable heavy chain region complementarity determining regions (CDRs) of antibody number 13 in Table 1; or (b) a variable light chain region comprising the variable light chain region CDRs of antibody number 13 in Table 2. In one embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region comprising the variable heavy chain region complementarity determining regions (CDRs) of antibody number 14 in Table 1; or (b) a variable light chain region comprising the variable light chain region CDRs of antibody number 14 in Table 2. In one embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region comprising the variable heavy chain region complementarity determining regions (CDRs) of antibody number 15 in Table 1; or (b) a variable light chain region comprising the variable light chain region CDRs of antibody number 15 in Table 1. In one embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region comprising the variable heavy chain region complementarity determining regions (CDRs) of antibody number 16 in Table 1; or (b) a variable light chain region comprising the variable light chain region CDRs of antibody number 16 in Table 2. In one embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region comprising the variable heavy chain region complementarity determining regions (CDRs) of antibody number 17 in Table 1; or (b) a variable light chain region comprising the variable light chain region CDRs of antibody

number 17 in Table 2. In one embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region comprising the variable heavy chain region complementarity determining regions (CDRs) of antibody number 18 in Table 1; or (b) a variable light chain region comprising the variable light chain region CDRs of antibody number 19 in Table 2. In one embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region comprising the variable heavy chain region complementarity determining regions (CDRs) of antibody number 20 in Table 1; or (b) a variable light chain region comprising the variable light chain region CDRs of antibody number 20 in Table 2. In one embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region comprising the variable heavy chain region complementarity determining regions (CDRs) of antibody number 21 in Table 1; or (b) a variable light chain region comprising the variable light chain region CDRs of antibody number 21 in Table 2. In one embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region comprising the variable heavy chain region complementarity determining regions (CDRs) of antibody number 22 in Table 1; or (b) a variable light chain region comprising the variable light chain region CDRs of antibody number 22 in Table 2. In one embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region comprising the variable heavy chain region complementarity determining regions (CDRs) of antibody number 23 in Table 1; or (b) a variable light chain region comprising the variable light chain region CDRs of antibody number 23 in Table 2. In one embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region comprising the variable heavy chain region complementarity determining regions (CDRs) of antibody number 24 in Table 1; or (b) a variable light chain region comprising the variable light chain region CDRs of antibody number 24 in Table 2. In one embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region comprising the variable heavy chain region complementarity determining regions (CDRs) of antibody number 25 in Table 1; or (b) a variable light chain region comprising the variable light chain region CDRs of antibody number 25 in Table 2. In one embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region comprising the variable heavy chain region complementarity determining regions (CDRs) of antibody number 26 in Table 1; or (b) a variable light chain region comprising the variable light chain region CDRs of antibody number 26 in Table 2. In one embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region comprising the variable heavy chain region complementarity determining regions (CDRs) of antibody number 27 in Table 1; or (b) a variable light chain region comprising the variable light chain region CDRs of antibody number 27 in Table 2. In one embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region comprising the variable heavy chain region complementarity determining regions (CDRs) of antibody number 28 in Table 1; or (b) a variable light chain region comprising the variable light chain region CDRs of antibody number 28 in Table 2. In one embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region comprising the variable heavy chain region complementarity determining regions (CDRs) of antibody number 29 in Table 1; or (b) a variable light chain region comprising the variable light chain region CDRs of antibody number 29 in Table 2.

[0007] In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein, wherein the antibody comprises a variable heavy chain region comprising the amino acid sequence of antibody number 1 in Table 1 and a variable light chain region comprising the amino acid sequence of antibody number 1 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein, wherein the antibody comprises a variable heavy chain region comprising the amino acid sequence of antibody number 2 in Table 1 and a variable light chain region comprising the amino acid sequence of antibody number 2 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein, wherein the antibody comprises a variable heavy chain region comprising the amino acid sequence of antibody number 3 in Table 1 and a variable light chain region comprising the amino acid sequence of antibody number 3 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein, wherein the antibody comprises a variable heavy chain region comprising the amino acid sequence of antibody number 4 in Table 1 and a variable light chain region comprising the amino acid sequence of antibody number 4 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein, wherein the antibody comprises a variable heavy chain region comprising the amino acid sequence of antibody number 5 in Table 1 and a variable light chain region comprising the amino acid sequence of antibody number 5 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein, wherein the antibody comprises a variable heavy chain region comprising the amino acid sequence of antibody number 6 in Table 1 and a variable light chain region comprising the amino acid sequence of antibody number 6 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein, wherein the antibody comprises a variable heavy chain region comprising the amino acid sequence of antibody number 7 in Table 1 and a variable light chain region comprising the amino acid sequence of antibody number 7 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein, wherein the antibody comprises a variable heavy chain region comprising the amino acid sequence of antibody number 8 in Table 1 and a variable light chain region comprising the amino acid sequence of antibody number 8 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein, wherein the antibody comprises a variable heavy chain region comprising the amino acid sequence of antibody number 9 in Table 1 and a variable light chain region comprising the amino acid sequence of antibody

number 9 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein, wherein the antibody comprises a variable heavy chain region comprising the amino acid sequence of antibody number 10 in Table 1 and a variable light chain region comprising the amino acid sequence of antibody number 10 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein, wherein the antibody comprises a variable heavy chain region comprising the amino acid sequence of antibody number 11 in Table 1 and a variable light chain region comprising the amino acid sequence of antibody number 11 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein, wherein the antibody comprises a variable heavy chain region comprising the amino acid sequence of antibody number 12 in Table 1 and a variable light chain region comprising the amino acid sequence of antibody number 12 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein, wherein the antibody comprises a variable heavy chain region comprising the amino acid sequence of antibody number 13 in Table 1 and a variable light chain region comprising the amino acid sequence of antibody number 13 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein, wherein the antibody comprises a variable heavy chain region comprising the amino acid sequence of antibody number 14 in Table 1 and a variable light chain region comprising the amino acid sequence of antibody number 14 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein, wherein the antibody comprises a variable heavy chain region comprising the amino acid sequence of antibody number 15 in Table 1 and a variable light chain region comprising the amino acid sequence of antibody number 15 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein, wherein the antibody comprises a variable heavy chain region comprising the amino acid sequence of antibody number 16 in Table 1 and a variable light chain region comprising the amino acid sequence of antibody number 16 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein, wherein the antibody comprises variable heavy chain region comprising the amino acid sequence of antibody number 17 in Table 1 and a variable light chain region comprising the amino acid sequence of antibody number 17 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein, wherein the antibody comprises a variable heavy chain region comprising the amino acid sequence of antibody number 18 in Table 1 and a variable light chain region comprising the amino acid sequence of antibody number 18 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein, wherein the antibody comprises a variable heavy chain region comprising the amino acid sequence of antibody number 19 in Table 1 and a variable light chain region comprising the amino acid sequence of antibody number 19 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein, wherein the antibody comprises variable heavy chain region comprising the amino acid sequence of antibody number 20 in Table 1 and a variable light chain region comprising the amino acid sequence of antibody number 20 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein, wherein the antibody comprises variable heavy chain region comprising the amino acid sequence of antibody number 21 in Table 1 and a variable light chain region comprising the amino acid sequence of antibody number 21 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein, wherein the antibody comprises variable heavy chain region comprising the amino acid sequence of antibody number 22 in Table 1 and a variable light chain region comprising the amino acid sequence of antibody number 22 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein, wherein the antibody comprises variable heavy chain region comprising the amino acid sequence of antibody number 23 in Table 1 and a variable light chain region comprising the amino acid sequence of antibody number 23 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein, wherein the antibody comprises variable heavy chain region comprising the amino acid sequence of antibody number 24 in Table 1 and a variable light chain region comprising the amino acid sequence of antibody number 24 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein, wherein the antibody comprises variable heavy chain region comprising the amino acid sequence of antibody number 25 in Table 1 and a variable light chain region comprising the amino acid sequence of antibody number 25 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein, wherein the antibody comprises variable heavy chain region comprising the amino acid sequence of antibody number 26 in Table 1 and a variable light chain region comprising the amino acid sequence of antibody number 26 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein, wherein the antibody comprises variable heavy chain region comprising the amino acid sequence of antibody number 27 in Table 1 and a variable light chain region comprising the amino acid sequence of antibody number 27 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein, wherein the antibody comprises variable heavy chain region comprising the amino acid sequence of antibody number 28 in Table 1 and a variable light chain region comprising the amino acid sequence of antibody number 28 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein, wherein the antibody comprises variable heavy chain region comprising the amino acid sequence of antibody number 29 in Table 1 and a variable light chain region comprising the amino acid sequence of antibody number 29 in Table 2.

[0008] In another embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 1 in Table 1; or (b) a variable light chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 1 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the

antibody are identical to the CDRs of the variable heavy chain region of antibody number 1 in Table 1. In one embodiment, the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 1 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 1 in Table 1 and the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 1 in Table 2.

[0009] In another embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 2 in Table 1; or (b) a variable light chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 2 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 2 in Table 1. In one embodiment, the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 2 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 2 in Table 1 and the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 2 in Table 2.

[0010] In another embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 3 in Table 1; or (b) a variable light chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 3 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 3 in Table 1. In one embodiment, the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 3 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 3 in Table 1 and the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 3 in Table 2.

[0011] In another embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 4 in Table 1; or (b) a variable light chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 4 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 4 in Table 1. In one embodiment, the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 4 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 4 in Table 1 and the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 4 in Table 2.

[0012] In another embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 5 in Table 1; or (b) a variable light chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 5 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 5 in Table 1. In one embodiment, the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 5 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 5 in Table 1 and the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 5 in Table 2.

[0013] In another embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 6 in Table 1; or (b) a variable light chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 6 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 6 in Table 1. In one embodiment, the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 6 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 6 in Table 1 and the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 6 in Table 2.

[0014] In another embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 7 in Table 1; or (b) a variable light chain region that is at least 80%, at

least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 7 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 7 in Table 1. In one embodiment, the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 7 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 7 in Table 1 and the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 7 in Table 2.

[0015] In another embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 8 in Table 1; or (b) a variable light chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 8 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 8 in Table 1. In one embodiment, the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 8 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 8 in Table 1 and the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 8 in Table 2.

[0016] In another embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 9 in Table 1; or (b) a variable light chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 9 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 9 in Table 1. In one embodiment, the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 9 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 9 in Table 1 and the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 9 in Table 2.

[0017] In another embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 10 in Table 1; or (b) a variable light chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 10 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 10 in Table 1. In one embodiment, the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 10 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 10 in Table 1 and the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 10 in Table 2.

[0018] In another embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 11 in Table 1; or (b) a variable light chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 11 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 11 in Table 1. In one embodiment, the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 11 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 11 in Table 1 and the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 11 in Table 2.

[0019] In another embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 12 in Table 1; or (b) a variable light chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 12 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 12 in Table 1. In one embodiment, the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 12 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 12 in Table 1 and the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 12 in Table 2.

[0020] In another embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region that is at

least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 13 in Table 1; or (b) a variable light chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 13 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 13 in Table 1. In one embodiment, the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 13 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 13 in Table 1 and the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 13 in Table 2.

[0021] In another embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 14 in Table 1; or (b) a variable light chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 14 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 14 in Table 1. In one embodiment, the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 14 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 14 in Table 1 and the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 14 in Table 2.

[0022] In another embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 15 in Table 1; or (b) a variable light chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 15 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 15 in Table 1. In one embodiment, the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 15 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 15 in Table 1 and the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 15 in Table 2.

[0023] In another embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 16 in Table 1; or (b) a variable light chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 16 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 16 in Table 1. In one embodiment, the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 16 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 16 in Table 1 and the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 16 in Table 2.

[0024] In another embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 17 in Table 1; or (b) a variable light chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 17 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 17 in Table 1. In one embodiment, the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 17 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 17 in Table 1 and the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 17 in Table 2.

[0025] In another embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 18 in Table 1; or (b) a variable light chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 18 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 18 in Table 1. In one embodiment, the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 18 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 18 in Table 1 and the CDRs of the variable light chain region of the antibody are iden-

tical to the CDRs of the variable heavy light region of antibody number 18 in Table 2.

[0026] In another embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 19 in Table 1; or (b) a variable light chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 19 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 19 in Table 1. In one embodiment, the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 19 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 19 in Table 1 and the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 19 in Table 2.

[0027] In another embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 20 in Table 1; or (b) a variable light chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 20 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 20 in Table 1. In one embodiment, the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 20 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 20 in Table 1 and the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 20 in Table 2.

[0028] In another embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 21 in Table 1; or (b) a variable light chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 21 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 21 in Table 1. In one embodiment, the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 21 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 21 in Table 1 and the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 21 in Table 2.

[0029] In another embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 22 in Table 1; or (b) a variable light chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 22 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 22 in Table 1. In one embodiment, the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 22 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 22 in Table 1 and the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 22 in Table 2.

[0030] In another embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 23 in Table 1; or (b) a variable light chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 23 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 23 in Table 1. In one embodiment, the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 23 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 23 in Table 1 and the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 23 in Table 2.

[0031] In another embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 24 in Table 1; or (b) a variable light chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 24 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 24 in Table 1. In one embodiment, the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 24 in Table 2. In one

embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 24 in Table 1 and the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 24 in Table 2.

[0032] In another embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 25 in Table 1; or (b) a variable light chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 25 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 25 in Table 1. In one embodiment, the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 25 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 25 in Table 1 and the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 25 in Table 2.

[0033] In another embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 26 in Table 1; or (b) a variable light chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 26 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 26 in Table 1. In one embodiment, the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 26 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 26 in Table 1 and the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 26 in Table 2.

[0034] In another embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 27 in Table 1; or (b) a variable light chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 27 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 27 in Table 1. In one embodiment, the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 27 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 27 in Table 1 and the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 27 in Table 2.

[0035] In another embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 28 in Table 1; or (b) a variable light chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 28 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 28 in Table 1. In one embodiment, the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 28 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 28 in Table 1 and the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 28 in Table 2.

[0036] In another embodiment, an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprises: (a) a variable heavy chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 29 in Table 1; or (b) a variable light chain region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of antibody number 29 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 29 in Table 1. In one embodiment, the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 29 in Table 2. In one embodiment, the CDRs of the variable heavy chain region of the antibody are identical to the CDRs of the variable heavy chain region of antibody number 29 in Table 1 and the CDRs of the variable light chain region of the antibody are identical to the CDRs of the variable heavy light region of antibody number 29 in Table 2.

[0037] Provided herein is an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprising a variable heavy chain region and a variable light chain region wherein:

[0038] a) the variable heavy chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:59 and the variable light chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:88;

[0039] b) the variable heavy chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:60 and the variable light chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:89;

[0040] c) the variable heavy chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:61 and the variable light chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:90;

[0041] d) the variable heavy chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:62 and the variable light chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:91;

[0042] e) the variable heavy chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:63 and the variable light chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:92;

[0043] f) the variable heavy chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:64 and the variable light chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:93;

[0044] g) the variable heavy chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:65 and the variable light chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:94;

[0045] h) the variable heavy chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:66 and the variable light chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:95;

[0046] i) the variable heavy chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:67 and the variable light chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:96;

[0047] j) the variable heavy chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:68 and the variable light chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:97;

[0048] k) the variable heavy chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:69 and the variable light chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:98;

[0049] l) the variable heavy chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:70 and the variable light chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:99;

[0050] m) the variable heavy chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:71 and the variable light chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:100;

[0051] n) the variable heavy chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:72 and the variable light chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:101;

[0052] o) the variable heavy chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:73 and the variable light chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:102;

[0053] p) the variable heavy chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:74 and the variable light chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:103;

[0054] q) the variable heavy chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:75 and the variable light chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:104;

[0055] r) the variable heavy chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:76 and the variable light chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:105;

[0056] s) the variable heavy chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:77 and the variable light chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:106;

[0057] t) the variable heavy chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:78 and the variable light chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:107;

[0058] u) the variable heavy chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:79 and the variable light chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:108;

[0059] v) the variable heavy chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:80 and the variable light chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:109;

[0060] w) the variable heavy chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:81 and the variable light chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:110;

[0061] x) the variable heavy chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:82 and the variable light chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:111;

[0062] y) the variable heavy chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:83 and the variable light chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:112;

[0063] z) the variable heavy chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:84 and the variable light chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:113;

[0064] aa) the variable heavy chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:85 and the variable light chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:114;

[0065] bb) the variable heavy chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:86 and the variable light chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:115; or

[0066] cc) the variable heavy chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:87 and the variable light chain region comprises a sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at last 98%, or least 99% identical to SEQ ID NO:116.

[0067] Provided herein is an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprising a variable heavy chain region and a variable light chain region wherein:

[0068] a) the variable heavy chain region comprises SEQ ID NO:59 and the variable light chain region comprises SEQ ID NO:88;

[0069] b) the variable heavy chain region comprises SEQ ID NO:60 and the variable light chain region comprises SEQ ID NO:89;

[0070] c) the variable heavy chain region comprises SEQ ID NO:61 and the variable light chain region comprises SEQ ID NO:90;

[0071] d) the variable heavy chain region comprises SEQ ID NO:62 and the variable light chain region comprises SEQ ID NO:91;

[0072] e) the variable heavy chain region comprises SEQ ID NO:63 and the variable light chain region comprises SEQ ID NO:92;

[0073] f) the variable heavy chain region comprises SEQ ID NO:64 and the variable light chain region comprises SEQ ID NO:93;

[0074] g) the variable heavy chain region comprises SEQ ID NO:65 and the variable light chain region comprises SEQ ID NO:94;

[0075] h) the variable heavy chain region comprises SEQ ID NO:66 and the variable light chain region comprises SEQ ID NO:95;

[0076] i) the variable heavy chain region comprises SEQ ID NO:67 and the variable light chain region comprises SEQ ID NO:96;

[0077] j) the variable heavy chain region comprises SEQ ID NO:68 and the variable light chain region comprises SEQ ID NO:97;

[0078] k) the variable heavy chain region comprises SEQ ID NO:69 and the variable light chain region comprises SEQ ID NO:98;

[0079] l) the variable heavy chain region comprises SEQ ID NO:70 and the variable light chain region comprises SEQ ID NO:99;

[0080] m) the variable heavy chain region comprises SEQ ID NO:71 and the variable light chain region comprises SEQ ID NO:100;

[0081] n) the variable heavy chain region comprises SEQ ID NO:72 and the variable light chain region comprises SEQ ID NO:101;

[0082] o) the variable heavy chain region comprises SEQ ID NO:73 and the variable light chain region comprises SEQ ID NO:102;

[0083] p) the variable heavy chain region comprises SEQ ID NO:74 and the variable light chain region comprises SEQ ID NO:103;

[0084] q) the variable heavy chain region comprises SEQ ID NO:75 and the variable light chain region comprises SEQ ID NO:104;

[0085] r) the variable heavy chain region comprises SEQ ID NO:76 and the variable light chain region comprises SEQ ID NO:105;

[0086] s) the variable heavy chain region comprises SEQ ID NO:77 and the variable light chain region comprises SEQ ID NO:106;

[0087] t) the variable heavy chain region comprises SEQ ID NO:78 and the variable light chain region comprises SEQ ID NO:107;

[0088] u) the variable heavy chain region comprises SEQ ID NO:79 and the variable light chain region comprises SEQ ID NO:108;

[0089] v) the variable heavy chain region comprises SEQ ID NO:80 and the variable light chain region comprises SEQ ID NO:109;

[0090] w) the variable heavy chain region comprises SEQ ID NO:81 and the variable light chain region comprises SEQ ID NO:110;

[0091] x) the variable heavy chain region comprises SEQ ID NO:82 and the variable light chain region comprises SEQ ID NO:111;

[0092] y) the variable heavy chain region comprises SEQ ID NO:83 and the variable light chain region comprises SEQ ID NO:112;

[0093] z) the variable heavy chain region comprises SEQ ID NO:84 and the variable light chain region comprises SEQ ID NO:113;

[0094] aa) the variable heavy chain region comprises SEQ ID NO:85 and the variable light chain region comprises SEQ ID NO:114;

[0095] bb) the variable heavy chain region comprises SEQ ID NO:86 and the variable light chain region comprises SEQ ID NO:115; or

[0096] cc) the variable heavy chain region comprises SEQ ID NO:87 and the variable light chain region comprises SEQ ID NO:116.

[0097] Provided herein is an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) comprising a variable heavy chain region comprising a CDR1H, a CDR2H, and a CDR3H, and a variable light chain region comprising a CFR1L, a CDR2L, and a CDR3L, wherein:

[0098] a) CDR1H comprises SEQ ID NO:204, CDR2H comprises SEQ ID NO:233, CDR3H comprises SEQ ID NO:262, CDR1L comprises SEQ ID NO:378, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:407;

[0099] b) CDR1H comprises SEQ ID NO:205, CDR2H comprises SEQ ID NO:234, CDR3H comprises SEQ ID NO:263, CDR1L comprises SEQ ID NO:379, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:408;

[0100] c) CDR1H comprises SEQ ID NO:206, CDR2H comprises SEQ ID NO:235, CDR3H comprises SEQ ID NO:264, CDR1L comprises SEQ ID NO:380, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:409;

[0101] d) CDR1H comprises SEQ ID NO:207, CDR2H comprises SEQ ID NO:236, CDR3H comprises SEQ ID NO:265, CDR1L comprises SEQ ID NO:381, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:410;

[0102] e) CDR1H comprises SEQ ID NO:208, CDR2H comprises SEQ ID NO:237, CDR3H comprises SEQ ID NO:266, CDR1L comprises SEQ ID NO:382, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:411;

[0103] f) CDR1H comprises SEQ ID NO:209, CDR2H comprises SEQ ID NO:238, CDR3H comprises SEQ ID NO:267, CDR1L comprises SEQ ID NO:383, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:412;

[0104] g) CDR1H comprises SEQ ID NO:210, CDR2H comprises SEQ ID NO:239, CDR3H comprises SEQ ID NO:268, CDR1L comprises SEQ ID NO:384, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:413;

[0105] h) CDR1H comprises SEQ ID NO:211, CDR2H comprises SEQ ID NO:240, CDR3H comprises SEQ ID NO:269, CDR1L comprises SEQ ID NO:385, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:414;

[0106] i) CDR1H comprises SEQ ID NO:212, CDR2H comprises SEQ ID NO:241, CDR3H comprises SEQ ID NO:270, CDR1L comprises SEQ ID NO:386, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:415;

[0107] j) CDR1H comprises SEQ ID NO:213, CDR2H comprises SEQ ID NO:242, CDR3H comprises SEQ ID NO:271, CDR1L comprises SEQ ID NO:387, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:416;

[0108] k) CDR1H comprises SEQ ID NO:214, CDR2H comprises SEQ ID NO:243, CDR3H comprises SEQ ID NO:272, CDR1L comprises SEQ ID NO:388, CDR2L comprises sequence AAS, and CDR3L comprises SEQ ID NO:417;

[0109] l) CDR1H comprises SEQ ID NO:215, CDR2H comprises SEQ ID NO:244, CDR3H comprises SEQ ID NO:273, CDR1L comprises SEQ ID NO:389, CDR2L comprises sequence AAS, and CDR3L comprises SEQ ID NO:418;

[0110] m) CDR1H comprises SEQ ID NO:216, CDR2H comprises SEQ ID NO:245, CDR3H comprises SEQ ID NO:274, CDR1L comprises SEQ ID NO:390, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:419;

[0111] n) CDR1H comprises SEQ ID NO:217, CDR2H comprises SEQ ID NO:246, CDR3H comprises SEQ ID NO:275, CDR1L comprises SEQ ID NO:391, CDR2L comprises sequence LGS, and CDR3L comprises SEQ ID NO:420;

[0112] o) CDR1H comprises SEQ ID NO:218, CDR2H comprises SEQ ID NO:247, CDR3H comprises SEQ ID NO:276, CDR1L comprises SEQ ID NO:392, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:421;

[0113] p) CDR1H comprises SEQ ID NO:219, CDR2H comprises SEQ ID NO:248, CDR3H comprises SEQ ID NO:277, CDR1L comprises SEQ ID NO:393, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:422;

[0114] q) CDR1H comprises SEQ ID NO:220, CDR2H comprises SEQ ID NO:249, CDR3H comprises SEQ ID NO:278, CDR1L comprises SEQ ID NO:394, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:423;

[0115] r) CDR1H comprises SEQ ID NO:221, CDR2H comprises SEQ ID NO:250, CDR3H comprises SEQ ID NO:279, CDR1L comprises SEQ ID NO:395, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:424;

[0116] s) CDR1H comprises SEQ ID NO:222, CDR2H comprises SEQ ID NO:251, CDR3H comprises SEQ ID NO:280, CDR1L comprises SEQ ID NO:396, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:425;

[0117] t) CDR1H comprises SEQ ID NO:223, CDR2H comprises SEQ ID NO:252, CDR3H comprises SEQ ID NO:281, CDR1L comprises SEQ ID NO:397, CDR2L comprises sequence AAS, and CDR3L comprises SEQ ID NO:426;

[0118] u) CDR1H comprises SEQ ID NO:224, CDR2H comprises SEQ ID NO:253, CDR3H comprises SEQ ID NO:282, CDR1L comprises SEQ ID NO:398, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:427;

[0119] v) CDR1H comprises SEQ ID NO:225, CDR2H comprises SEQ ID NO:254, CDR3H comprises SEQ ID NO:283, CDR1L comprises SEQ ID NO:399, CDR2L comprises sequence AAS, and CDR3L comprises SEQ ID NO:428;

[0120] w) CDR1H comprises SEQ ID NO:226, CDR2H comprises SEQ ID NO:255, CDR3H comprises SEQ ID NO:284, CDR1L comprises SEQ ID NO:400, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:429;

[0121] x) CDR1H comprises SEQ ID NO:227, CDR2H comprises SEQ ID NO:256, CDR3H comprises SEQ ID NO:285, CDR1L comprises SEQ ID NO:401, CDR2L comprises sequence TS, and CDR3L comprises SEQ ID NO:430;

[0122] y) CDR1H comprises SEQ ID NO:228, CDR2H comprises SEQ ID NO:257, CDR3H comprises SEQ ID NO:286, CDR1L comprises SEQ ID NO:402, CDR2L comprises sequence AAS, and CDR3L comprises SEQ ID NO:431;

[0123] z) CDR1H comprises SEQ ID NO:229, CDR2H comprises SEQ ID NO:258, CDR3H comprises SEQ ID NO:287, CDR1L comprises SEQ ID NO:403, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:432;

[0124] aa) CDR1H comprises SEQ ID NO:230, CDR2H comprises SEQ ID NO:259, CDR3H comprises SEQ ID NO:288, CDR1L comprises SEQ ID NO:404, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:433;

[0125] bb) CDR1H comprises SEQ ID NO:231, CDR2H comprises SEQ ID NO:260, CDR3H comprises SEQ ID NO:289, CDR1L comprises SEQ ID NO:405, CDR2L comprises sequence AAS, and CDR3L comprises SEQ ID NO:434; or

[0126] cc) CDR1H comprises SEQ ID NO:232, CDR2H comprises SEQ ID NO:261, CDR3H comprises SEQ ID NO:290, CDR1L comprises SEQ ID NO:406, CDR2L comprises sequence AAS, and CDR3L comprises SEQ ID NO:435.

[0127] In one embodiment, an antibody provided herein comprises human-derived heavy and light chain constant regions. In one embodiment, the heavy chain constant region has an isotype selected from the group consisting of gamma1, gamma2, gamma3, and gamma4. In one embodiment, the light chain constant region has an isotype selected from the group consisting of kappa and lambda.

[0128] In one embodiment, an antibody provided herein is an immunoglobulin comprising two identical heavy chains and two identical light chains.

[0129] In one embodiment, an antibody provided herein is a monoclonal antibody. In one embodiment, an antibody provided herein is an antigen-binding fragment. In one embodiment, an antibody provided herein is a single-chain variable fragment (scFv).

[0130] In one embodiment, an antibody provided herein is conjugated to a detectable agent or a therapeutic agent.

[0131] In one embodiment, an antibody provide herein is isolated.

[0132] In another aspect, provided herein are polynucleotide sequences encoding antibodies described herein. See Tables 1 and 2 for the nucleotide sequences of the variable heavy chain region and variable light chain region of antibodies 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, and 29. In one embodiment, an antibody described herein is encoded by a nucleic acid sequence comprising the nucleotide sequences of the variable heavy chain region and variable light chain region of antibody 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, or 29 (see Tables 1 and 2). In one embodiment, the nucleic acid sequences are isolated.

[0133] Provided herein is a nucleic acid encoding an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), wherein the nucleic acid comprises one or more of SEQ ID NOs:1-58. Provided herein is a nucleic acid encoding an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), wherein the nucleic acid comprises one or more of SEQ ID NOs:117-203 or SEQ ID NOs:291-377.

[0134] In another aspect, provided herein are expression vectors comprising a nucleotide encoding an antibody described herein. In one embodiment, an expression vector provided herein is operably linked to one or more regulatory regions.

[0135] In another aspect, provided herein are host cells comprising a nucleotide encoding an antibody described herein. In one embodiment, provided herein are host cells engineered to express an antibody described herein. The host cells may be used to produce the antibody using techniques known to one of skill in the art or described herein.

[0136] In another aspect, provided herein are compositions comprising an antibody described herein. The compositions described herein may be used in the methods of prevention, treatment, or diagnosis described herein. In one embodiment, the compositions may be used to prevent COVID-19 In another embodiment, the compositions may be used to treat a SARS-CoV-2 infection or COVID-19.

[0137] In another aspect, provided herein are methods for preventing COVID-19 comprising administering to a subject in need thereof an antibody described herein, or a composition comprising such an antibody. In one embodiment, the subject is a human. In one embodiment, the subject is a human infant or human toddler. In one embodiment, the subject is an elderly human.

[0138] In another aspect, provided herein are methods for treating SARS-CoV-2 infection or COVID-19 comprising administering to a subject in need thereof an antibody described herein, or composition comprising such an antibody. In one embodiment, the subject is diagnosed with SARS-CoV-2 virus infection or COVID-19. In one embodiment, the subject is diagnosed as SARS-CoV-2 infection or COVID-19. In one embodiment, the subject is a human. In one embodiment, the subject is a human infant or human toddler. In one embodiment, the subject is an elderly human.

[0139] In another aspect, provided herein are methods for detecting SARS-CoV-2, or diagnosing SARS-CoV-2 infection using an antibody described herein.

[0140] In another aspect, provided herein are kits comprising an antibody described herein. In one embodiment, provided herein is a kit comprising an antibody described herein, and optionally instructions for use of the antibody in the prevention or treatment of SARS-CoV-2 infection, or COVID-19, or in the detection of SARS-CoV-2 infection.

[0141] In another aspect, provided herein is an isolated antigenic peptide comprising an epitope of an antibody described herein. In one embodiment, the peptide of the SARS-CoV-21 spike protein may be used to actively immunize a patient, or in a diagnostic to detect SARS-CoV-2.

5. DESCRIPTION OF THE DRAWINGS

[0142] FIG. **1** is a heat map that shows the diversity of mAb binding to the spike protein. The clones were screened in several assays that included binding to membrane bound whole spike on the cell surface (MFI/flow cytometry), binding to receptor binding domain (RBD) of spike protein (RBD ELISA), RBD/ACE2 competition assay (ACE2 inhibition), and pseudovirus neutralization assay (pseudovirus neutralization).

[0143] FIG. **2** is a graph illustrating the results of neutralizing titer testing. Mabs were evaluated for neutralization potency using SARS-CoV-2 Spike expressing/VSV pseudovirus assay system. Twenty-four hours post infection, cells were analyzed by flow cytometry. Max infection (100%) is the percent of cells infected with virus alone.

[0144] FIGS. **3**A, **3**B, **3**C, and **3**D are genetic trees illustrating grouping of antibodies in families based on CDR3 identity Antibody sequences were determined to belong to two sequence families based on CDR3 homologies, designated A (FIG. **3**A), B (FIG. **3**B), E (FIG. **3**C) and G (FIG. **3**D). Individual clones with variances from members within each family are shown in the above genetic trees, with identical clones (100% homology) in shaded boxes. All clones with some degree of uniqueness were chosen to move forward. Only one clone was chosen from the identical cluster sets.

[0145] FIGS. **4**A, **4**B, **4**C, and **4**D show results from a competitive ELISA. SARS-CoV RBD coated plates were exposed to supernatants (either undiluted (neat) or at a 1:10 dilution in sera free media) comprising clones from each family or rat IgG isotype control (1 μg/ml). Biotinylated purified antibody from family A (10D6) or B (16C5) was added after the supernatants. The plates were developed with streptavidin HRP. Representative clones included 19C4 (family A), 16C12 (family B), 2C1 (family D), 14G5 (family E), 7D2 (family F), and 10A3 (family G) (FIGS. **4**A and **4**B). Three family E clones (3E10, 14G5, and 14G11) were examined for competition with family A (FIG. **4**C) and B (FIG. **4**D) biotinylated monoclonals.

[0146] FIGS. **5**A, **5**B, and **5**C show neutralization experiments with WT (FIG. **5**A) and mutant-VSV pseudovriuses N501Y (FIG. **5**B) and E484K (FIG. **5**C). Representative clones included 19C4 (family A), 16C12 (family B), 2C1 (family D), 14G5 (family E), 7D2 (family F), and 10A3 (family G).

[0147] FIGS. **6**A, **6**B, **6**C, **6**D, **6**E, **6**F, **6**G, and **6**H show an ELISA experiment in which fusion proteins representing the RBD domains of the SARS-CoV2 Spike protein from the wild type, N501Y single mutant, or E484K single mutant (South African variant SA) were coated to ELISA plates and screened for binding as described in the materials and methods. Monoclonal antibodies representing each of the genetic families were added to coated ELISA plates at concentrations of 2 μg/ml, 200 ng/ml, 20 ng/ml, and 2 ng/ml (from left to right).

[0148] FIGS. **7**A, **7**B, and **7**C illustrate that anti-SARS-CoV2 RBD mAbs block virus proliferation in vivo. The timeline of sensivizing BALB/c mice with Ad5-hACE2, treatment with anti-RBD monoclonal antibodies, and challenge with SARS-CoV-2 (FIG. **7**A). Monoclonal antibodies 5H12, 10D6 (FIG. **7**B), 1D10, 16C5, and 19C4 (FIG. **7**C) were administered intraperitoneally into BALB/c mice that had been sensitized with Ad5-hACE2 at different doses. The SARS-CoV2 viral titer (PFU/ml) from harvested lungs two days post-infection was analyzed. PBS and human IgG (hIgG) were used as controls. The panel of mAbs effectively blocked virus replication in the lungs in contrast to human IgG negative control and PBS, with almost no detectable titers in some groups.

6. DETAILED DESCRIPTION

[0149] 6.1 Antibodies

[0150] Antibodies can include, for example, monoclonal antibodies, recombinantly produced antibodies, monospecific antibodies, multispecific antibodies (including bispecific antibodies), human antibodies, humanized antibodies, chimeric antibodies, synthetic antibodies, tetrameric anti-

bodies comprising two heavy chain and two light chain molecule, an antibody light chain monomer, an antibody heavy chain monomer, an antibody light chain dimer, an antibody heavy chain dimer, an antibody light chain-antibody heavy chain pair, intrabodies, heteroconjugate antibodies, single domain antibodies, monovalent antibodies, single chain antibodies or single-chain Fvs (scFv), camelized antibodies, affybodies, Fab fragments, F(ab') fragments, disulfide-linked Fvs (sdFv), anti-idiotypic (anti-Id) antibodies (including, e.g., anti-anti-Id antibodies), and antigen-binding fragments of any of the above. In certain embodiments, antibodies described herein refer to polyclonal antibody populations. Antibodies can be of any type (e.g., IgG, IgE, IgM, IgD, IgA or IgY), any class, (e.g., IgG1, IgG2, IgG3, IgG4, IgA1 or IgA2), or any subclass (e.g., IgG2a or IgG2b) of immunoglobulin molecule. In certain embodiments, antibodies described herein are IgG antibodies, or a class (e.g., human IgG1 or IgG2) or subclass (e.g., IgG2a) thereof. In one embodiment, an antibody described herein is isolated or purified.

[0151] In one embodiment, an antibody includes any molecule with an antigen-binding site that binds an antigen. In some embodiments, an antibody includes an antigen-binding fragment (e.g., the region(s) of an immunoglobulin that binds to an antigen or an epitope, such as a sequence comprising complementarity determining regions (e.g., the heavy and/or light chain variable regions)). In other embodiments, an antibody does not include antigen-binding fragments.

[0152] In one embodiment, an antibody described herein is a monoclonal antibody. As used herein, the term "monoclonal antibody" refers to an antibody obtained from a population of homogenous or substantially homogeneous antibodies. The term "monoclonal" is not limited to any particular method for making the antibody. Generally, a population of monoclonal antibodies can be generated by cells, a population of cells, or a cell line. In some embodiments, a "monoclonal antibody," as used herein, is an antibody produced by a single cell (e.g., hybridoma or host cell producing a recombinant antibody), wherein the antibody binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) as determined, e.g., by ELISA or other antigen-binding or competitive binding assay known in the art or in the Examples provided herein. In some embodiments, a monoclonal antibody can be a chimeric antibody, a human antibody, or a humanized antibody.

[0153] In certain embodiments, a monoclonal antibody is a monovalent antibody or multivalent (e.g., bivalent) antibody. In some embodiments, a monoclonal antibody is a monospecific or multispecific antibody (e.g., bispecific antibody). Monoclonal antibodies described herein can, for example, be made by the hybridoma method as described in Kohler et al.; Nature, 256:495 (1975) or can, e.g., be isolated from phage libraries using the techniques as described herein, for example. Other methods for the preparation of clonal cell lines and of monoclonal antibodies expressed thereby are well known in the art (see, for example, Chapter 11 in: *Short Protocols in Molecular Biology*, (2002) 5th Ed., Ausubel et al., eds., John Wiley and Sons, New York).

[0154] In one embodiment, an antibody described herein is an immunoglobulin, such as an IgG, IgE, IgM, IgD, IgA or IgY. In one embodiment, an antibody described herein is an IgG2a. In some embodiments, an antibody described herein is an IgG1 or IgG2a. In another embodiment, antibody described herein is an antigen-binding fragment, such as, e.g., a Fab fragment or $F(ab')_2$ fragment. In another embodiment, an antibody described herein is an scFv.

[0155] As used herein, the terms "SARS-CoV-2 spike protein" and "spike protein of SARS-CoV-2" refer to a SARS-CoV-2 spike protein known to those of skill in the art. In certain embodiments, the spike protein comprises the amino acid or nucleic acid sequence found at GenBank Accession No. MN908947.3. A typical spike protein comprises domains known to those of skill in the art including an S1 domain, a receptor binding domain, an S2 domain, a transmembrane domain and a cytoplasmic domain. See, e.g., Wrapp et al., 2020, Science 367: 1260-1263 for a description of SARS-CoV-2 spike protein (in particular, the structure of such protein). The spike protein may be characterized has having a signal peptide (e.g., a signal peptide of 1-14 amino acid residues of the amino acid sequence of GenBank Accession No. MN908947.3), a receptor binding domain (e.g., a receptor binding domain of 319-541 amino acid residues of GenBank Accession No. MN908947.3), an ectodomain (e.g., an ectodomain of 15-1213 amino acid residues of GenBank Accession No. MN908947.3), and a transmembrane and endodomain (e.g., a transmembrane and endodomain of 1214-1273 amino acid residues of GenBank Accession No. MN908947.3).

[0156] In certain embodiments, a fragment of a SARS-CoV-2 spike protein is at least 8, 10, 12, 15, or 20 amino acid residues in length. In some embodiments, a fragment of a SARS-CoV-2 spike protein comprises or consists of the receptor binding domain (RBD) of the spike protein. In certain embodiments, fragment of a SARS-CoV-2 spike protein consists of the RBD of the spike protein and 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acid residues at the N-terminus, C-terminus or both. In some embodiments, fragment of a SARS-CoV-2 spike protein comprises or consists of the S1 domain, S2 domain or ectodomain of the spike protein. In certain embodiments, fragment of a SARS-CoV-2 spike protein consists of the S1 domain, S2 domain or ectodomain of the spike protein and 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acid residues at the N-terminus, C-terminus or both.

[0157] In another aspect, the antibodies provided herein bind to SARS-CoV-2 spike protein with a certain affinity. "Binding affinity" generally refers to the strength of the sum total of non-covalent interactions between a single binding site of a molecule (e.g., an antibody) and its binding partner (e.g., an antigen). In one embodiment, "binding affinity" refers to intrinsic binding affinity which reflects a 1:1 interaction between members of a binding pair (e.g., antibody and antigen). The affinity of a molecule X for its partner Y can generally be represented by the dissociation constant (K_D). Affinity can be measured and/or expressed in a number of ways known in the art, including, but not limited to, equilibrium dissociation constant (K_D), equilibrium association constant (K_A), and IC_{50}. The K_D is calculated from the quotient of k_{off}/k_{on}, whereas K_A is calculated from the quotient of k_{on}/k_{off}. k_{on} refers to the association rate constant of, e.g., an antibody to an antigen, and k_{off} refers to the dissociation of, e.g., an antibody to an antigen. The k_{on} and k_{off} can be determined by techniques known to one of ordinary skill in the art, such as BIAcore™, Kinexa, or biolayer interferometry.

[0158] Affinity can be measured by common methods known in the art, including those described herein. For example, individual association (k_{on}) and dissociation (k_{off})

rate constants can be calculated from the resulting binding curves using the BIAevaluation software available through the vendor. Data can then be fit to a 1:1 binding model, which includes a term to correct for mass transport limited binding, should it be detected. From these rate constants, the apparent dissociation binding constant (K_D) for the interaction of the antibody (e.g., IgG) with the antigen (e.g., SARS-CoV-2 spike) can be calculated from the quotient of k_{off}/k_{on}. Low-affinity antibodies generally bind antigen slowly and tend to dissociate readily, whereas high-affinity antibodies generally bind antigen faster and tend to remain bound longer. A variety of methods of measuring binding affinity are known in the art, any of which can be used for purposes of the described herein.

[0159] In another embodiment, an antibody described herein binds to SARS-CoV-2 spike protein present in the virion particle. In one embodiment, an antibody described herein binds to a SARS-CoV-2 spike protein on the surface of a cell infected with SARS-CoV-2.

[0160] In some embodiments, an antibody described herein binds to SARS-CoV-2 spike protein as assessed by techniques known in the art, e.g., ELISA, Western blot, biolayer interferometry, FACS or BIACore, or described herein. In other embodiments, an antibody described herein does not cross-react with spike protein from another type of coronavirus (e.g., other betacoronaviruses) as assessed by techniques known in the art, e.g., ELISA, Western blot, biolayer interferometry, FACS or BIACore, or described herein. In certain embodiments, provided herein is an antibody that selectively binds to SARS-CoV-2 spike protein relative to a spike protein of another type of coronavirus as assessed by techniques known in the art, e.g., ELISA, Western blot, biolayer interferometry, FACS or BIACore, or described herein. In some embodiments, provided herein is an antibody that selectively binds to SARS-CoV-2 spike protein relative to a spike protein of other betacoronaviruses as assessed by techniques known in the art, e.g., ELISA, Western blot, biolayer interferometry, FACS or BIACore, or described herein. In certain embodiments, provided herein is an antibody that selectively binds to SARS-CoV-2 spike protein relative to a surface protein of a non-coronavirus as assessed by techniques known in the art, e.g., ELISA, Western blot, biolayer interferometry, FACS or BIACore, or described herein.

[0161] In certain embodiments, an antibody that binds to a SARS-CoV-2 spike protein inhibits the binding of the spike protein to a host cell receptor. In certain embodiments, an antibody that binds to a SARS-CoV-2 spike protein inhibits the binding of the spike protein to a host cell receptor (e.g., human receptor angiotensin converting enzyme 2 (ACE2)). The inhibition of binding may be complete or partial as assessed by a technique known to one of skill in the art or described herein.

[0162] In another aspect, an antibody provided herein has one, two or more, or all of the characteristics/properties of one of the antibodies described herein (e.g., an antibody described in Section 5, infra). For example, in certain embodiments, an antibody described herein has neutralizing activity as assessed by a technique known to one of skill in the art.

[0163] In another aspect, an antibody described herein binds to the receptor binding domain of SARS-CoV-2 spike protein or a fragment thereof as assessed by a technique known to one of skill in the art or described herein. For example, an antibody described herein binds to a fragment of the SARS-CoV-2 spike protein comprising the receptor binding domain. Such fragment may comprise amino acid resides 258 to 572 or amino acid residues 498-572 of the SARS-CoV-2 spike protein.

[0164] As used herein, the terms "variable region" or "variable domain" are used interchangeably and are common in the art. The variable region typically refers to a portion of an antibody, generally, a portion of a light or heavy chain, typically about the amino-terminal 110 to 120 amino acids in a mature heavy chain and about the amino-terminal 90 to 100 amino acids in a mature light chain, which differs extensively in sequence among antibodies and is used in the binding and specificity of a particular antibody for its particular antigen. The variability in sequence is concentrated in those regions called complementarity determining regions (CDRs) while the more highly conserved regions in the variable domain are called framework regions (FR). CDRs are flanked by FRs. Generally, the spatial orientation of CDRs and FRs are as follows, in an N-terminal to C-terminal direction: FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4. Without wishing to be bound by any particular mechanism or theory, it is believed that the CDRs of the light and heavy chains are primarily responsible for the interaction and specificity of the antibody with antigen. In certain embodiments, the variable region is a rodent (e.g., mouse or rat) variable region. In certain embodiments, the variable region is a human variable region. In certain embodiments, the variable region comprises rodent (e.g., mouse or rat) CDRs and human framework regions (FRs). In some embodiments, the variable region is a primate (e.g., non-human primate) variable region. In certain embodiments, the variable region comprises rodent or murine CDRs and primate (e.g., non-human primate) framework regions (FRs).

[0165] In another aspect, an antibody provided herein comprises one, two or three of the complementarity determining regions (CDRs) of the variable heavy chain region ("VH" domain) or one, two or three of the CDRs of the variable light chain region ("VL" domain) of an antibody described herein. In another aspect, an antibody provided herein comprises one, two or three of the complementarity determining regions (CDRs) of the variable heavy chain region ("VH" domain) and one, two or three of the CDRs of the variable light chain region ("VL" domain) of an antibody described herein. In another aspect, an antibody provided herein comprises the complementarity determining regions (CDRs) of the variable heavy chain region ("VH" domain) and the CDRs of the variable light chain region ("VL" domain) of an antibody described herein.

[0166] In certain aspects, the CDRs of an antibody can be determined according to the Kabat numbering system. The terms "Kabat numbering," and like terms are recognized in the art and refer to a system of numbering amino acid residues in the heavy and light chain variable regions of an antibody, or an antigen-binding portion thereof. In certain aspects, the CDRs of an antibody can be determined according to the Kabat numbering system (see, e.g., Kabat et al. (1971) Ann. NY Acad. Sci. 190:382-391 and, Kabat et al. (1991) Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242). With respect to the Kabat numbering system, (i) the VH CDR1 is typically present at amino acid positions 31 to 35 of the heavy chain,

which can optionally include one or two additional amino acids following amino acid position 35 (referred to in the Kabat numbering scheme as 35A and 35B); (ii) the VH CDR2 is typically present at amino acid positions 50 to 65 of the heavy chain; and (iii) the VH CDR2 is typically present at amino acid positions 95 to 102 of the heavy chain (Kabat, Elvin A. et al., Sequences of Proteins of Immunological Interest. Bethesda: National Institutes of Health, 1983). With respect to the Kabat numbering system, (i) the VL CDR1 is typically present at amino acid positions 24 to 34 of the light chain; (ii) the VL CDR2 is typically present at amino acid positions 50 to 56 of the light chain; and (iii) the VL CDR3 is typically present at amino acid positions 89 to 97 of the light chain (Kabat, Elvin A. et al., Sequences of Proteins of Immunological Interest. Bethesda: National Institutes of Health, 1983). As is well known to those of skill in the art, using the Kabat numbering system, the actual linear amino acid sequence of the antibody variable domain can contain fewer or additional amino acids due to a shortening or lengthening of a FR and/or CDR and, as such, an amino acid's Kabat number is not necessarily the same as its linear amino acid number.

[0167] In certain aspects, the CDRs of an antibody can be determined according to the Chothia numbering scheme, which refers to the location of immunoglobulin structural loops (see, e.g., Chothia and Lesk, 1987, J. Mol. Biol., 196:901-917; Al-Lazikani et al., 1997, J. Mol. Biol., 273: 927-948; Chothia et al., 1992, J. Mol. Biol., 227:799-817; Tramontano A et al., 1990, J. Mol. Biol. 215(1):175-82; and U.S. Pat. No. 7,709,226). The Chothia definition is based on the location of the structural loop regions (Chothia et al., (1987) J Mol Biol 196: 901-917; and U.S. Pat. No. 7,709, 226). The term "Chothia CDRs," and like terms are recognized in the art and refer to antibody CDR sequences as determined according to the method of Chothia and Lesk, 1987, J. Mol. Biol., 196:901-917, which will be referred to herein as the "Chothia CDRs" (see also, e.g., U.S. Pat. No. 7,709,226 and Martin, A., "Protein Sequence and Structure Analysis of Antibody Variable Domains," in Antibody Engineering, Kontermann and DObe, eds., Chapter 31, pp. 422-439, Springer-Verlag, Berlin (2001)). With respect to the Chothia numbering system, using the Kabat numbering system of numbering amino acid residues in the VH region, (i) the VH CDR1 is typically present at amino acid positions 26 to 32 of the heavy chain; (ii) the VH CDR2 is typically present at amino acid positions 53 to 55 of the heavy chain; and (iii) the VH CDR3 is typically present at amino acid positions 96 to 101 of the heavy chain. In one embodiment, with respect to the Chothia numbering system, using the Kabat numbering system of numbering amino acid residues in the VH region, (i) the VH CDR1 is typically present at amino acid positions 26 to 32 or 34 of the heavy chain; (ii) the VH CDR2 is typically present at amino acid positions 52 to 56 (in one embodiment, CDR2 is at positions 52A-56, wherein 52A follows position 52) of the heavy chain; and (iii) the VH CDR3 is typically present at amino acid positions 95 to 102 of the heavy chain (in one embodiment, there is no amino acid at positions numbered 96-100). With respect to the Chothia numbering system, using the Kabat numbering system of numbering amino acid residues in the VL region, (i) the VL CDR1 is typically present at amino acid positions 26 to 33 of the light chain; (ii) the VL CDR2 is typically present at amino acid positions 50 to 52 of the light chain; and (iii) the VL CDR3 is typically present at amino acid positions 91 to 96 of the light chain. In one embodiment, with respect to the Chothia numbering system, using the Kabat numbering system of numbering amino acid residues in the VL region, (i) the VL CDR1 is typically present at amino acid positions 24 to 34 of the light chain; (ii) the VL CDR2 is typically present at amino acid positions 50 to 56 of the light chain; and (iii) the VL CDR3 is typically present at amino acid positions 89 to 97 of the light chain (in one embodiment, there is no amino acid at positions numbered 96-100). These Chothia CDR positions may vary depending on the antibody, and may be determined according to methods known in the art.

[0168] In certain aspects, the CDRs of an antibody can be determined according to the IMGT numbering system as described in Lefranc, M.-P., 1999, The Immunologist, 7:132-136 and Lefranc, M.-P. et al., 1999, Nucleic Acids Res., 27:209-212. The IMGT definition is from the IMGT ("IMGT®, the international ImMunoGeneTics information System® website imgt.org, founder and director: Marie-Paule Lefranc, Montpellier, France; see, e.g., Lefranc, M.-P., 1999, The Immunologist, 7:132-136 and Lefranc, M.-P. et al., 1999, Nucleic Acids Res., 27:209-212, both of which are incorporated herein by reference in their entirety). With respect to the IMGT numbering system, (i) the VH CDR1 is typically present at amino acid positions 25 to 35 of the heavy chain; (ii) the VH CDR2 is typically present at amino acid positions 51 to 57 of the heavy chain; and (iii) the VH CDR2 is typically present at amino acid positions 93 to 102 of the heavy chain. With respect to the IMGT numbering system, (i) the VL CDR1 is typically present at amino acid positions 27 to 32 of the light chain; (ii) the VL CDR2 is typically present at amino acid positions 50 to 52 of the light chain; and (iii) the VL CDR3 is typically present at amino acid positions 89 to 97 of the light chain.

[0169] In certain aspects, the CDRs of an antibody can be determined according to MacCallum et al., 1996, J. Mol. Biol., 262:732-745. See also, e.g., Martin, A., "Protein Sequence and Structure Analysis of Antibody Variable Domains," in *Antibody Engineering*, Kontermann and Dübel, eds., Chapter 31, pp. 422-439, Springer-Verlag, Berlin (2001).

[0170] In certain aspects, the CDRs of an antibody can be determined according to the AbM numbering scheme, which refers AbM hypervariable regions which represent a compromise between the Kabat CDRs and Chothia structural loops, and are used by Oxford Molecular's AbM antibody modeling software. A person of ordinary skill in the art would be able to determine the CDRs and framework regions of the variable regions of the 2B3, 1C7C7 or 22C7C4 antibody sequence based on known numbering systems, such as the Kabat numbering system, Chothia system, Oxford's AbM system, and/or contact system.

[0171] A person skilled in the art would be able to identify the CDRs of the provided variable region sequences using techniques known to a person skilled in the art, such as described herein. In one embodiment, the position of a CDR along the VH and/or VL domain of an antibody described herein may vary by one, two, three or four amino acid positions so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA). For example, in one embodiment, the position defining a CDR of antibody described

herein may vary by shifting the N-terminal and/or C-terminal boundary of the CDR by one, two, three, or four amino acids, relative to the CDR position, so long as binding to herein SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA).

[0172] In another aspect, provided herein are antibodies that bind to SARS-CoV-2 spike protein comprising one, two or three complementarity determining regions (CDRs) of the variable heavy chain region of an antibody described herein (e.g., antibody number 1 in Table 1) and one, two or three CDRs of the variable light chain region of that antibody (e.g., antibody number 1 in Table 2). In certain embodiments, an antibody that binds to a SARS-CoV-2 spike protein, comprises (or alternatively, consists of) a VH CDR1 and a VL CDR1; a VH CDR1 and a VL CDR2; a VH CDR1 and a VL CDR3; a VH CDR2 and a VL CDR1; VH CDR2 and a VL CDR2; a VH CDR2 and a VL CDR3; a VH CDR3 and a VL CDR1; a VH CDR3 and a VL CDR2; a VH CDR3 and a VL CDR3; a VH1 CDR1, a VH CDR2 and a VL CDR1; a VH CDR1, a VH CDR2 and a VL CDR2; a VH CDR1, a VH CDR2 and a VL CDR3; a VH CDR2, a VH CDR3 and a VL CDR1; a VH CDR2, a VH CDR3 and a VL CDR2; a VH CDR2, a VH CDR3 and a VL CDR3; a VH CDR1, a VL CDR1 and a VL CDR2; a VH CDR1, a VL CDR1 and a VL CDR3; a VH CDR2, a VL CDR1 and a VL CDR2; a VH CDR2, a VL CDR1 and a VL CDR3; a VH CDR3, a VL CDR1 and a VL CDR2; a VH CDR3, a VL CDR1 and a VL CDR3; a VH CDR1, a VH CDR2, a VH CDR3 and a VL CDR1; a VH CDR1, a VH CDR2, a VH CDR3 and a VL CDR2; a VH CDR1, a VH CDR2, a VH CDR3 and a VL CDR3; a VH CDR1, a VH CDR2, a VL CDR1 and a VL CDR2; a VH CDR1, a VH CDR2, a VL CDR1 and a VL CDR3; a VH CDR1, a VH CDR3, a VL CDR1 and a VL CDR2; a VH CDR1, a VH CDR3, a VL CDR1 and a VL CDR3; a VH CDR2, a VH CDR3, a VL CDR1 and a VL CDR2; a VH CDR2, a VH CDR3, a VL CDR1 and a VL CDR3; a VH CDR2, a VH CDR3, a VL CDR2 and a VL CDR3; a VH CDR1, a VH CDR2, a VH CDR3, a VL CDR1 and a VL CDR2; a VH CDR1, a VH CDR2, a VH CDR3, a VL CDR1 and a VL CDR3; a VH CDR1, a VH CDR2, a VL CDR1, a VL CDR2, and a VL CDR3; a VH CDR1, a VH CDR3, a VL CDR1, a VL CDR2, and a VL CDR3; a VH CDR2, a VH CDR3, a VL CDR1, a VL CDR2, and a VL CDR3; a VH CDR1, VH CDR2, a VH CDR3, a VL CDR1, a VL CDR2, and a VL CDR3; or any combination thereof of the VH CDRs and VL CDRs of an antibody described herein (e.g., antibody number 1 in Tables 1 and 2).

[0173] In one embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising the three CDRs of the variable heavy chain region of antibody number 1 in Table 1 and the three CDRs of the variable light chain region of antibody number 1 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising the three CDRs of the variable heavy chain region of antibody number 2 in Table 1 and the three CDRs of the variable light chain region of antibody number 2 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising the three CDRs of the variable heavy chain region of antibody number 3 in Table 1 and the three CDRs of the variable light chain region of antibody number 3 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising the three CDRs of the variable heavy chain region of antibody number 4 in Table 1 and the three CDRs of the variable light chain region of antibody number 4 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising the three CDRs of the variable heavy chain region of antibody number 5 in Table 1 and the three CDRs of the variable light chain region of antibody number 5 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising the three CDRs of the variable heavy chain region of antibody number 6 in Table 1 and the three CDRs of the variable light chain region of antibody number 6 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising the three CDRs of the variable heavy chain region of antibody number 7 in Table 1 and the three CDRs of the variable light chain region of antibody number 7 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising the three CDRs of the variable heavy chain region of antibody number 8 in Table 1 and the three CDRs of the variable light chain region of antibody number 8 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising the three CDRs of the variable heavy chain region of antibody number 9 in Table 1 and the three CDRs of the variable light chain region of antibody number 9 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising the three CDRs of the variable heavy chain region of antibody number 10 in Table 1 and the three CDRs of the variable light chain region of antibody number 10 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising the three CDRs of the variable heavy chain region of antibody number 11 in Table 1 and the three CDRs of the variable light chain region of antibody number 11 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising the three CDRs of the variable heavy chain region of antibody number 12 in Table 1 and the three CDRs of the variable light chain region of antibody number 12 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising the three CDRs of the variable heavy chain region of antibody number 13 in Table 1 and the three CDRs of the variable light chain region of antibody number 13 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising the three CDRs of the variable heavy chain region of antibody number 14 in Table 1 and the three CDRs of the variable light chain region of antibody number 14 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising the three CDRs of the variable heavy chain region of antibody number 15 in Table 1 and the three CDRs of the variable light chain region of antibody number 15 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising the three CDRs of the variable heavy chain region of antibody number 16 in Table 1 and the three CDRs of the variable light chain region of antibody number 16 in Table

2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising the three CDRs of the variable heavy chain region of antibody number 17 in Table 1 and the three CDRs of the variable light chain region of antibody number 17 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising the three CDRs of the variable heavy chain region of antibody number 18 in Table 1 and the three CDRs of the variable light chain region of antibody number 18 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising the three CDRs of the variable heavy chain region of antibody number 19 in Table 1 and the three CDRs of the variable light chain region of antibody number 19 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising the three CDRs of the variable heavy chain region of antibody number 20 in Table 1 and the three CDRs of the variable light chain region of antibody number 20 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising the three CDRs of the variable heavy chain region of antibody number 21 in Table 1 and the three CDRs of the variable light chain region of antibody number 21 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising the three CDRs of the variable heavy chain region of antibody number 22 in Table 1 and the three CDRs of the variable light chain region of antibody number 22 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising the three CDRs of the variable heavy chain region of antibody number 23 in Table 1 and the three CDRs of the variable light chain region of antibody number 23 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising the three CDRs of the variable heavy chain region of antibody number 24 in Table 1 and the three CDRs of the variable light chain region of antibody number 24 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising the three CDRs of the variable heavy chain region of antibody number 25 in Table 1 and the three CDRs of the variable light chain region of antibody number 25 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising the three CDRs of the variable heavy chain region of antibody number 26 in Table 1 and the three CDRs of the variable light chain region of antibody number 26 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising the three CDRs of the variable heavy chain region of antibody number 27 in Table 1 and the three CDRs of the variable light chain region of antibody number 27 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising the three CDRs of the variable heavy chain region of antibody number 28 in Table 1 and the three CDRs of the variable light chain region of antibody number 28 in Table 2. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising the three CDRs of the variable heavy chain region of antibody number 29 in Table 1 and the three CDRs of the variable light chain region of antibody number 29 in Table 2.

[0174] In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, or CDR3 of the variable heavy chain region of antibody number 1 in Table 6 and CDR1, CDR2, or CDR3 of the variable light chain region of antibody number 1 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising two of CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 1 in Table 6 and two of CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 1 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 1 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 1 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 1 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 1 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain one, two, three or four amino acid substitutions (e.g., a conservative amino acid substitution) so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA). In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 1 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 1 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain are one, two or three amino acid residues longer or shorter at the N-terminus, C-terminus or both so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA).

[0175] In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, or CDR3 of the variable heavy chain region of antibody number 2 in Table 6 and CDR1, CDR2, or CDR3 of the variable light chain region of antibody number 2 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising two of CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 2 in Table 6 and two of CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 2 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 2 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 2 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 2 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 2 in

Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain one, two, three or four amino acid substitutions (e.g., a conservative amino acid substitution) so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA). In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 2 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 2 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain are one, two or three amino acid residues longer or shorter at the N-terminus, C-terminus or both so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA).

[0176] In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, or CDR3 of the variable heavy chain region of antibody number 3 in Table 6 and CDR1, CDR2, or CDR3 of the variable light chain region of antibody number 3 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising two of CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 3 in Table 6 and two of CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 3 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 3 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 3 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 3 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 3 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain one, two, three or four amino acid substitutions (e.g., a conservative amino acid substitution) so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA). In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 3 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 3 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain are one, two or three amino acid residues longer or shorter at the N-terminus, C-terminus or both so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA).

[0177] In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, or CDR3 of the variable heavy chain region of antibody number 4 in Table 6 and CDR1, CDR2, or CDR3 of the variable light chain region of antibody number 4 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising two of CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 4 in Table 6 and two of CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 4 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 4 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 4 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 4 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 4 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain one, two, three or four amino acid substitutions (e.g., a conservative amino acid substitution) so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA). In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 4 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 4 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain are one, two or three amino acid residues longer or shorter at the N-terminus, C-terminus or both so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA).

[0178] In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, or CDR3 of the variable heavy chain region of antibody number 5 in Table 6 and CDR1, CDR2, or CDR3 of the variable light chain region of antibody number 5 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising two of CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 5 in Table 6 and two of CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 5 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 5 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 5 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1,

CDR2, and CDR3 of the variable heavy chain region of antibody number 5 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 5 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain one, two, three or four amino acid substitutions (e.g., a conservative amino acid substitution) so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA). In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 5 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 5 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain are one, two or three amino acid residues longer or shorter at the N-terminus, C-terminus or both so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA).

[0179] In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, or CDR3 of the variable heavy chain region of antibody number 6 in Table 6 and CDR1, CDR2, or CDR3 of the variable light chain region of antibody number 6 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising two of CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 6 in Table 6 and two of CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 6 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 6 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 6 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 6 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 6 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain one, two, three or four amino acid substitutions (e.g., a conservative amino acid substitution) so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA). In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 6 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 6 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain are one, two or three amino acid residues longer or shorter at the N-terminus, C-terminus or both so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA).

[0180] In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, or CDR3 of the variable heavy chain region of antibody number 7 in Table 6 and CDR1, CDR2, or CDR3 of the variable light chain region of antibody number 7 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising two of CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 7 in Table 6 and two of CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 7 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 7 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 7 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 7 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 7 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain one, two, three or four amino acid substitutions (e.g., a conservative amino acid substitution) so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA). In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 7 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 7 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain are one, two or three amino acid residues longer or shorter at the N-terminus, C-terminus or both so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA).

[0181] In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, or CDR3 of the variable heavy chain region of antibody number 8 in Table 6 and CDR1, CDR2, or CDR3 of the variable light chain region of antibody number 8 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising two of CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 8 in Table 6 and two of CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 8 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 8 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 8 in Table 8. In another embodiment, provided herein is an antibody that

binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 8 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 8 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain one, two, three or four amino acid substitutions (e.g., a conservative amino acid substitution) so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA). In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 8 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 8 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain are one, two or three amino acid residues longer or shorter at the N-terminus, C-terminus or both so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA).

[0182] In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, or CDR3 of the variable heavy chain region of antibody number 9 in Table 6 and CDR1, CDR2, or CDR3 of the variable light chain region of antibody number 9 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising two of CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 9 in Table 6 and two of CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 9 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 9 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 9 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 9 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 9 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain one, two, three or four amino acid substitutions (e.g., a conservative amino acid substitution) so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA). In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 9 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 9 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain are one, two or three amino acid residues longer or shorter at the N-terminus, C-terminus or both so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA).

[0183] In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, or CDR3 of the variable heavy chain region of antibody number 10 in Table 6 and CDR1, CDR2, or CDR3 of the variable light chain region of antibody number 10 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising two of CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 10 in Table 6 and two of CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 10 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 10 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 10 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 10 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 10 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain one, two, three or four amino acid substitutions (e.g., a conservative amino acid substitution) so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA). In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 10 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 10 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain are one, two or three amino acid residues longer or shorter at the N-terminus, C-terminus or both so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA).

[0184] In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, or CDR3 of the variable heavy chain region of antibody number 11 in Table 6 and CDR1, CDR2, or CDR3 of the variable light chain region of antibody number 11 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising two of CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 11 in Table 6 and two of CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 11 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 11 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 11 in Table

8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 11 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 11 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain one, two, three or four amino acid substitutions (e.g., a conservative amino acid substitution) so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA). In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 11 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 11 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain are one, two or three amino acid residues longer or shorter at the N-terminus, C-terminus or both so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA).

[0185] In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, or CDR3 of the variable heavy chain region of antibody number 12 in Table 6 and CDR1, CDR2, or CDR3 of the variable light chain region of antibody number 12 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising two of CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 12 in Table 6 and two of CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 12 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 12 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 12 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 12 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 12 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain one, two, three or four amino acid substitutions (e.g., a conservative amino acid substitution) so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA). In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 12 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 12 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain are one, two or three amino acid residues longer or shorter at the N-terminus, C-terminus or both so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA).

[0186] In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, or CDR3 of the variable heavy chain region of antibody number 13 in Table 6 and CDR1, CDR2, or CDR3 of the variable light chain region of antibody number 13 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising two of CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 13 in Table 6 and two of CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 13 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 13 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 13 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 13 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 13 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain one, two, three or four amino acid substitutions (e.g., a conservative amino acid substitution) so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA). In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 13 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 13 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain are one, two or three amino acid residues longer or shorter at the N-terminus, C-terminus or both so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA).

[0187] In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, or CDR3 of the variable heavy chain region of antibody number 14 in Table 6 and CDR1, CDR2, or CDR3 of the variable light chain region of antibody number 14 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising two of CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 14 in Table 6 and two of CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 14 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 14 in Table 6 and CDR1, CDR2, and CDR3 of the

variable light chain region of antibody number 14 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 14 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 14 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain one, two, three or four amino acid substitutions (e.g., a conservative amino acid substitution) so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA). In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 14 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 14 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain are one, two or three amino acid residues longer or shorter at the N-terminus, C-terminus or both so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA).

[0188] In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, or CDR3 of the variable heavy chain region of antibody number 15 in Table 6 and CDR1, CDR2, or CDR3 of the variable light chain region of antibody number 15 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising two of CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 15 in Table 6 and two of CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 15 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 15 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 15 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 15 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 15 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain one, two, three or four amino acid substitutions (e.g., a conservative amino acid substitution) so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA). In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 15 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 15 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain are one, two or three amino acid residues longer or shorter at the N-terminus, C-terminus or both so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA).

[0189] In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, or CDR3 of the variable heavy chain region of antibody number 16 in Table 6 and CDR1, CDR2, or CDR3 of the variable light chain region of antibody number 16 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising two of CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 16 in Table 6 and two of CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 16 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 16 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 16 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 16 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 16 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain one, two, three or four amino acid substitutions (e.g., a conservative amino acid substitution) so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA). In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 16 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 16 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain are one, two or three amino acid residues longer or shorter at the N-terminus, C-terminus or both so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA).

[0190] In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, or CDR3 of the variable heavy chain region of antibody number 17 in Table 6 and CDR1, CDR2, or CDR3 of the variable light chain region of antibody number 17 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising two of CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 17 in Table 6 and two of CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 17 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody

number 17 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 17 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 17 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 17 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain one, two, three or four amino acid substitutions (e.g., a conservative amino acid substitution) so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA). In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 17 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 17 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain are one, two or three amino acid residues longer or shorter at the N-terminus, C-terminus or both so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA).

[0191] In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, or CDR3 of the variable heavy chain region of antibody number 18 in Table 6 and CDR1, CDR2, or CDR3 of the variable light chain region of antibody number 18 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising two of CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 18 in Table 6 and two of CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 18 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 18 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 18 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 18 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 18 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain one, two, three or four amino acid substitutions (e.g., a conservative amino acid substitution) so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA). In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 18 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 18 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain are one, two or three amino acid residues longer or shorter at the N-terminus, C-terminus or both so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA).

[0192] In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, or CDR3 of the variable heavy chain region of antibody number 19 in Table 6 and CDR1, CDR2, or CDR3 of the variable light chain region of antibody number 19 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising two of CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 19 in Table 6 and two of CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 19 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 19 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 19 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 19 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 19 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain one, two, three or four amino acid substitutions (e.g., a conservative amino acid substitution) so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA). In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 19 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 19 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain are one, two or three amino acid residues longer or shorter at the N-terminus, C-terminus or both so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA).

[0193] In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, or CDR3 of the variable heavy chain region of antibody number 20 in Table 6 and CDR1, CDR2, or CDR3 of the variable light chain region of antibody number 20 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising two of CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 20 in Table 6 and two of CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 20 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and

CDR3 of the variable heavy chain region of antibody number 20 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 20 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 20 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 20 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain one, two, three or four amino acid substitutions (e.g., a conservative amino acid substitution) so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA). In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 20 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 20 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain are one, two or three amino acid residues longer or shorter at the N-terminus, C-terminus or both so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA).

[0194] In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, or CDR3 of the variable heavy chain region of antibody number 21 in Table 6 and CDR1, CDR2, or CDR3 of the variable light chain region of antibody number 21 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising two of CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 21 in Table 6 and two of CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 21 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 21 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 21 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 21 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 21 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain one, two, three or four amino acid substitutions (e.g., a conservative amino acid substitution) so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA). In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 21 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 21 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain are one, two or three amino acid residues longer or shorter at the N-terminus, C-terminus or both so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA).

[0195] In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, or CDR3 of the variable heavy chain region of antibody number 22 in Table 6 and CDR1, CDR2, or CDR3 of the variable light chain region of antibody number 22 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising two of CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 22 in Table 6 and two of CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 22 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 22 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 22 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 22 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 22 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain one, two, three or four amino acid substitutions (e.g., a conservative amino acid substitution) so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA). In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 22 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 22 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain are one, two or three amino acid residues longer or shorter at the N-terminus, C-terminus, or both so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA).

[0196] In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, or CDR3 of the variable heavy chain region of antibody number 23 in Table 6 and CDR1, CDR2, or CDR3 of the variable light chain region of antibody number 23 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising two of CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 23 in Table 6 and two of CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 23 in Table 8. In another embodiment, provided herein is an antibody that binds to

SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 23 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 23 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 23 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 23 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain one, two, three or four amino acid substitutions (e.g., a conservative amino acid substitution) so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA). In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 23 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 23 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain are one, two or three amino acid residues longer or shorter at the N-terminus, C-terminus or both so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA).

[0197] In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, or CDR3 of the variable heavy chain region of antibody number 24 in Table 6 and CDR1, CDR2, or CDR3 of the variable light chain region of antibody number 24 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising two of CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 24 in Table 6 and two of CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 24 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 24 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 24 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 24 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 24 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain one, two, three or four amino acid substitutions (e.g., a conservative amino acid substitution) so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA). In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 24 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 24 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain are one, two or three amino acid residues longer or shorter at the N-terminus, C-terminus or both so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA).

[0198] In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, or CDR3 of the variable heavy chain region of antibody number 25 in Table 6 and CDR1, CDR2, or CDR3 of the variable light chain region of antibody number 25 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising two of CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 25 in Table 6 and two of CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 25 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 25 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 25 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 25 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 25 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain one, two, three or four amino acid substitutions (e.g., a conservative amino acid substitution) so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA). In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 25 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 25 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain are one, two or three amino acid residues longer or shorter at the N-terminus, C-terminus or both so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA).

[0199] In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, or CDR3 of the variable heavy chain region of antibody number 26 in Table 6 and CDR1, CDR2, or CDR3 of the variable light chain region of antibody number 26 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising two of CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 26 in Table 6 and two of CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 26 in Table 8. In another

embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 26 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 26 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 26 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 26 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain one, two, three or four amino acid substitutions (e.g., a conservative amino acid substitution) so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA). In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 26 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 26 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain are one, two or three amino acid residues longer or shorter at the N-terminus, C-terminus or both so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA).

[0200] In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, or CDR3 of the variable heavy chain region of antibody number 27 in Table 6 and CDR1, CDR2, or CDR3 of the variable light chain region of antibody number 27 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising two of CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 27 in Table 6 and two of CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 27 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 27 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 27 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 27 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 27 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain one, two, three or four amino acid substitutions (e.g., a conservative amino acid substitution) so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA). In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 27 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 27 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain are one, two or three amino acid residues longer or shorter at the N-terminus, C-terminus or both so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA).

[0201] In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, or CDR3 of the variable heavy chain region of antibody number 28 in Table 6 and CDR1, CDR2, or CDR3 of the variable light chain region of antibody number 28 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising two of CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 28 in Table 6 and two of CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 28 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 28 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 28 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 28 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 28 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain one, two, three or four amino acid substitutions (e.g., a conservative amino acid substitution) so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA). In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 28 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 28 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain are one, two or three amino acid residues longer or shorter at the N-terminus, C-terminus or both so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA).

[0202] In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, or CDR3 of the variable heavy chain region of antibody number 29 in Table 6 and CDR1, CDR2, or CDR3 of the variable light chain region of antibody number 29 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising two of CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 29 in Table 6 and two of CDR1, CDR2, and CDR3 of the variable light

chain region of antibody number 29 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 29 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 29 in Table 8. In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 29 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 29 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain one, two, three or four amino acid substitutions (e.g., a conservative amino acid substitution) so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA). In another embodiment, provided herein is an antibody that binds to SARS-CoV-2 spike protein comprising CDR1, CDR2, and CDR3 of the variable heavy chain region of antibody number 29 in Table 6 and CDR1, CDR2, and CDR3 of the variable light chain region of antibody number 29 in Table 8, wherein one, two or three of the CDRs of the variable heavy chain region, the variable light chain region, or both contain are one, two or three amino acid residues longer or shorter at the N-terminus, C-terminus or both so long as binding to SARS-CoV-2 spike protein is maintained or substantially maintained (for example, by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% in an assay known in the art or described herein, such as an ELISA).

[0203] In certain embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises a variable heavy chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable heavy chain region of an antibody described herein (e.g., an antibody in Table 1). In some embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises a variable light chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable light chain region of an antibody described herein (e.g., an antibody in Table 2). In certain embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable heavy chain region of an antibody described herein (e.g., an antibody in Table 1) and (b) a variable light chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%95%, 96%, 97% or 98% identical to the amino acid sequence of a variable light chain region of an antibody described herein (e.g., an antibody in Table 2). In accordance with these embodiments, the CDRs of the antibody may, in certain embodiments, be identical to one, two, three, four, five, or all six of the CDRs of the antibody described herein.

[0204] In certain embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable heavy chain region of antibody number 1 in Table 1; and (b) a variable light chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable light chain region of antibody number 1 in Table 2. In accordance with these embodiments, the CDRs of the antibody may, in certain embodiments, be identical to one, two, three, four, five, or all six of the CDRs of antibody number 1. In one embodiment, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising the amino acid sequence of a variable heavy chain region of antibody number 1 in Table 1; and (b) a variable light chain region comprising the amino acid sequence of a variable light chain region of antibody number 1 in Table 2.

[0205] In certain embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable heavy chain region of antibody number 2 in Table 1; and (b) a variable light chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable light chain region of antibody number 2 in Table 2. In accordance with these embodiments, the CDRs of the antibody may, in certain embodiments, be identical to one, two, three, four, five, or all six of the CDRs of antibody number 2. In one embodiment, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising the amino acid sequence of a variable heavy chain region of antibody number 2 in Table 1; and (b) a variable light chain region comprising the amino acid sequence of a variable light chain region of antibody number 2 in Table 2.

[0206] In certain embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable heavy chain region of antibody number 3 in Table 1; and (b) a variable light chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable light chain region of antibody number 3 in Table 2. In accordance with these embodiments, the CDRs of the antibody may, in certain embodiments, be identical to one, two, three, four, five, or all six of the CDRs of antibody number 3. In one embodiment, an antibody described herein,

which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising the amino acid sequence of a variable heavy chain region of antibody number 3 in Table 1; and (b) a variable light chain region comprising the amino acid sequence of a variable light chain region of antibody number 3 in Table 2.

[0207] In certain embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable heavy chain region of antibody number 4 in Table 1; and (b) a variable light chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable light chain region of antibody number 4 in Table 2. In accordance with these embodiments, the CDRs of the antibody may, in certain embodiments, be identical to one, two, three, four, five, or all six of the CDRs of antibody number 4. In one embodiment, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising the amino acid sequence of a variable heavy chain region of antibody number 4 in Table 1; and (b) a variable light chain region comprising the amino acid sequence of a variable light chain region of antibody number 4 in Table 2.

[0208] In certain embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable heavy chain region of antibody number 5 in Table 1; and (b) a variable light chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable light chain region of antibody number 5 in Table 2. In accordance with these embodiments, the CDRs of the antibody may, in certain embodiments, be identical to one, two, three, four, five, or all six of the CDRs of antibody number 5. In one embodiment, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising the amino acid sequence of a variable heavy chain region of antibody number 5 in Table 1; and (b) a variable light chain region comprising the amino acid sequence of a variable light chain region of antibody number 5 in Table 2.

[0209] In certain embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable heavy chain region of antibody number 6 in Table 1; and (b) a variable light chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable light chain region of antibody number 6 in Table 2. In accordance with these embodiments, the CDRs of the antibody may, in certain embodiments, be identical to one, two, three, four, five, or all six of the CDRs of antibody number 6. In one embodiment, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising the amino acid sequence of a variable heavy chain region of antibody number 6 in Table 1; and (b) a variable light chain region comprising the amino acid sequence of a variable light chain region of antibody number 6 in Table 2.

[0210] In certain embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable heavy chain region of antibody number 7 in Table 1; and (b) a variable light chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable light chain region of antibody number 7 in Table 2. In accordance with these embodiments, the CDRs of the antibody may, in certain embodiments, be identical to one, two, three, four, five, or all six of the CDRs of antibody number 7. In one embodiment, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising the amino acid sequence of a variable heavy chain region of antibody number 7 in Table 1; and (b) a variable light chain region comprising the amino acid sequence of a variable light chain region of antibody number 7 in Table 2.

[0211] In certain embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable heavy chain region of antibody number 8 in Table 1; and (b) a variable light chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable light chain region of antibody number 8 in Table 2. In accordance with these embodiments, the CDRs of the antibody may, in certain embodiments, be identical to one, two, three, four, five, or all six of the CDRs of antibody number 8. In one embodiment, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising the amino acid sequence of a variable heavy chain region of antibody number 8 in Table 1; and (b) a variable light chain region comprising the amino acid sequence of a variable light chain region of antibody number 8 in Table 2.

[0212] In certain embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino

acid sequence of a variable heavy chain region of antibody number 9 in Table 1; and (b) a variable light chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable light chain region of antibody number 9 in Table 2. In accordance with these embodiments, the CDRs of the antibody may, in certain embodiments, be identical to one, two, three, four, five, or all six of the CDRs of antibody number 9. In one embodiment, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising the amino acid sequence of a variable heavy chain region of antibody number 9 in Table 1; and (b) a variable light chain region comprising the amino acid sequence of a variable light chain region of antibody number 9 in Table 2.

[0213] In certain embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable heavy chain region of antibody number 10 in Table 1; and (b) a variable light chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable light chain region of antibody number 10 in Table 2. In accordance with these embodiments, the CDRs of the antibody may, in certain embodiments, be identical to one, two, three, four, five, or all six of the CDRs of the antibody number 10. In one embodiment, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising the amino acid sequence of a variable heavy chain region of antibody number 10 in Table 1; and (b) a variable light chain region comprising the amino acid sequence of a variable light chain region of antibody number 10 in Table 2.

[0214] In certain embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable heavy chain region of antibody number 11 in Table 1; and (b) a variable light chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable light chain region of antibody number 11 in Table 2. In accordance with these embodiments, the CDRs of the antibody may, in certain embodiments, be identical to one, two, three, four, five, or all six of the CDRs of the antibody number 11. In one embodiment, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising the amino acid sequence of a variable heavy chain region of antibody number 11 in Table 1; and (b) a variable light chain region comprising the amino acid sequence of a variable light chain region of antibody number 11 in Table 2.

[0215] In certain embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable heavy chain region of antibody number 12 in Table 1; and (b) a variable light chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable light chain region of antibody number 12 in Table 2. In accordance with these embodiments, the CDRs of the antibody may, in certain embodiments, be identical to one, two, three, four, five, or all six of the CDRs of the antibody number 12. In one embodiment, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising the amino acid sequence of a variable heavy chain region of antibody number 12 in Table 1; and (b) a variable light chain region comprising the amino acid sequence of a variable light chain region of antibody number 12 in Table 2.

[0216] In certain embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable heavy chain region of antibody number 13 in Table 1; and (b) a variable light chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable light chain region of antibody number 13 in Table 2. In accordance with these embodiments, the CDRs of the antibody may, in certain embodiments, be identical to one, two, three, four, five, or all six of the CDRs of the antibody number 13. In one embodiment, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising the amino acid sequence of a variable heavy chain region of antibody number 13 in Table 1; and (b) a variable light chain region comprising the amino acid sequence of a variable light chain region of antibody number 13 in Table 2.

[0217] In certain embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable heavy chain region of antibody number 14 in Table 1; and (b) a variable light chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable light chain region of antibody number 14 in Table 2. In accordance with these embodiments, the CDRs of the antibody may, in certain embodiments, be identical to one, two, three, four, five, or all six of the CDRs of the antibody number 14. In one embodiment, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable

heavy chain region comprising the amino acid sequence of a variable heavy chain region of antibody number 14 in Table 1; and (b) a variable light chain region comprising the amino acid sequence of a variable light chain region of antibody number 14 in Table 2.

[0218] In certain embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable heavy chain region of antibody number 15 in Table 1; and (b) a variable light chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable light chain region of antibody number 15 in Table 2. In accordance with these embodiments, the CDRs of the antibody may, in certain embodiments, be identical to one, two, three, four, five, or all six of the CDRs of the antibody number 15. In one embodiment, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising the amino acid sequence of a variable heavy chain region of antibody number 15 in Table 1; and (b) a variable light chain region comprising the amino acid sequence of a variable light chain region of antibody number 15 in Table 2.

[0219] In certain embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable heavy chain region of antibody number 16 in Table 1; and (b) a variable light chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable light chain region of antibody number 16 in Table 2. In accordance with these embodiments, the CDRs of the antibody may, in certain embodiments, be identical to one, two, three, four, five, or all six of the CDRs of the antibody number 16. In one embodiment, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising the amino acid sequence of a variable heavy chain region of antibody number 16 in Table 1; and (b) a variable light chain region comprising the amino acid sequence of a variable light chain region of antibody number 16 in Table 2.

[0220] In certain embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable heavy chain region of antibody number 17 in Table 1; and (b) a variable light chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable light chain region of antibody number 17 in Table 2. In accordance with these embodiments, the CDRs of the antibody may, in certain embodiments, be identical to one, two, three, four, five, or all six of the CDRs of the antibody number 17. In one embodiment, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising the amino acid sequence of a variable heavy chain region of antibody number 17 in Table 1; and (b) a variable light chain region comprising the amino acid sequence of a variable light chain region of antibody number 17 in Table 2.

[0221] In certain embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable heavy chain region of antibody number 18 in Table 1; and (b) a variable light chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable light chain region of antibody number 18 in Table 2. In accordance with these embodiments, the CDRs of the antibody may, in certain embodiments, be identical to one, two, three, four, five, or all six of the CDRs of the antibody number 18. In one embodiment, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising the amino acid sequence of a variable heavy chain region of antibody number 18 in Table 1; and (b) a variable light chain region comprising the amino acid sequence of a variable light chain region of antibody number 18 in Table 2.

[0222] In certain embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable heavy chain region of antibody number 19 in Table 1; and (b) a variable light chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable light chain region of antibody number 19 in Table 2. In accordance with these embodiments, the CDRs of the antibody may, in certain embodiments, be identical to one, two, three, four, five, or all six of the CDRs of the antibody number 19. In one embodiment, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising the amino acid sequence of a variable heavy chain region of antibody number 19 in Table 1; and (b) a variable light chain region comprising the amino acid sequence of a variable light chain region of antibody number 19 in Table 2.

[0223] In certain embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable heavy chain region of antibody number 20 in Table 1; and (b) a variable light chain region

comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable light chain region of antibody number 20 in Table 2. In accordance with these embodiments, the CDRs of the antibody may, in certain embodiments, be identical to one, two, three, four, five, or all six of the CDRs of the antibody number 20. In one embodiment, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising the amino acid sequence of a variable heavy chain region of antibody number 20 in Table 1; and (b) a variable light chain region comprising the amino acid sequence of a variable light chain region of antibody number 20 in Table 2.

[0224] In certain embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable heavy chain region of antibody number 21 in Table 1; and (b) a variable light chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable light chain region of antibody number 21 in Table 2. In accordance with these embodiments, the CDRs of the antibody may, in certain embodiments, be identical to one, two, three, four, five, or all six of the CDRs of the antibody number 21. In one embodiment, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising the amino acid sequence of a variable heavy chain region of antibody number 21 in Table 1; and (b) a variable light chain region comprising the amino acid sequence of a variable light chain region of antibody number 21 in Table 2.

[0225] In certain embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable heavy chain region of antibody number 22 in Table 1; and (b) a variable light chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable light chain region of antibody number 22 in Table 2. In accordance with these embodiments, the CDRs of the antibody may, in certain embodiments, be identical to one, two, three, four, five, or all six of the CDRs of the antibody number 22. In one embodiment, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising the amino acid sequence of a variable heavy chain region of antibody number 22 in Table 1; and (b) a variable light chain region comprising the amino acid sequence of a variable light chain region of antibody number 22 in Table 2.

[0226] In certain embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable heavy chain region of antibody number 23 in Table 1; and (b) a variable light chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable light chain region of antibody number 23 in Table 2. In accordance with these embodiments, the CDRs of the antibody may, in certain embodiments, be identical to one, two, three, four, five, or all six of the CDRs of the antibody number 23. In one embodiment, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising the amino acid sequence of a variable heavy chain region of antibody number 23 in Table 1; and (b) a variable light chain region comprising the amino acid sequence of a vaable light chain region of antibody number 23 in Table 2.

[0227] In certain embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable heavy chain region of antibody number 24 in Table 1; and (b) a variable light chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable light chain region of antibody number 24 in Table 2. In accordance with these embodiments, the CDRs of the antibody may, in certain embodiments, be identical to one, two, three, four, five, or all six of the CDRs of the antibody number 24. In one embodiment, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising the amino acid sequence of a variable heavy chain region of antibody number 24 in Table 1; and (b) a variable light chain region comprising the amino acid sequence of a variable light chain region of antibody number 24 in Table 2.

[0228] In certain embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable heavy chain region of antibody number 25 in Table 1; and (b) a variable light chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable light chain region of antibody number 25 in Table 2. In accordance with these embodiments, the CDRs of the antibody may, in certain embodiments, be identical to one, two, three, four, five, or all six of the CDRs of the antibody number 25. In one embodiment, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising the amino acid sequence of a variable heavy chain region of antibody number 25 in Table 1; and (b) a variable light chain region comprising the

amino acid sequence of a variable light chain region of antibody number 25 in Table 2.

[0229] In certain embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable heavy chain region of antibody number 26 in Table 1; and (b) a variable light chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable light chain region of antibody number 26 in Table 2. In accordance with these embodiments, the CDRs of the antibody may, in certain embodiments, be identical to one, two, three, four, five, or all six of the CDRs of the antibody number 26. In one embodiment, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising the amino acid sequence of a variable heavy chain region of antibody number 26 in Table 1; and (b) a variable light chain region comprising the amino acid sequence of a variable light chain region of antibody number 26 in Table 2.

[0230] In certain embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable heavy chain region of antibody number 27 in Table 1; and (b) a variable light chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable light chain region of antibody number 27 in Table 2. In accordance with these embodiments, the CDRs of the antibody may, in certain embodiments, be identical to one, two, three, four, five, or all six of the CDRs of the antibody number 27. In one embodiment, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising the amino acid sequence of a variable heavy chain region of antibody number 27 in Table 1; and (b) a variable light chain region comprising the amino acid sequence of a variable light chain region of antibody number 27 in Table 2.

[0231] In certain embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable heavy chain region of antibody number 28 in Table 1; and (b) a variable light chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable light chain region of antibody number 28 in Table 2. In accordance with these embodiments, the CDRs of the antibody may, in certain embodiments, be identical to one, two, three, four, five, or all six of the CDRs of the antibody number 28. In one embodiment, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising the amino acid sequence of a variable heavy chain region of antibody number 28 in Table 1; and (b) a variable light chain region comprising the amino acid sequence of a variable light chain region of antibody number 28 in Table 2.

[0232] In certain embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable heavy chain region of antibody number 29 in Table 1; and (b) a variable light chain region comprising an amino acid sequence that is at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97% or 98% identical to the amino acid sequence of a variable light chain region of antibody number 29 in Table 2. In accordance with these embodiments, the CDRs of the antibody may, in certain embodiments, be identical to one, two, three, four, five, or all six of the CDRs of the antibody number 29. In one embodiment, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises (a) a variable heavy chain region comprising the amino acid sequence of a variable heavy chain region of antibody number 29 in Table 1; and (b) a variable light chain region comprising the amino acid sequence of a variable light chain region of antibody number 29 in Table 2.

[0233] Techniques known to one of skill in the art can be used to determine the percent identity between two amino acid sequences or between two nucleotide sequences. Generally, to determine the percent identity of two amino acid sequences or of two nucleic acid sequences, the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in the sequence of a first amino acid or nucleic acid sequence for optimal alignment with a second amino acid or nucleic acid sequence). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position. The percent identity between the two sequences is a function of the number of identical positions shared by the sequences (i.e., % identity=number of identical overlapping positions/total number of positions×100%). In one embodiment, the two sequences are the same length. In a certain embodiment, the percent identity is determined over the entire length of an amino acid sequence or nucleotide sequence.

[0234] The determination of percent identity between two sequences (e.g., amino acid sequences or nucleic acid sequences) can also be accomplished using a mathematical algorithm. A preferred, non-limiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul, 1990, Proc. Natl. Acad. Sci. U.S.A. 87:2264 2268, modified as in Karlin and Altschul, 1993, Proc. Natl. Acad. Sci. U.S.A. 90:5873 5877. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul et al., 1990, J. Mol. Biol. 215:403. BLAST nucleotide searches can be performed with the NBLAST nucleotide program parameters set, e.g., for score=100, wordlength=12 to obtain

nucleotide sequences homologous to nucleic acid molecules described herein. BLAST protein searches can be performed with the XBLAST program parameters set, e.g., to score 50, wordlength=3 to obtain amino acid sequences homologous to a protein molecule described herein. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al., 1997, Nucleic Acids Res. 25:3389 3402. Alternatively, PSI BLAST can be used to perform an iterated search which detects distant relationships between molecules (Id.). When utilizing BLAST, Gapped BLAST, and PSI Blast programs, the default parameters of the respective programs (e.g., of XBLAST and NBLAST) can be used (see, e.g., National Center for Biotechnology Information (NCBI) on the world-wide web, ncbi.nlm.nih.gov). Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller, 1988, CABIOS 4:11 17. Such an algorithm is incorporated in the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used.

[0235] The percent identity between two sequences can be determined using techniques similar to those described above, with or without allowing gaps. In calculating percent identity, typically only exact matches are counted.

[0236] In some embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises the variable heavy chain region or variable light chain region of an antibody described herein (e.g., a variable heavy chain region or variable light chain region an antibody in Table 1 or 2, respectively) with one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15 or 20) amino acid substitutions (e.g., conservative amino acid substitutions), deletions, or additions. In certain embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises the variable heavy chain region and variable light chain region of an antibody described herein (e.g., a variable heavy chain region and variable light chain region an antibody with the same name in Tables 1 and 2) with one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, or 20) amino acid substitutions (e.g., conservative amino acid substitutions), deletions, or additions. In specific embodiments, none of the amino acid substitutions are located within the CDRs. In specific embodiments, all of the amino acid substitutions are in the framework regions.

[0237] As used herein, a "conservative amino acid substitution" has the meaning known to one of skill in the art. In one embodiment, a conservative amino acid substitution is one in which the amino acid residue is replaced with an amino acid residue having a side chain with a similar charge. Families of amino acid residues having side chains with similar charges have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine).

[0238] In one embodiment, an antibody provided herein comprises a variable heavy chain region and a variable light chain region, wherein the variable heavy chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody number 1 in Table 1 and the variable light chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody 1 in Table 2. In one embodiment, an antibody provided herein comprises a variable heavy chain region and a variable light chain region, wherein the variable heavy chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody number 2 in Table 1 and the variable light chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody 2 in Table 2. In one embodiment, an antibody provided herein comprises a variable heavy chain region and a variable light chain region, wherein the variable heavy chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody number 3 in Table 1 and the variable light chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody 3 in Table 2. In one embodiment, an antibody provided herein comprises a variable heavy chain region and a variable light chain region, wherein the variable heavy chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody number 3 in Table 1 and the variable light chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody 3 in Table 2. In one embodiment, an antibody provided herein comprises a variable heavy chain region and a variable light chain region, wherein the variable heavy chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody number 4 in Table 1 and the variable light chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody 4 in Table 2. In one embodiment, an antibody provided herein comprises a variable heavy chain region and a variable light chain region, wherein the variable heavy chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody number 5 in Table 1 and the variable light chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody 5 in Table 2. In one embodiment, an antibody provided herein comprises a variable heavy chain region and a variable light chain region, wherein the variable heavy chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody number 6 in Table 1 and the variable light chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody 6 in Table 2. In one embodiment, an antibody provided herein comprises a variable heavy chain region and a variable light chain region, wherein the variable heavy chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody number 7 in Table 1 and the variable light chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody 7 in Table 2. In one embodiment, an antibody provided herein comprises a variable heavy chain region and a variable light chain region, wherein the variable heavy chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody number 8 in Table 1 and the variable light chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody 8 in Table 2. In one embodiment, an antibody provided herein com-

prises a variable heavy chain region and a variable light chain region, wherein the variable heavy chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody number 9 in Table 1 and the variable light chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody 9 in Table 2. In one embodiment, an antibody provided herein comprises a variable heavy chain region and a variable light chain region, wherein the variable heavy chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody number 10 in Table 1 and the variable light chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody 10 in Table 2. In one embodiment, an antibody provided herein comprises a variable heavy chain region and a variable light chain region, wherein the variable heavy chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody number 11 in Table 1 and the variable light chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody 11 in Table 2. In one embodiment, an antibody provided herein comprises a variable heavy chain region and a variable light chain region, wherein the variable heavy chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody number 11 in Table 1 and the variable light chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody 11 in Table 2. In one embodiment, an antibody provided herein comprises a variable heavy chain region and a variable light chain region, wherein the variable heavy chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody number 12 in Table 1 and the variable light chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody 12 in Table 2. In one embodiment, an antibody provided herein comprises a variable heavy chain region and a variable light chain region, wherein the variable heavy chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody number 13 in Table 1 and the variable light chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody 13 in Table 2. In one embodiment, an antibody provided herein comprises a variable heavy chain region and a variable light chain region, wherein the variable heavy chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody number 14 in Table 1 and the variable light chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody 14 in Table 2. In one embodiment, an antibody provided herein comprises a variable heavy chain region and a variable light chain region, wherein the variable heavy chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody number 15 in Table 1 and the variable light chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody 15 in Table 2. In one embodiment, an antibody provided herein comprises a variable heavy chain region and a variable light chain region, wherein the variable heavy chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody number 16 in Table 1 and the variable light chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody 16 in Table 2. In one embodiment, an antibody provided herein comprises a variable heavy chain region and a variable light chain region, wherein the variable heavy chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody number 17 in Table 1 and the variable light chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody 17 in Table 2. In one embodiment, an antibody provided herein comprises a variable heavy chain region and a variable light chain region, wherein the variable heavy chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody number 18 in Table 1 and the variable light chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody 18 in Table 2. In one embodiment, an antibody provided herein comprises a variable heavy chain region and a variable light chain region, wherein the variable heavy chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody number 19 in Table 1 and the variable light chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody 19 in Table 2. In one embodiment, an antibody provided herein comprises a variable heavy chain region and a variable light chain region, wherein the variable heavy chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody number 20 in Table 1 and the variable light chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody 20 in Table 2. In one embodiment, an antibody provided herein comprises a variable heavy chain region and a variable light chain region, wherein the variable heavy chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody number 21 in Table 1 and the variable light chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody 21 in Table 2. In one embodiment, an antibody provided herein comprises a variable heavy chain region and a variable light chain region, wherein the variable heavy chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody number 22 in Table 1 and the variable light chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody 22 in Table 2. In one embodiment, an antibody provided herein comprises a variable heavy chain region and a variable light chain region, wherein the variable heavy chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody number 23 in Table 1 and the variable light chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody 23 in Table 2. In one embodiment, an antibody provided herein comprises a variable heavy chain region and a variable light chain region, wherein the variable heavy chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody number 24 in Table 1 and the variable light chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody 24 in Table 2. In one embodiment, an antibody provided herein comprises a variable heavy chain region and a variable light chain region, wherein the variable heavy chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody number 25 in Table 1 and the variable light chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody 25 in Table 2. In one embodiment, an antibody provided herein comprises a variable heavy chain region and a variable light chain region, wherein the variable heavy chain region com-

prises the amino acid sequence encoded by the nucleotide sequence of antibody number 26 in Table 1 and the variable light chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody 26 in Table 2. In one embodiment, an antibody provided herein comprises a variable heavy chain region and a variable light chain region, wherein the variable heavy chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody number 27 in Table 1 and the variable light chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody 27 in Table 2. In one embodiment, an antibody provided herein comprises a variable heavy chain region and a variable light chain region, wherein the variable heavy chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody number 28 in Table 1 and the variable light chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody 28 in Table 2. In one embodiment, an antibody provided herein comprises a variable heavy chain region and a variable light chain region, wherein the variable heavy chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody number 29 in Table 1 and the variable light chain region comprises the amino acid sequence encoded by the nucleotide sequence of antibody 29 in Table 2.

[0239] In another aspect, provided herein are antibodies that bind to the same or an overlapping epitope of an antibody described herein. e.g., antibodies that compete for binding to SARS-CoV-2 spike protein with an antibody described herein, or antibodies which bind to an epitope which overlaps with an epitope to which an antibody described herein binds. As used herein, an "epitope" is a term in the art and refers to a localized region of an antigen to which an antibody can specifically bind. An epitope can be, for example, contiguous amino acids of a polypeptide (linear or contiguous epitope) or an epitope can, for example, come together from two or more non-contiguous regions of a polypeptide or polypeptides (conformational, non-linear, discontinuous, or non-contiguous epitope). In certain aspects, epitope mapping assays, well known to one of skill in the art, can be performed to ascertain the epitope (e.g., conformational epitope) to which an antibody described herein binds. In certain embodiments, the epitope can be determined by, e.g., structural mapping using negative electron microscopy, X-ray diffraction crystallography studies (see, e.g., Blechman et al., 1993, J. Biol. Chem. 268:4399-4406; Cho et al., 2003, Nature, 421:756-760), ELISA assays, hydrogen/deuterium exchange coupled with mass spectrometry (e.g., MALDI mass spectrometry), array-based oligo-peptide scanning assays, mutagenesis mapping (e.g., site-directed mutagenesis mapping) and/or escape binding assays.

[0240] Antibodies that recognize such epitopes can be identified using routine techniques such as an immunoassay, for example, by showing the ability of one antibody to block the binding of another antibody to a target antigen, i.e., a competitive binding assay. Competition binding assays also can be used to determine whether two antibodies have similar binding specificity for an epitope. Competitive binding can be determined in an assay in which the immunoglobulin under test inhibits specific binding of a reference antibody to a common antigen, such as SARS-CoV-2 spike protein. Numerous types of competitive binding assays are known, for example: solid phase direct or indirect radioimmunoassay (RIA), solid phase direct or indirect enzyme immunoassay (EIA), sandwich competition assay (see Stahli et al., (1983) Methods in Enzymology 9:242); solid phase direct biotin-avidin EIA (see Kirkland et al., (1986) J. Immunol. 137:3614); solid phase direct labeled assay, solid phase direct labeled sandwich assay (see Harlow and Lane, (1988) Antibodies: A Laboratory Manual, Cold Spring Harbor Press); solid phase direct label RIA using I-125 label (see Morel et al., (1988) Mol. Immunol. 25(1):7); solid phase direct biotin-avidin EIA (Cheung et al., (1990) Virology 176:546); and direct labeled RIA. (Moldenhauer et al., (1990) Scand J. Immunol. 32:77). Typically, such an assay involves the use of purified antigen (e.g., SARS-CoV-2 spike proteinfragment thereof (e.g., RBD)) bound to a solid surface or cells bearing either of these, an unlabeled test immunoglobulin and a labeled reference immunoglobulin. Competitive inhibition can be measured by determining the amount of label bound to the solid surface or cells in the presence of the test immunoglobulin. Usually the test immunoglobulin is present in excess. Usually, when a competing antibody is present in excess, it will inhibit specific binding of a reference antibody to a common antigen by at least 50-55%, 55-60%, 60-65%, 65-70% 70-75% or more. A competition binding assay can be configured in a large number of different formats using either labeled antigen or labeled antibody. In a common version of this assay, the antigen is immobilized on a 96-well plate. The ability of unlabeled antibodies to block the binding of labeled antibodies to the antigen is then measured using radioactive or enzyme labels. For further details see, for example, Wagener et al., J. Immunol., 1983, 130:2308-2315; Wagener et al., J. Immunol. Methods, 1984, 68:269-274; Kuroki et al., Cancer Res., 1990, 50:4872-4879; Kuroki et al., Immunol. Invest., 1992, 21:523-538; Kuroki et al., Hybridoma, 1992, 11:391-407, and *Using Antibodies: A Laboratory Manual*, Ed Harlow and David Lane editors (Cold Springs Harbor Laboratory Press, Cold Springs Harbor, N.Y., 1999), pp. 386-389.

[0241] In certain aspects, competition binding assays can be used to determine whether an antibody is competitively blocked, e.g., in a dose dependent manner, by another antibody for example, an antibody binds essentially the same epitope, or overlapping epitopes, as a reference antibody, when the two antibodies recognize identical or sterically overlapping epitopes in competition binding assays such as competition ELISA assays, which can be configured in all number of different formats, using either labeled antigen or labeled antibody. In one embodiment, an antibody can be tested in competition binding assays with an antibody described herein.

[0242] In specific embodiments, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g. RBD), comprises framework regions (e.g., framework regions of the VL domain and/or VH domain) that are human framework regions or derived from human framework regions. The framework region may be naturally occurring or consensus framework regions (see, e.g., Sui et al., 2009, Nature Structural & Molecular Biology 16:265-273). Non-limiting examples of human framework regions are described in the art, e.g., see Kabat et al. (1991) *Sequences of Proteins of Immunological Interest*, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242). In certain embodiment, an antibody described herein comprises framework regions (e.g.,

framework regions of the VL domain and/or VH domain) that are primate (e.g., non-human primate) framework regions or derived from primate (e.g., non-human primate) framework regions.

[0243] In specific aspects, provided herein is an antibody comprising an antibody light chain and heavy chain, e.g., a separate light chain and heavy chain.

[0244] With respect to the light chain, in one embodiment, the light chain of an antibody described herein is a kappa light chain. In one embodiment, the light chain of an antibody described herein is a lambda light chain. In yet one embodiment, the light chain of an antibody described herein is a human kappa light chain or a human lambda light chain. In one embodiment, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises a light chain wherein the amino acid sequence of the variable light chain region can comprise any amino acid sequence described herein (e.g., variable light chain region of an antibody in Table 2), and wherein the constant region of the light chain comprises the amino acid sequence of a human kappa or lamda light chain constant region. Non-limiting examples of human constant region sequences have been described in the art, e.g., see U.S. Pat. No. 5,693,780 and Kabat et al. (1991) *Sequences of Proteins of Immunological Interest*, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242.

[0245] In one embodiment, an antibody described herein comprises (i) a heavy chain comprising a variable heavy chain region described herein and a constant region; or (ii) a light chain comprising a variable light chain region described herein and a constant region. In one embodiment, an antibody described herein comprises comprises (i) a heavy chain comprising a variable heavy chain region described herein and a constant region; and (ii) a light chain comprising a variable light chain region described herein and a constant region. As used herein, the term "constant region" or "constant domain" is interchangeable and has its meaning common in the art. The constant region refers to an antibody portion, e.g., a carboxyl terminal portion of a light and/or heavy chain which is not directly involved in binding of an antibody to antigen but which can exhibit various effector functions, such as interaction with the Fc receptor. The terms refer to a portion of an immunoglobulin molecule having a generally more conserved amino acid sequence relative to an immunoglobulin variable domain.

[0246] As used herein, the term"heavy chain" when used in reference to an antibody can refer to any distinct types, e.g., alpha (α), delta (δ), epsilon (ε), gamma (γ) and mu (μ), based on the amino acid sequence of the constant domain, which give rise to IgA, IgD, IgE, IgG and IgM classes of antibodies, respectively, including subclasses of IgG, e.g., IgG_1, IgG_2, IgG_3 and IgG_4.

[0247] As used herein, the term "light chain" when used in reference to an antibody can refer to any distinct types, e.g., kappa (κ) of lambda (λ) based on the amino acid sequence of the constant domains. Light chain amino acid sequences are well known in the art. In specific embodiments, the light chain is a human light chain.

[0248] With respect to the heavy chain, in one embodiment, the heavy chain of an antibody described herein can be an alpha (α), delta (δ), epsilon (ε), gamma (γ) or mu (μ) heavy chain. In one embodiment, the heavy chain of an antibody described can comprise a human alpha (α), delta (δ), epsilon (ε), gamma (γ) or mu (μ) heavy chain. In one embodiment, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises a heavy chain wherein the amino acid sequence of the variable heavy chain region can comprise any amino acid sequence described herein (e.g., variable heavy chain region of an antibody in Table 1), and wherein the constant region of the heavy chain comprises the amino acid sequence of a human gamma (γ) heavy chain constant region. Non-limiting examples of human constant region sequences have been described in the art, e.g., see U.S. Pat. No. 5,693,780 and Kabat et al. (1991) *Sequences of Proteins of Immunological Interest*, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242.

[0249] In one embodiment, an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises a variable heavy chain region and a variable light chain region comprising any amino acid sequences described herein, and wherein the constant regions comprise the amino acid sequences of the constant regions of an IgG, IgE, IgM, IgD, IgA or IgY immunoglobulin molecule, or a human IgG, IgE, IgM, IgD, IgA or IgY immunoglobulin molecule. In one embodiment, an antibody described herein, which binds SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), comprises a variable heavy chain region and a variable light chain region comprising any amino acid sequences described herein, and wherein the constant regions comprise the amino acid sequences of the constant regions of an IgG, IgE, IgM, IgD, IgA or IgY immunoglobulin molecule, any class (e.g., IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2), or any subclass (e.g., IgG2a and IgG2b) of immunoglobulin molecule. In some embodiments, an antibody described herein is an IgG2a antibody, and optionally comprises a kappa light chain.

[0250] The antibodies described herein can be affinity matured using techniques known to one of skill in the art.

[0251] The antibodies provided herein include derivatives that are chemically modified, i.e., by the covalent attachment of any type of molecule to the antibody. For example, but not by way of limitation, the antibody derivatives include antibodies that have been chemically modified, e.g., by glycosylation, acetylation, pegylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to a cellular ligand or other protein, etc. Any of numerous chemical modifications may be carried out by known techniques, including, but not limited to specific chemical cleavage, acetylation, formylation, metabolic synthesis of tunicamycin, etc. Additionally, the derivative may contain one or more non-classical amino acids.

[0252] In some embodiments, the glycosylation of antibodies described herein, in particular glycosylation of a variable region of an antibody described herein, is modified. For example, an aglycoslated antibody can be made (i.e., the antibody lacks glycosylation) or an antibody comprising a mutation or substitution at one or more glycosylation sites to eliminate glycosylation at the one or more glycosylation sites can be be made. Glycosylation can be altered to, for example, increase the affinity of the antibody for SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD). Such carbohydrate modifications can be accomplished by, for example, altering one or more sites of glycosylation within the antibody sequence. For example, one or more amino acid substitutions can be made that result in elimination of one or more variable region (e.g., variable heavy chain region

CDRS and/or variable light chain region CDRs or variable heavy chain region FRs and/or variable light chain region FRs) glycosylation sites to thereby eliminate glycosylation at that site. Such aglycosylation can increase the affinity of the antibody for SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD). Such an approach is described in further detail in U.S. Pat. Nos. 5,714,350 and 6,350,861.

[0253] Glycosylation can occur via N-linked (or asparagine-linked) glycosylation or O-linked glycosylation. N-linked glycosylation involves carbohydrate modification at the side-chain NH_2 group of an asparagine amino acid in a polypeptide. O-linked glycosylation involves carbohydrate modification at the hydroxyl group on the side chain of a serine, threonine, or hydroxylysine amino acid.

[0254] In certain embodiments, aglycosylated antibodies can be produced in bacterial cells which lack the necessary glycosylation machinery. Cells with altered glycosylation machinery have been described in the art and can be used as host cells in which to express recombinant antibodies described herein to thereby produce an antibody with altered glycosylation. See, for example, Shields, R. L. et al. (2002) J. Biol. Chem. 277:26733-26740; Umana et al. (1999) Nat. Biotech. 17:176-1, as well as, European Patent No: EP 1,176,195; PCT Publications WO 03/035835; WO 99/54342.

[0255] Antibodies with reduced fucose content have been reported to have an increased affinity for Fc receptors, such as, e.g., FcγRIIIa. Accordingly, in certain embodiments, the antibodies described herein have reduced fucose content or no fucose content. Such antibodies can be produced using techniques known to one skilled in the art. For example, the antibodies can be expressed in cells deficient or lacking the ability to fucosylate. In one example, cell lines with a knockout of both alleles of α1,6-fucosyltransferase can be used to produce antibodies with reduced fucose content. The Potelligent® system (Lonza) is an example of such a system that can be used to produce antibodies with reduced fucose content.

[0256] In certain embodiments, one, two or more mutations (e.g., amino acid substitutions) are introduced into the Fc region of an antibody described herein or a fragment thereof (e.g., CH2 domain (residues 231-340 of human IgG1) and/or CH3 domain (residues 341-447 of human IgG1) and/or the hinge region, with numbering according to the Kabat numbering system (e.g., the EU index in Kabat)) to increase the affinity of the antibody for an Fc receptor (e.g., an activated Fc receptor) on the surface of an effector cell. Mutations in the Fc region of an antibody or fragment thereof that increase the affinity of an antibody for an Fc receptor and techniques for introducting such mutations into the Fc receptor or fragment thereof are known to one of skill in the art. Examples of mutations in the Fc receptor of an antibody that can be made to increase the affinity of the antibody for an Fc receptor are described in, e.g., Smith, P., et al. (2012) PNAS. 109:6181-6186, which is incorporated herein by reference.

[0257] In some aspects, provided herein are antibodies, conjugated or recombinantly fused to a diagnostic, detectable or therapeutic agent or any other molecule. The conjugated or recombinantly fused antibodies can be useful, e.g., for monitoring or prognosing the onset, development, progression and/or severity of COVID-19 as part of a clinical testing procedure, such as determining the efficacy of a particular therapy. In certain aspects, the conjugated or recombinantly fused antibodies can be useful in preventing, treating, or both COVID-19. Antibodies described herein can also be conjugated to a molecule (e.g., polyethylene glycol) which can affect one or more biological and/or molecular properties of the antibodies, for example, stability (e.g., in serum), half-life, solubility, and antigenicity.

[0258] In some embodiments, a conjugate comprises an antibody described herein and a molecule (e.g., therapeutic or drug moiety), wherein the antibody is linked directly to the molecule, or by way of one or more linkers. In certain embodiments, an antibody is covalently conjugated to a molecule. In one embodiment, an antibody is noncovalently conjugated to a molecule. In one embodiment, provided herein is an antibody drug conjugate comprising an antibody moiety and a drug (e.g., therapeutic or prophylactic agent), wherein the antibody moiety is an antibody described herein and wherein the conjugate may comprise one or more linkers.

[0259] In certain embodiments, an antibody described herein is conjugated to one or more molecules (e.g., therapeutic or drug moiety) directly or indirectly via one or more linker molecules. In one embodiments, a linker comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 20 amino acid residues. In certain embodiments, a linker consists of 1 to 10 amino acid residues, 1 to 15 amino acid residues, 5 to 20 amino acid residues, 10 to 25 amino acid residues, 10 to 30 amino acid residues, or 10 to 50 amino acid residues. In some embodiments, a linker is an enzyme-cleavable linker or a disulfide linker. In one embodiment, the cleavable linker is cleavable via an enzyme such an aminopeptidase, an aminoesterase, a dipeptidyl carboxy peptidase, or a protease of the blood clotting cascade. In one embodiment, the linker that may be conjugated to the antibody does not interfere with the antibody binding to either recombinant SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), the virion of SARS-CoV-2, or both, using techniques known in the art or described herein.

[0260] In certain aspects, diagnosis and detection can be accomplished, for example, by coupling the antibody to a detectable substance(s) including, but not limited to, various enzymes, such as, but not limited to, horseradish peroxidase, alkaline phosphatase, beta-galactosidase, or acetylcholinesterase; prosthetic groups, such as, but not limited to, streptavidin/biotin and avidin/biotin; fluorescent materials, such as, but not limited to, umbelliferone, fluorescein, fluorescein isothiocynate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; luminescent materials, such as, but not limited to, luminol; bioluminescent materials, such as but not limited to, luciferase, luciferin, and aequorin; radioactive materials, such as, but not limited to, iodine (^{131}I, ^{125}I, ^{123}I, and ^{121}I), carbon (^{14}C), sulfur (^{35}S), tritium (^{3}H), indium (^{115}In, ^{113}In, ^{112}In, and ^{111}In,), technetium (^{99}Tc), thallium (^{201}Ti), gallium (^{68}Ga, ^{67}Ga), palladium (^{103}Pd), molybdenum (^{99}Mo), xenon (^{133}Xe), fluorine (^{18}F), ^{153}Sm, ^{177}Lu, ^{159}Gd, ^{149}Pm, ^{140}La, ^{175}Yb, ^{166}Ho, ^{90}Y, ^{47}Sc, ^{186}Re, ^{188}Re, ^{142}Pr, ^{105}Rh, ^{97}Ru, ^{68}Ge, ^{57}Co, ^{65}Zn, ^{85}Sr, ^{32}P, ^{153}Gd, ^{169}Yb, ^{51}Cr, ^{54}Mn, ^{113}Sn, and ^{117}Sn; and positron emitting metals using various positron emission tomographies, and non-radioactive paramagnetic metal ions.

[0261] Provided are antibodies described herein conjugated or recombinantly fused to a therapeutic moiety (or one or more therapeutic moieties) and uses of such antibodies. The antibody can be conjugated or recombinantly fused to a

therapeutic moiety, such as a cytotoxin, e.g., a cytostatic or cytocidal agent, a therapeutic agent or a radioactive metal ion, e.g., alpha-emitters.

[0262] Further, provided herein are uses of the antibodies conjugated or recombinantly fused to a therapeutic moiety or drug moiety that modifies a given biological response. Therapeutic moieties or drug moieties are not to be construed as limited to classical chemical therapeutic agents. For example, the drug moiety may be a protein, peptide, or polypeptide possessing a desired biological activity.

[0263] In addition, an antibody described herein can be conjugated to therapeutic moieties such as a radioactive metal ion, such as alpha-emitters such as ^{213}Bi or macrocyclic chelators useful for conjugating radiometal ions, including but not limited to, ^{131}In, ^{131}LU, ^{131}Y, ^{131}Ho, ^{131}Sm, to polypeptides.

[0264] Moreover, antibodies can be fused to marker sequences, such as a peptide to facilitate purification. In some embodiments, the marker amino acid sequence is a hexa-histidine peptide (i.e., His-tag), such as the tag provided in a pQE vector (QIAGEN, Inc.), among others, many of which are commercially available. As described in Gentz et al., 1989, Proc. Natl. Acad. Sci. USA 86:821-824, for instance, hexa-histidine provides for convenient purification of the fusion protein. Other peptide tags useful for purification include, but are not limited to, the hemagglutinin ("HA") tag, which corresponds to an epitope derived from the influenza hemagglutinin protein (Wilson et al., 1984, Cell 37:767), and the "flag" tag.

[0265] Methods for fusing or conjugating therapeutic moieties (including polypeptides) to antibodies are well known, see, e.g., Amon et al., "Monoclonal Antibodies For Immunotargeting Of Drugs In Cancer Therapy", in Monoclonal Antibodies And Cancer Therapy, Reisfeld et al. (eds.), pp. 243-56 (Alan R. Liss, Inc. 1985); Hellstrom et al., "Antibodies For Drug Delivery", in Controlled Drug Delivery (2nd Ed.), Robinson et al. (eds.), pp. 623-53 (Marcel Dekker, Inc. 1987); Thorpe, "Antibody Carriers Of Cytotoxic Agents In Cancer Therapy: A Review", in Monoclonal Antibodies 84: Biological And Clinical Applications, Pinchera et al. (eds.), pp. 475-506 (1985); "Analysis, Results, And Future Prospective Of The Therapeutic Use Of Radiolabeled Antibody In Cancer Therapy", in Monoclonal Antibodies For Cancer Detection And Therapy, Baldwin et al. (eds.), pp. 303-16 (Academic Press 1985), Thorpe et al., 1982, Immunol. Rev. 62:119-58; U.S. Pat. Nos. 5,336,603, 5,622,929, 5,359,046, 5,349,053, 5,447,851, 5,723,125, 5,783,181, 5,908,626, 5,844,095, and 5,112,946; EP 307,434; EP 367,166; EP 394,827; PCT publications WO 91/06570, WO 96/04388, WO 96/22024, WO 97/34631, and WO 99/04813; Ashkenazi et al., Proc. Natl. Acad. Sci. USA, 88: 10535-10539, 1991; Traunecker et al., Nature, 331:84-86, 1988; Zheng et al., J. Immunol., 154:5590-5600, 1995; Vil et al., Proc. Natl. Acad. Sci. USA, 89:11337-11341, 1992; which are incorporated herein by reference in their entireties.

[0266] Fusion proteins may be generated, for example, through the techniques of gene-shuffling, motif-shuffling, exon-shuffling, and/or codon-shuffling (collectively referred to as "DNA shuffling"). DNA shuffling may be employed to alter the activities of the monoclonal antibodies described herein (or an antigen-binding fragment thereof) (e.g., antibodies with higher affinities and lower dissociation rates). See, generally, U.S. Pat. Nos. 5,605,793, 5,811,238, 5,830,721, 5,834,252, and 5,837,458; Patten et al., 1997, Curr. Opinion Biotechnol. 8:724-33; Harayama, 1998, Trends Biotechnol. 16(2):76-82; Hansson, et al., 1999, J. Mol. Biol. 287:265-76; and Lorenzo and Blasco, 1998, Biotechniques 24(2):308-313 (each of these patents and publications are hereby incorporated by reference in its entirety). Antibodies, or the encoded antibodies, may be altered by being subjected to random mutagenesis by error-prone PCR, random nucleotide insertion or other methods prior to recombination. A polynucleotide encoding a monoclonal antibody described herein (or an antigen-binding fragment thereof) may be recombined with one or more components, motifs, sections, parts, domains, fragments, etc. of one or more heterologous molecules.

[0267] An antibody can also be conjugated to a second antibody to form an antibody heteroconjugate as described by Segal in U.S. Pat. No. 4,676,980, which is incorporated herein by reference in its entirety.

[0268] An antibody can also be linked directly or indirectly to one or more antibodies to produce bispecific/multispecific antibodies.

[0269] An antibody can also be attached to solid supports, which are particularly useful for immunoassays or purification of an antigen. Such solid supports include, but are not limited to, glass, cellulose, polyacrylamide, nylon, polystyrene, polyvinyl chloride or polypropylene.

[0270] 6.2 Polynucleotides

[0271] In certain aspects, provided herein are polynucleotides comprising a nucleotide sequence encoding an antibody described herein or a fragment thereof (e.g., a variable heavy chain region and/or variable light chain region) that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g. RBD), and vectors, e.g., vectors comprising such polynucleotides for recombinant expression in host cells (e.g., *E. coli* and mammalian cells). Provided herein are polynucleotides comprising nucleotide sequences encoding any of the antibodies provided herein, as well as vectors comprising such polynucleotide sequences, e.g., expression vectors for their efficient expression in host cells, e.g., mammalian cells.

[0272] In one embodiment, an "isolated" polynucleotide or nucleic acid molecule is one that is separated from other nucleic acid molecules that are present in the natural source (e.g., in a mouse or a human) of the nucleic acid molecule. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized. For example, the language "substantially free" includes preparations of polynucleotide or nucleic acid molecule having less than about 15%, 10%, 5%, 2%, 1%, 0.5% or 0.1% (in particular less than about 10%) of other material, e.g., cellular material, culture medium, other nucleic acid molecules, chemical precursors and/or other chemicals. In one embodiment, a nucleic acid molecule(s) encoding an antibody described herein is isolated or purified.

[0273] As used herein, the terms "polynucleotide(s)" "nucleic acid" and "nucleotide" include deoxyribonucleotides, deoxyribonucleic acids, ribonucleotides, and ribonucleic acids, and polymeric forms thereof, and includes either single- or double-stranded forms. In certain embodiments, the terms "polynucleotide(s)" "nucleic acid" and "nucleotide" include known analogues of natural nucleotides, for example, peptide nucleic acids ("PNA"s), that have

similar binding properties as the reference nucleic acid. In some embodiments, the terms "polynucleotide(s)" "nucleic acid" and "nucleotide" refer to deoxyribonucleic acids (e.g., cDNA or DNA). In other embodiments, the terms "polynucleotide(s)" "nucleic acid" and "nucleotide" refer to ribonucleic acids (e.g., mRNA or RNA).

[0274] In some aspects, provided herein are polynucleotides comprising nucleotide sequences encoding antibodies, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) and comprises an amino acid sequence as described herein, as well as antibodies which compete with such antibodies for binding to SARS-CoV-2 spike protein or a fragment thereof (e.g., in a dose-dependent manner), or which binds to the same epitope as that of such antibodies. In one embodiments, a polynucleotide described herein an antibody which comprises a variable heavy chain region and/or variable light chain region of an antibody with the same name in Tables 1 and 2.

[0275] In one embodiment, a polynucleotide described herein comprises a nucleotide sequence encoding an antibody which comprises a variable heavy chain region comprising the amino acid sequence of an antibody in Table 1 and/or a variable light chain region comprising the amino acid sequence of an antibody in Table 2 with the same name. In some embodiments, a polynucleotide described herein comprises a nucleotide sequence encoding for an antibody that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), wherein the antibody comprises 1, 2, or 3 VH CDRs and/or 1, 2, or 3 VL CDRs of an antibody in Tables 1 and 2.

[0276] In certain aspects, provided herein are polynucleotides comprising a nucleotide sequence encoding the light chain or heavy chain of an antibody described herein. The polynucleotides can comprise nucleotide sequences encoding a light chain or a VL domain, comprising the VL FRs and CDRs of an antibody described herein. The polynucleotides can comprise nucleotide sequences encoding a heavy chain, or a VH domain, comprising the VH FRs and CDRs of antibodies described herein.

[0277] In some embodiments, a polynucleotide described herein encodes a variable heavy chain region, wherein the polynucleotide comprises a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable heavy chain region of an antibody in Table 1. In some embodiments, a polynucleotide described herein encodes a variable light chain region, wherein the polynucleotide comprises a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable light chain region of an antibody in Table 1. In one embodiment, the variable heavy chain region and/or variable light chain region encoded the polynucleotide(s) does not affect the amino acid sequence of the variable heavy chain region and/or variable light chain region.

[0278] In some embodiments, a polynucleotide described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide comprises (i) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable heavy chain region of an antibody in Table 1, and (ii) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable light chain region of an antibody in Table 2. In one embodiment, the variable heavy chain region and/or variable light chain region encoded by the polynucleotide(s) does not affect the amino acid sequence of the variable heavy chain region and/or variable light chain region.

[0279] In some embodiments, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable heavy chain region of antibody number 1 in Table 1, and (ii) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable light chain region of antibody number 1 in Table 2. In one embodiment, the variable heavy chain region and/or variable light chain region encoded by the polynucleotide(s)(s) does not affect the amino acid sequence of the variable heavy chain region and/or variable light chain region. In one embodiment, the CDRs of the variable heavy chain region are identical to the CDRs of antibody number 1 in Tables 1 or 6, and the CDRs of the variable light chain region are identical to the CDRs of antibody number 1 in Tables 2 or 8. In another embodiment, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence identical to the nucleic acid sequence of a variable heavy chain region of antibody number 1 in Table 1, and (ii) a nucleic acid sequence identical to the nucleic acid sequence of a variable light chain region of antibody number 1 in Table 2.

[0280] In some embodiments, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable heavy chain region of antibody number 2 in Table 1, and (ii) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable light chain region of antibody number 2 in Table 2. In one embodiment, the variable heavy chain region and/or variable light chain region encoded by the polynucleotide(s)(s) does not affect the amino acid sequence of the variable heavy chain region and/or variable light chain region. In one embodiment, the CDRs of the variable heavy chain region are identical to the CDRs of antibody number 2 in Tables 1 or 6, and the CDRs of the variable light chain region are identical to the CDRs of antibody number 2 in Tables 2 or 8. In another embodiment, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light the nucleic acid sequence of a variable heavy chain region of antibody number 2 in Table 1, and (ii) a nucleic acid sequence identical to the nucleic acid sequence of a variable light chain region of antibody number 2 in Table 2.

[0281] In some embodiments, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable heavy

chain region of antibody number 3 in Table 1, and (ii) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable light chain region of antibody number 3 in Table 2. In one embodiment, the variable heavy chain region and/or variable light chain region encoded by the polynucleotide(s)(s) does not affect the amino acid sequence of the variable heavy chain region and/or variable light chain region. In one embodiment, the CDRs of the variable heavy chain region are identical to the CDRs of antibody number 3 in Tables 1 or 6, and the CDRs of the variable light chain region are identical to the CDRs of antibody number 3 in Tables 2 or 8. In another embodiment, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence identical to the nucleic acid sequence of a variable heavy chain region of antibody number 3 in Table 1, and (ii) a nucleic acid sequence identical to the nucleic acid sequence of a variable light chain region of antibody number 3 in Table 2.

[0282] In some embodiments, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable heavy chain region of antibody number 4 in Table 1, and (ii) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable light chain region of antibody number 4 in Table 2. In one embodiment, the variable heavy chain region and/or variable light chain region encoded by the polynucleotide(s)(s) does not affect the amino acid sequence of the variable heavy chain region and/or variable light chain region. In one embodiment, the CDRs of the variable heavy chain region are identical to the CDRs of antibody number 4 in Tables 1 or 6, and the CDRs of the variable light chain region are identical to the CDRs of antibody number 4 in Tables 2 or 8. In another embodiment, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light the nucleic acid sequence of a variable heavy chain region of antibody number 4 in Table 1, and (ii) a nucleic acid sequence identical to the nucleic acid sequence of a variable light chain region of antibody number 4 in Table 2.

[0283] In some embodiments, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable heavy chain region of antibody number 5 in Table 1, and (ii) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable light chain region of antibody number 5 in Table 2. In one embodiment, the variable heavy chain region and/or variable light chain region encoded by the polynucleotide(s)(s) does not affect the amino acid sequence of the variable heavy chain region and/or variable light chain region. In one embodiment, the CDRs of the variable heavy chain region are identical to the CDRs of antibody number 5 in Tables 1 or 6, and the CDRs of the variable light chain region are identical to the CDRs of antibody number 5 in Tables 2 or 8. In another embodiment, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence identical to the nucleic acid sequence of a variable heavy chain region of antibody number 5 in Table 1, and (ii) a nucleic acid sequence identical to the nucleic acid sequence of a variable light chain region of antibody number 5 in Table 2.

[0284] In some embodiments, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable heavy chain region of antibody number 6 in Table 1, and (ii) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable light chain region of antibody number 6 in Table 2. In one embodiment, the variable heavy chain region and/or variable light chain region encoded by the polynucleotide(s)(s) does not affect the amino acid sequence of the variable heavy chain region and/or variable light chain region. In one embodiment, the CDRs of the variable heavy chain region are identical to the CDRs of antibody number 6 in Tables 1 or 6, and the CDRs of the variable light chain region are identical to the CDRs of antibody number 6 in Tables 2 or 8. In another embodiment, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light the nucleic acid sequence of a variable heavy chain region of antibody number 6 in Table 1, and (ii) a nucleic acid sequence identical to the nucleic acid sequence of a variable light chain region of antibody number 6 in Table 2.

[0285] In some embodiments, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable heavy chain region of antibody number 7 in Table 1, and (ii) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable light chain region of antibody number 7 in Table 2. In one embodiment, the variable heavy chain region and/or variable light chain region encoded by the polynucleotide(s)(s) does not affect the amino acid sequence of the variable heavy chain region and/or variable light chain region. In one embodiment, the CDRs of the variable heavy chain region are identical to the CDRs of antibody number 7 in Tables 1 or 6, and the CDRs of the variable light chain region are identical to the CDRs of antibody number 7 in Tables 2 or 8. In another embodiment, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence identical to the nucleic acid sequence of a variable heavy chain region of antibody number 7 in Table 1, and (ii) a nucleic acid sequence identical to the nucleic acid sequence of a variable light chain region of antibody number 7 in Table 2.

[0286] In some embodiments, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s)

comprises (i) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable heavy chain region of antibody number 8 in Table 1, and (ii) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable light chain region of antibody number 8 in Table 2. In one embodiment, the variable heavy chain region and/or variable light chain region encoded by the polynucleotide(s)(s) does not affect the amino acid sequence of the variable heavy chain region and/or variable light chain region. In one embodiment, the CDRs of the variable heavy chain region are identical to the CDRs of antibody number 8 in Tables 1 or 6, and the CDRs of the variable light chain region are identical to the CDRs of antibody number 8 in Tables 2 or 8. In another embodiment, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light the nucleic acid sequence of a variable heavy chain region of antibody number 8 in Table 1, and (ii) a nucleic acid sequence identical to the nucleic acid sequence of a variable light chain region of antibody number 8 in Table 2.

[0287] In some embodiments, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable heavy chain region of antibody number 9 in Table 1, and (ii) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable light chain region of antibody number 9 in Table 2. In one embodiment, the variable heavy chain region and/or variable light chain region encoded by the polynucleotide(s)(s) does not affect the amino acid sequence of the variable heavy chain region and/or variable light chain region. In one embodiment, the CDRs of the variable heavy chain region are identical to the CDRs of antibody number 9 in Tables 1 or 6, and the CDRs of the variable light chain region are identical to the CDRs of antibody number 9 in Tables 2 or 8. In another embodiment, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence identical to the nucleic acid sequence of a variable heavy chain region of antibody number 9 in Table 1, and (ii) a nucleic acid sequence identical to the nucleic acid sequence of a variable light chain region of antibody number 9 in Table 2.

[0288] In some embodiments, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable heavy chain region of antibody number 10 in Table 1, and (ii) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable light chain region of antibody number 10 in Table 2. In one embodiment, the variable heavy chain region and/or variable light chain region encoded by the polynucleotide(s)(s) does not affect the amino acid sequence of the variable heavy chain region and/or variable light chain region. In one embodiment, the CDRs of the variable heavy chain region are identical to the CDRs of antibody number 10 in Tables 1 or 6, and the CDRs of the variable light chain region are identical to the CDRs of antibody number 10 in Tables 2 or 8. In another embodiment, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light the nucleic acid sequence of a variable heavy chain region of antibody number 10 in Table 1, and (ii) a nucleic acid sequence identical to the nucleic acid sequence of a variable light chain region of antibody number 10 in Table 2.

[0289] In some embodiments, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable heavy chain region of antibody number 11 in Table 1, and (ii) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable light chain region of antibody number 11 in Table 2. In one embodiment, the variable heavy chain region and/or variable light chain region encoded by the polynucleotide(s)(s) does not affect the amino acid sequence of the variable heavy chain region and/or variable light chain region. In one embodiment, the CDRs of the variable heavy chain region are identical to the CDRs of antibody number 11 in Tables 1 or 6, and the CDRs of the variable light chain region are identical to the CDRs of antibody number 11 in Tables 2 or 8. In another embodiment, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence identical to the nucleic acid sequence of a variable heavy chain region of antibody number 11 in Table 1, and (ii) a nucleic acid sequence identical to the nucleic acid sequence of a variable light chain region of antibody number 11 in Table 2.

[0290] In some embodiments, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable heavy chain region of antibody number 12 in Table 1, and (ii) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable light chain region of antibody number 12 in Table 2. In one embodiment, the variable heavy chain region and/or variable light chain region encoded by the polynucleotide(s)(s) does not affect the amino acid sequence of the variable heavy chain region and/or variable light chain region. In one embodiment, the CDRs of the variable heavy chain region are identical to the CDRs of antibody number 12 in Tables 1 or 6, and the CDRs of the variable light chain region are identical to the CDRs of antibody number 12 in Tables 2 or 8. In another embodiment, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light the nucleic acid sequence of a variable heavy chain region of antibody number 12 in Table 1, and (ii) a nucleic acid sequence identical to the nucleic acid sequence of a variable light chain region of antibody number 12 in Table 2.

[0291] In some embodiments, a polynucleotide(s) described herein encodes a variable heavy chain region and

a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable heavy chain region of antibody number 13 in Table 1, and (ii) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable light chain region of antibody number 13 in Table 2. In one embodiment, the variable heavy chain region and/or variable light chain region encoded by the polynucleotide(s)(s) does not affect the amino acid sequence of the variable heavy chain region and/or variable light chain region. In one embodiment, the CDRs of the variable heavy chain region are identical to the CDRs of antibody number 13 in Tables 1 or 6, and the CDRs of the variable light chain region are identical to the CDRs of antibody number 13 in Tables 2 or 8. In another embodiment, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence identical to the nucleic acid sequence of a variable heavy chain region of antibody number 13 in Table 1, and (ii) a nucleic acid sequence identical to the nucleic acid sequence of a variable light chain region of antibody number 13 in Table 2.

[0292] In some embodiments, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable heavy chain region of antibody number 14 in Table 1, and (ii) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable light chain region of antibody number 14 in Table 2. In one embodiment, the variable heavy chain region and/or variable light chain region encoded by the polynucleotide(s)(s) does not affect the amino acid sequence of the variable heavy chain region and/or variable light chain region. In one embodiment, the CDRs of the variable heavy chain region are identical to the CDRs of antibody number 14 in Tables 1 or 6, and the CDRs of the variable light chain region are identical to the CDRs of antibody number 14 in Tables 2 or 8. In another embodiment, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light the nucleic acid sequence of a variable heavy chain region of antibody number 14 in Table 1, and (ii) a nucleic acid sequence identical to the nucleic acid sequence of a variable light chain region of antibody number 14 in Table 2.

[0293] In some embodiments, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable heavy chain region of antibody number 15 in Table 1, and (ii) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable light chain region of antibody number 15 in Table 2. In one embodiment, the variable heavy chain region and/or variable light chain region encoded by the polynucleotide(s)(s) does not affect the amino acid sequence of the variable heavy chain region and/or variable light chain region. In one embodiment, the CDRs of the variable heavy chain region are identical to the CDRs of antibody number 15 in Tables 1 or 6, and the CDRs of the variable light chain region are identical to the CDRs of antibody number 15 in Tables 2 or 8. In another embodiment, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence identical to the nucleic acid sequence of a variable heavy chain region of antibody number 15 in Table 1, and (ii) a nucleic acid sequence identical to the nucleic acid sequence of a variable light chain region of antibody number 15 in Table 2.

[0294] In some embodiments, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable heavy chain region of antibody number 16 in Table 1, and (ii) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable light chain region of antibody number 16 in Table 2. In one embodiment, the variable heavy chain region and/or variable light chain region encoded by the polynucleotide(s)(s) does not affect the amino acid sequence of the variable heavy chain region and/or variable light chain region. In one embodiment, the CDRs of the variable heavy chain region are identical to the CDRs of antibody number 16 in Tables 1 or 6, and the CDRs of the variable light chain region are identical to the CDRs of antibody number 16 in Tables 2 or 8. In another embodiment, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light the nucleic acid sequence of a variable heavy chain region of antibody number 16 in Table 1, and (ii) a nucleic acid sequence identical to the nucleic acid sequence of a variable light chain region of antibody number 16 in Table 2.

[0295] In some embodiments, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable heavy chain region of antibody number 17 in Table 1, and (ii) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable light chain region of antibody number 17 in Table 2. In one embodiment, the variable heavy chain region and/or variable light chain region encoded by the polynucleotide(s)(s) does not affect the amino acid sequence of the variable heavy chain region and/or variable light chain region. In one embodiment, the CDRs of the variable heavy chain region are identical to the CDRs of antibody number 17 in Tables 1 or 6, and the CDRs of the variable light chain region are identical to the CDRs of antibody number 17 in Tables 2 or 8. In another embodiment, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence identical to the nucleic acid sequence of a variable heavy chain region of antibody number 17 in Table 1, and

(ii) a nucleic acid sequence identical to the nucleic acid sequence of a variable light chain region of antibody number 17 in Table 2.

[0296] In some embodiments, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable heavy chain region of antibody number 18 in Table 1, and (ii) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable light chain region of antibody number 18 in Table 2. In one embodiment, the variable heavy chain region and/or variable light chain region encoded by the polynucleotide(s)(s) does not affect the amino acid sequence of the variable heavy chain region and/or variable light chain region. In one embodiment, the CDRs of the variable heavy chain region are identical to the CDRs of antibody number 18 in Tables 1 or 6, and the CDRs of the variable light chain region are identical to the CDRs of antibody number 18 in Tables 2 or 8. In another embodiment, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light the nucleic acid sequence of a variable heavy chain region of antibody number 18 in Table 1, and (ii) a nucleic acid sequence identical to the nucleic acid sequence of a variable light chain region of antibody number 18 in Table 2.

[0297] In some embodiments, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable heavy chain region of antibody number 19 in Table 1, and (ii) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable light chain region of antibody number 19 in Table 2. In one embodiment, the variable heavy chain region and/or variable light chain region encoded by the polynucleotide(s)(s) does not affect the amino acid sequence of the variable heavy chain region and/or variable light chain region. In one embodiment, the CDRs of the variable heavy chain region are identical to the CDRs of antibody number 19 in Tables 1 or 6, and the CDRs of the variable light chain region are identical to the CDRs of antibody number 19 in Tables 2 or 8. In another embodiment, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence identical to the nucleic acid sequence of a variable heavy chain region of antibody number 19 in Table 1, and (ii) a nucleic acid sequence identical to the nucleic acid sequence of a variable light chain region of antibody number 19 in Table 2.

[0298] In some embodiments, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable heavy chain region of antibody number 20 in Table 1, and (ii) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable light chain region of antibody number 20 in Table 2. In one embodiment, the variable heavy chain region and/or variable light chain region encoded by the polynucleotide(s)(s) does not affect the amino acid sequence of the variable heavy chain region and/or variable light chain region. In one embodiment, the CDRs of the variable heavy chain region are identical to the CDRs of antibody number 20 in Tables 1 or 6, and the CDRs of the variable light chain region are identical to the CDRs of antibody number 20 in Tables 2 or 8. In another embodiment, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light the nucleic acid sequence of a variable heavy chain region of antibody number 20 in Table 1, and (ii) a nucleic acid sequence identical to the nucleic acid sequence of a variable light chain region of antibody number 20 in Table 2.

[0299] In some embodiments, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable heavy chain region of antibody number 21 in Table 1, and (ii) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable light chain region of antibody number 21 in Table 2. In one embodiment, the variable heavy chain region and/or variable light chain region encoded by the polynucleotide(s)(s) does not affect the amino acid sequence of the variable heavy chain region and/or variable light chain region. In one embodiment, the CDRs of the variable heavy chain region are identical to the CDRs of antibody number 21 in Tables 1 or 6, and the CDRs of the variable light chain region are identical to the CDRs of antibody number 21 in Tables 2 or 8. In another embodiment, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence identical to the nucleic acid sequence of a variable heavy chain region of antibody number 21 in Table 1, and (ii) a nucleic acid sequence identical to the nucleic acid sequence of a variable light chain region of antibody number 21 in Table 2.

[0300] In some embodiments, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable heavy chain region of antibody number 22 in Table 1, and (ii) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable light chain region of antibody number 22 in Table 2. In one embodiment, the variable heavy chain region and/or variable light chain region encoded by the polynucleotide(s)(s) does not affect the amino acid sequence of the variable heavy chain region and/or variable light chain region. In one embodiment, the CDRs of the variable heavy chain region are identical to the CDRs of antibody number 22 in Tables 1 or 6, and the CDRs of the variable light chain region are identical to the CDRs of antibody number 22 in Tables 2 or 8. In another embodiment, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light the nucleic acid

sequence of a variable heavy chain region of antibody number 22 in Table 1, and (ii) a nucleic acid sequence identical to the nucleic acid sequence of a variable light chain region of antibody number 22 in Table 2.

[0301] In some embodiments, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable heavy chain region of antibody number 23 in Table 1, and (ii) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable light chain region of antibody number 23 in Table 2. In one embodiment, the variable heavy chain region and/or variable light chain region encoded by the polynucleotide(s)(s) does not affect the amino acid sequence of the variable heavy chain region and/or variable light chain region. In one embodiment, the CDRs of the variable heavy chain region are identical to the CDRs of antibody number 23 in Tables 1 or 6, and the CDRs of the variable light chain region are identical to the CDRs of antibody number 23 in Tables 2 or 8. In another embodiment, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence identical to the nucleic acid sequence of a variable heavy chain region of antibody number 23 in Table 1, and (ii) a nucleic acid sequence identical to the nucleic acid sequence of a variable light chain region of antibody number 23 in Table 2.

[0302] In some embodiments, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable heavy chain region of antibody number 24 in Table 1, and (ii) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable light chain region of antibody number 24 in Table 2. In one embodiment, the variable heavy chain region and/or variable light chain region encoded by the polynucleotide(s)(s) does not affect the amino acid sequence of the variable heavy chain region and/or variable light chain region. In one embodiment, the CDRs of the variable heavy chain region are identical to the CDRs of antibody number 24 in Tables 1 or 6, and the CDRs of the variable light chain region are identical to the CDRs of antibody number 24 in Tables 2 or 8. In another embodiment, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light the nucleic acid sequence of a variable heavy chain region of antibody number 24 in Table 1, and (ii) a nucleic acid sequence identical to the nucleic acid sequence of a variable light chain region of antibody number 24 in Table 2.

[0303] In some embodiments, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable heavy chain region of antibody number 215 in Table 1, and (ii) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable light chain region of antibody number 25 in Table 2. In one embodiment, the variable heavy chain region and/or variable light chain region encoded by the polynucleotide(s)(s) does not affect the amino acid sequence of the variable heavy chain region and/or variable light chain region. In one embodiment, the CDRs of the variable heavy chain region are identical to the CDRs of antibody number 25 in Tables 1 or 6, and the CDRs of the variable light chain region are identical to the CDRs of antibody number 25 in Tables 2 or 8. In another embodiment, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence identical to the nucleic acid sequence of a variable heavy chain region of antibody number 25 in Table 1, and (ii) a nucleic acid sequence identical to the nucleic acid sequence of a variable light chain region of antibody number 25 in Table 2.

[0304] In some embodiments, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable heavy chain region of antibody number 26 in Table 1, and (ii) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable light chain region of antibody number 26 in Table 2. In one embodiment, the variable heavy chain region and/or variable light chain region encoded by the polynucleotide(s)(s) does not affect the amino acid sequence of the variable heavy chain region and/or variable light chain region. In one embodiment, the CDRs of the variable heavy chain region are identical to the CDRs of antibody number 26 in Tables 1 or 6, and the CDRs of the variable light chain region are identical to the CDRs of antibody number 26 in Tables 2 or 8. In another embodiment, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light the nucleic acid sequence of a variable heavy chain region of antibody number 26 in Table 1, and (ii) a nucleic acid sequence identical to the nucleic acid sequence of a variable light chain region of antibody number 26 in Table 2.

[0305] In some embodiments, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable heavy chain region of antibody number 27 in Table 1, and (ii) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable light chain region of antibody number 27 in Table 2. In one embodiment, the variable heavy chain region and/or variable light chain region encoded by the polynucleotide(s)(s) does not affect the amino acid sequence of the variable heavy chain region and/or variable light chain region. In one embodiment, the CDRs of the variable heavy chain region are identical to the CDRs of antibody number 27 in Tables 1 or 6, and the CDRs of the variable light chain region are identical to the CDRs of antibody number 27 in Tables 2 or 8. In another embodiment, a polynucleotide(s) described herein encodes a vari-

able heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence identical to the nucleic acid sequence of a variable heavy chain region of antibody number 27 in Table 1, and (ii) a nucleic acid sequence identical to the nucleic acid sequence of a variable light chain region of antibody number 27 in Table 2.

[0306] In some embodiments, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable heavy chain region of antibody number 28 in Table 1, and (ii) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable light chain region of antibody number 28 in Table 2. In one embodiment, the variable heavy chain region and/or variable light chain region encoded by the polynucleotide(s)(s) does not affect the amino acid sequence of the variable heavy chain region and/or variable light chain region. In one embodiment, the CDRs of the variable heavy chain region are identical to the CDRs of antibody number 28 in Tables 1 or 6, and the CDRs of the variable light chain region are identical to the CDRs of antibody number 28 in Tables 2 or 8. In another embodiment, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light the nucleic acid sequence of a variable heavy chain region of antibody number 28 in Table 1, and (ii) a nucleic acid sequence identical to the nucleic acid sequence of a variable light chain region of antibody number 28 in Table 2.

[0307] In some embodiments, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable heavy chain region of antibody number 29 in Table 1, and (ii) a nucleic acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% identical to the nucleic acid sequence of a variable light chain region of antibody number 29 in Table 2. In one embodiment, the variable heavy chain region and/or variable light chain region encoded by the polynucleotide(s)(s) does not affect the amino acid sequence of the variable heavy chain region and/or variable light chain region. In one embodiment, the CDRs of the variable heavy chain region are identical to the CDRs of antibody number 29 in Tables 1 or 6, and the CDRs of the variable light chain region are identical to the CDRs of antibody number 29 in Tables 2 or 8. In another embodiment, a polynucleotide(s) described herein encodes a variable heavy chain region and a variable light chain region, wherein the polynucleotide(s) comprises (i) a nucleic acid sequence identical to the nucleic acid sequence of a variable heavy chain region of antibody number 29 in Table 1, and (ii) a nucleic acid sequence identical to the nucleic acid sequence of a variable light chain region of antibody number 29 in Table 2.

[0308] In one embodiment, a polynucleotide provided herein comprises a nucleotide sequence encoding a kappa light chain (e.g., human kappa light chain). In one embodiment, a polynucleotide provided herein comprises a nucleotide sequence encoding a lambda light chain (e.g., human lambda light chain).

[0309] In one embodiment, a polynucleotide provided herein comprises a nucleotide sequence encoding an IgG1 heavy chain (e.g., human IgG1 heavy chain) of an antibody described herein. In one embodiment, a polynucleotide provided herein comprises a nucleotide sequence encoding IgG4 heavy chain (e.g., human IgG4 heavy chain). In one embodiment, a polynucleotide provided herein comprises a nucleotide sequence encoding IgG2 heavy chain (e.g., human IgG2 heavy chain).

[0310] In one embodiment, a polynucleotide provided herein encodes an antigen-binding domain, e.g., an Fab or $F(ab')_2$.

[0311] Also provided are polynucleotides that hybridize under high stringency, intermediate or lower stringency hybridization conditions to antisense polynucleotides of polynucleotides that encode an antibody described herein or a fragment thereof (e.g., variable heavy chain region and/or variable light chain region). In specific embodiments, a polynucleotide described herein hybridizes under high stringency, or intermediate stringency hybridization conditions to an antisense polynucleotide of a polynucleotide encoding a variable light chain region, provided herein. In another specific embodiments, a polynucleotide described herein hybridizes under high stringency, or intermediate stringency hybridization conditions to an antisense polynucleotide of a polynucleotide encoding a variable heavy chain region, provided herein.

[0312] Hybridization conditions have been described in the art and are known to one of skill in the art. For example, hybridization under stringent conditions can involve hybridization to filter-bound DNA in 6×sodium chloride/sodium citrate (SSC) at about 45° C. followed by one or more washes in 0.2×SSC/0.1% SDS at about 50-65° C.; hybridization under highly stringent conditions can involve hybridization to filter-bound nucleic acid in 6×SSC at about 45° C. followed by one or more washes in 0.1×SSC/0.2% SDS at about 68° C. Hybridization under other stringent hybridization conditions are known to those of skill in the art and have been described, see, for example, Ausubel, F. M. et al., eds., 1989, Current Protocols in Molecular Biology, Vol. I, Green Publishing Associates, Inc. and John Wiley & Sons, Inc., New York at pages 6.3.1-6.3.6 and 2.10.3.

[0313] Also provided herein are polynucleotides encoding an antibody that are optimized, e.g., by codon/RNA optimization, replacement with heterologous signal sequences, and elimination of mRNA instability elements. Methods to generate optimized nucleic acids encoding an antibody or a fragment thereof (e.g., light chain, heavy chain, a variable heavy chain region, or a variable light chain region) for recombinant expression by introducing codon changes and/or eliminating inhibitory regions in the mRNA can be carried out by adapting the optimization methods described in, e.g., U.S. Pat. Nos. 5,965,726; 6,174,666; 6,291,664; 6,414,132; and 6,794,498, accordingly. For example, potential splice sites and instability elements (e.g., A/T or A/U rich elements) within the RNA can be mutated without altering the amino acids encoded by the nucleic acid sequences to increase stability of the RNA for recombinant expression. The alterations utilize the degeneracy of the genetic code, e.g., using an alternative codon for an identical amino acid. In some embodiments, it can be desirable to alter one or

more codons to encode a conservative mutation, e.g., a similar amino acid with similar chemical structure and properties and/or function as the original amino acid. Such methods can increase expression of an antibody or fragment thereof by at least 1 fold, 2 fold, 3 fold, 4 fold, 5 fold, 10 fold, 20 fold, 30 fold, 40 fold, 50 fold, 60 fold, 70 fold, 80 fold, 90 fold, or 100 fold or more relative to the expression of an antibody encoded by polynucleotides that have not been optimized.

[0314] In certain embodiments, an optimized polynucleotide sequence encoding an antibody described herein or a fragment thereof (e.g., a variable light chain region and/or a variable heavy chain region) can hybridize to an antisense polynucleotide of an unoptimized polynucleotide encoding an antibody described herein or a fragment thereof (e.g., a variable light chain region and/or a variable heavy chain region). In specific embodiments, an optimized nucleotide sequence encoding an antibody described herein or a fragment thereof (e.g., a variable light chain region and/or a variable heavy chain region) hybridizes under high stringency conditions to an antisense polynucleotide of an unoptimized polynucleotide encoding an antibody described herein or a fragment thereof (e.g., a variable light chain region and/or a variable heavy chain region). In one embodiment, an optimized nucleotide sequence encoding an antibody described herein or a fragment thereof (e.g., a variable light chain region and/or a variable heavy chain region) hybridizes under intermediate or lower stringency hybridization conditions to an antisense polynucleotide of an unoptimized polynucleotide encoding an antibody described herein or a fragment thereof (e.g., a variable light chain region and/or a variable heavy chain region). Information regarding hybridization conditions have been described, see, e.g., U.S. Patent Application Publication No. US 2005/0048549 (e.g., paragraphs 72-73), which is incorporated herein by reference in its entirety.

[0315] The polynucleotides can be obtained, and the nucleotide sequence of the polynucleotides determined, by any method known in the art. Nucleotide sequences encoding antibodies described herein, and modified forms of these antibodies can be determined using methods well known in the art, i.e., nucleotide codons known to encode particular amino acids are assembled in such a way to generate a nucleic acid that encodes the antibody. Such a polynucleotide encoding the antibody can be assembled from chemically synthesized oligonucleotides (e.g., as described in Kutmeier et al., 1994, BioTechniques 17:242), which, briefly, involves the synthesis of overlapping oligonucleotides containing portions of the sequence encoding the antibody, annealing and ligating of those oligonucleotides, and then amplification of the ligated oligonucleotides by PCR.

[0316] Alternatively, a polynucleotide encoding an antibody described herein can be generated from nucleic acid from a suitable source (e.g., a hybridoma) using methods well known in the art (e.g., PCR and other molecular cloning methods). For example, PCR amplification using synthetic primers hybridizable to the 3' and 5' ends of a known sequence can be performed using genomic DNA obtained from hybridoma cells producing the antibody of interest. Such PCR amplification methods can be used to obtain nucleic acids comprising the sequence encoding the light chain and/or heavy chain of an antibody. Such PCR amplification methods can be used to obtain nucleic acids comprising the sequence encoding the variable light domain and/or the variable heavy domain of an antibody. The amplified nucleic acids can be cloned into vectors for expression in host cells and for further cloning, for example, to generate chimeric and humanized antibodies.

[0317] If a clone containing a nucleic acid encoding a particular antibody is not available, but the sequence of the antibody molecule is known, a nucleic acid encoding the immunoglobulin can be chemically synthesized or obtained from a suitable source (e.g., an antibody cDNA library or a cDNA library generated from, or nucleic acid, preferably poly A+RNA, isolated from, any tissue or cells expressing the antibody, such as hybridoma cells selected to express an antibody described herein) by PCR amplification using synthetic primers hybridizable to the 3' and 5' ends of the sequence or by cloning using an oligonucleotide probe specific for the particular gene sequence to identify, e.g., a cDNA clone from a cDNA library that encodes the antibody. Amplified nucleic acids generated by PCR can then be cloned into replicable cloning vectors using any method well known in the art.

[0318] DNA encoding an antibody can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of the antibody). Hybridoma cells can serve as a source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as *E. coli* cells, simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of antibodies in the recombinant host cells.

[0319] In phage display methods, functional antibody domains are displayed on the surface of phage particles which carry the polynucleotide sequences encoding them. In particular, a library of DNA sequences encoding a variable light chain region and/or a variable heavy chain region are generated (e.g., amplified from animal cDNA libraries such as human cDNA libraries or random libraries are generated by chemical synthesis). The DNA encoding the variable light chain region and a variable heavy chain region are recombined together with an scFv linker by PCR and cloned into a phagemid vector. The vector is electroporated in *E. coli* and the *E. coli* is infected with helper phage. Phage expressing an antigen-binding domain that binds to a particular antigen can be selected or identified with antigen, e.g., using labeled antigen or antigen bound or captured to a solid surface or bead. After phage selection, the antibody coding regions from the phage can be isolated and used to generate whole antibodies, including human antibodies, or any other desired antigen-binding fragment, and expressed in any desired host, including mammalian cells, insect cells, plant cells, yeast, and bacteria, e.g., as described below. Techniques to recombinantly produced Fab, Fab' and $F(ab')_2$ fragments can also be employed using methods known in the art such as those disclosed in PCT Publication No. WO 92/22324; Mullinax et al., 1992, *BioTechniques,* 12(6):864-869; Sawai et al., 1995, *AJRI,* 34:26-34; and Better et al., 1988, *Science,* 240:1041-1043.

[0320] Antibodies can be isolated from antibody phage libraries generated using the techniques described in McCafferty et al., *Nature,* 348:552-554 (1990). Clackson et al., *Nature,* 352:624-628 (1991). Marks et al., *J Mol. Biol.,* 222:581-597 (1991) describe the isolation of murine and

human antibodies, respectively, using phage libraries. Chain shuffling can be used in the production of high affinity (nM range) human antibodies (Marks et al., *Bio/Technology,* 10:779-783 (1992)), as well as combinatorial infection and in vivo recombination as a strategy for constructing very large phage libraries (Waterhouse et al., *Nuc. Acids. Res.,* 21:2265-2266 (1993)).

[0321] To generate whole antibodies, PCR primers including a variable light chain region and a variable heavy chain region nucleotide sequences, a restriction site, and a flanking sequence to protect the restriction site can be used to amplify the VH or VL sequences in scFv clones. Utilizing cloning techniques known to those of skill in the art, the PCR amplified VH domains can be cloned into vectors expressing a heavy chain constant region, e.g., the human gamma 4 constant region, and the PCR amplified VL domains can be cloned into vectors expressing a light chain constant region, e.g., human kappa or lambda constant regions. In certain embodiments, the vectors for expressing the VH or VL domains comprise a promoter, a secretion signal, a cloning site for the variable domain, constant domains, and a selection marker such as neomycin. The VH and VL domains can also be cloned into one vector expressing the necessary constant regions. The heavy chain conversion vectors and light chain conversion vectors are then co-transfected into cell lines to generate stable or transient cell lines that express full-length antibodies, e.g., IgG, using techniques known to those of skill in the art.

[0322] In one embodiment, provided herein are two vectors (e.g., plasmids or viruses), wherein one vector comprises the variable heavy chain region of an antibody described herein, and the second vector comprises the variable light chain region of an antibody described herein.

[0323] In a non-limiting example, the Dyax (Cambridge, MA) technology platform can be used to convert Fab-phage or Fabs to complete IgG antibodies, such as the Dyax pR rapid reformatting vectors (RR). Briefly, by PCR, a Fab-encoding DNA fragment is inserted into a Dyax pR-RRV between a eukaryotic leader sequence and an IgG heavy chain constant region cDNA. Antibody expression is driven by the human cytomegalovirus (hCMV). In a second cloning step, bacterial regulatory elements are replaced by the appropriate eukaryotic sequences (i.e., the IRES (internal ribosome entry site) motif). The expression vector can also include the SV40 origin of replication. The Dyax pRh1(a,z), pRh1(f), pRh4 and pRm2a are expression vectors allowing expression of reformatted FAbs as human IgG1 (isotype a,z), human IgG1 (isotype F), human IgG4, and mouse IgG2a, respectively. Expressing vectors can be introduced into a suitable host cell (e.g., HEK293T cells, CHO cells)) for expression and purification.

[0324] In some embodiments, a polynucleotide(s) encoding an antibody provided herein is isolated. In other embodiments, a polynucleotide(s) encoding an antibody provided herein is not isolated. In yet other embodiments, a polynucleotide(s) encoding an antibody provided herein is integrated, e.g., into chromosomal DNA or an expression vector. In specific embodiments, a polynucleotide(s) encoding an antibody provided herein is not integrated into chromosomal DNA.

[0325] 6.3 Antibody Production

[0326] In one aspect, provided herein are methods for making an antibody described herein, which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g. RBD). In one embodiment, an antibody described herein (e.g., an antigen-binding fragment), which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g. RBD), may be prepared, expressed, created or isolated by any means that involves creation, e.g., via synthesis or genetic engineering of sequences. In one embodiment, such an antibody comprises sequences that are encoded by DNA sequences that do not naturally exist withing the antibody germline repertoire of an animal or mammal (e.g., a human).

[0327] In certain aspects, a method for making an antibody described herein, which binds to SARS-CoV-2 or fragment thereof (e.g. RBD), comprises the step of culturing a cell (e.g., host cell or hybridoma cell) that expresses the antibody. In certain embodiments, the method for making an antibody described herein further comprises the step of purifying the antibody expressed by the cell. In certain aspects, a method for making an antibody described herein (e.g., an antigen-binding fragment thereof), which binds to SARS-CoV-2 spike protein or a fragment thereof (e.g. RBD), comprises the step of culturing a cell (e.g., host cell or hybridoma cell) that comprises polynucleotides or vectors encoding the antibody. In one aspect, provided herein are methods for producing an antibody described herein (e.g., an antigen-binding fragment thereof), comprising expressing such antibody from a host cell.

[0328] In certain aspects, provided herein are cells (e.g., host cells) expressing (e.g., recombinantly expressing) the antibodies described herein (e.g., an antigen-binding fragment thereof) and related expression vectors. In another aspect, provided herein are vectors (e.g., expression vectors) comprising polynucleotides comprising nucleotide sequences encoding antibodies (e.g., an antigen-binding fragment) for recombinant expression in host cells, preferably in mammalian cells. Also provided herein are host cells comprising a polynucleotide encoding an antibody, or vectors comprising a polynucleotide encoding an antibody for recombinantly expressing an antibody described herein. In one embodiment, provided herein is a host cell comprising two vectors, wherein the first vector comprises a polynucleotide of an antibody described herein, and the second vector comprises a polynucleotide encoding an antibody for recombinantly expressing an antibody described herein. The cells may be primary cells or cell lines. In one aspect, provided herein are hybridoma cells expressing an antibody described herein. In one embodiment, the host cell is isolated from other cells. In another embodiment, the host cell is not found within the body of a subject.

[0329] Antibodies described herein (e.g., monoclonal antibodies, such as chimeric or humanized antibodies, or an antigen-binding fragment thereof) that bind to SARS-CoV-2 spike protein or a fragment thereof (e.g. RBD) can be produced by any method known in the art for the synthesis of antibodies, for example, by chemical synthesis or by recombinant expression techniques. The methods described herein employ, unless otherwise indicated, conventional techniques in molecular biology, microbiology, genetic analysis, recombinant DNA, organic chemistry, biochemistry, PCR, oligonucleotide synthesis and modification, nucleic acid hybridization, and related fields within the skill of the art. These techniques are described in the references cited herein and are fully explained in the literature. See, e.g., Maniatis et al. (1982) *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press; Sambrook et al. (1989), *Molecular Cloning: A Laboratory Manual*, Sec-

ond Edition, Cold Spring Harbor Laboratory Press; Sambrook et al. (2001) *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY; Ausubel et al., *Current Protocols in Molecular Biology*, John Wiley & Sons (1987 and annual updates); *Current Protocols in Immunology*, John Wiley & Sons (1987 and annual updates) Gait (ed.) (1984) *Oligonucleotide Synthesis: A Practical Approach*, IRL Press; Eckstein (ed.) (1991) *Oligonucleotides and Analogues: A Practical Approach*, IRL Press; Birren et al. (eds.) (1999) *Genome Analysis: A Laboratory Manual*, Cold Spring Harbor Laboratory Press.

[0330] Monoclonal antibodies can be prepared using a wide variety of techniques known in the art including the use of hybridoma, recombinant, and phage display technologies, or a combination thereof. For example, monoclonal antibodies can be produced using hybridoma techniques including those known in the art and taught, for example, in Harlow et al., *Antibodies: A Laboratory Manual*, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988); Hammerling et al., in: *Monoclonal Antibodies and T-Cell Hybridomas* 563 681 (Elsevier, N.Y., 1981). The term "monoclonal antibody" as used herein is not limited to antibodies produced through hybridoma technology.

[0331] Methods for producing and screening for specific antibodies using hybridoma technology are routine and well known in the art. For example, in the hybridoma method, a mouse or other appropriate host animal, such as a sheep, goat, rabbit, rat, hamster or macaque monkey, is immunized to elicit lymphocytes that produce or are capable of producing antibodies that will bind to the protein (e.g., SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD)) used for immunization. Alternatively, lymphocytes may be immunized in vitro. Lymphocytes then are fused with myeloma cells using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, *Monoclonal Antibodies: Principles and Practice*, pp. 59-103 (Academic Press, 1986)).

[0332] Additionally, a RIMMS (repetitive immunization multiple sites) technique can be used to immunize an animal (Kilptrack et al., 1997 Hybridoma 16:381-9, incorporated by reference in its entirety).

[0333] The hybridoma cells thus prepared are seeded and grown in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, parental myeloma cells. For example, if the parental myeloma cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine (HAT medium), which substances prevent the growth of HGPRT-deficient cells.

[0334] Specific embodiments employ myeloma cells that fuse efficiently, support stable high-level production of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. Among these myeloma cell lines are murine myeloma lines, such as those derived from MOPC-21 and MPC-11 mouse tumors available from the Salk Institute Cell Distribution Center, San Diego, CA, USA, and SP-2 or X63-Ag8.653 cells available from the American Type Culture Collection, Rockville, MD, USA. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, *J. Immunol.*, 133: 3001 (1984); Brodeur et al., *Monoclonal Antibody Production Techniques and Applications*, pp. 51-63 (Marcel Dekker, Inc., New York, 1987)).

[0335] Culture medium in which hybridoma cells are growing is assayed for production of monoclonal antibodies directed against SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD). The binding specificity of monoclonal antibodies produced by hybridoma cells is determined by methods known in the art, for example, immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA).

[0336] After hybridoma cells are identified that produce antibodies of the desired specificity, affinity, and/or activity, the clones may be subcloned by limiting dilution procedures and grown by standard methods (Goding, *Monoclonal Antibodies: Principles and Practice*, pp. 59-103 (Academic Press, 1986)). Suitable culture media for this purpose include, for example, D-MEM or RPMI 1640 medium. Alternatively, clonal cells can be isolated using a semi-solid agar supplemented with HAT (Stemcell Technologies). In addition, the hybridoma cells may be grown in vivo as ascites tumors in an animal.

[0337] The monoclonal antibodies secreted by the subclones are suitably separated from the culture medium, ascites fluid, or serum by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

[0338] In some embodiments, mice (or other animals, such as rats, monkeys, donkeys, pigs, sheep, goats, hamsters, or dogs) can be immunized with an antigen (e.g., SARS-CoV-2 spike proteina fragment thereof (e.g., RBD)) and once an immune response is detected, e.g., antibodies specific for the antigen are detected in the mouse serum, the mouse spleen is harvested and splenocytes isolated. The splenocytes are then fused by well known techniques to any suitable myeloma cells, for example cells from cell line SP2/0 available from the American Type Culture Collection (ATCC®) (Manassas, VA), to form hybridomas. Hybridomas are selected and cloned by limited dilution.

[0339] In certain embodiments, lymph nodes of the immunized mice are harvested and fused with NS0 myeloma cells.

[0340] The hybridoma clones are then assayed by methods known in the art for cells that secrete antibodies capable of binding a polypeptide of the antigen. Ascites fluid, which generally contains high levels of antibodies, can be generated by immunizing mice with positive hybridoma clones.

[0341] Accordingly, described herein are methods of making antibodies described herein by culturing a hybridoma cell secreting an antibody. In certain embodiments, the method of making an antibody described herein further comprises the step of purifying the antibody.

[0342] In some embodiments, the hybridoma is generated by fusing splenocytes isolated from a mouse (or other animal, such as rat, monkey, donkey, pig, sheep, or dog) immunized with SARS-CoV-2 spike proteina fragment thereof (e.g. RBD) with myeloma cells and then screening the hybridomas resulting from the fusion for hybridoma clones that secrete an antibody able to bind to the SARS-CoV-2 spike protein or a fragment thereof (e.g. RBD). In certain embodiments, the hybridoma is generated by fusing lymph nodes isolated from a mouse (or other animal, such as rat, monkey, donkey, pig, sheep, or dog) immunized with a SARS-CoV-2 spike protein or a fragment thereof (e.g.

RBD) with myeloma cells, and then screening the hybridomas resulting from the fusion for hybridoma clones that secrete an antibody able to bind to the SARS-CoV-2 spike protein or a fragment thereof (e.g. RBD).

[0343] Antibodies described herein include antibody fragments that recognize SARS-CoV-2 spike protein or a fragment thereof (e.g. RBD) and can be generated by any technique known to those of skill in the art. For example, Fab and $F(ab')_2$ fragments described herein can be produced by proteolytic cleavage of immunoglobulin molecules, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce $F(ab')_2$ fragments). A Fab fragment corresponds to one of the two identical arms of an antibody molecule and contains the complete light chain paired with the VH and CH1 domains of the heavy chain. A $F(ab')_2$ fragment contains the two antigen-binding arms of an antibody molecule linked by disulfide bonds in the hinge region.

[0344] Further, the antibodies described herein can also be generated using various phage display methods known in the art. Examples of phage display methods that can be used to make the antibodies described herein include those disclosed in Brinkman et al., 1995, J. Immunol. Methods 182:41-50; Ames et al., 1995, J. Immunol. Methods 184:177-186; Kettleborough et al., 1994, Eur. J. Immunol. 24:952-958; Persic et al., 1997, Gene 187:9-18; Burton et al., 1994, Advances in Immunology 57:191-280; PCT Application No. PCT/GB91/O1 134; International Publication Nos. WO 90/02809, WO 91/10737, WO 92/01047, WO 92/18619, WO 93/1 1236, WO 95/15982, WO 95/20401, and WO97/13844; and U.S. Pat. Nos. 5,698,426, 5,223,409, 5,403,484, 5,580,717, 5,427,908, 5,750,753, 5,821,047, 5,571,698, 5,427,908, 5,516,637, 5,780,225, 5,658,727, 5,733,743 and 5,969,108.

[0345] As described in the above references, after phage selection, the antibody coding regions from the phage can be isolated and used to generate whole antibodies, including human antibodies, or any other desired antigen binding fragment, and expressed in any desired host, including mammalian cells, insect cells, plant cells, yeast, and bacteria, e.g., as described below. Techniques to recombinantly produce antibody fragments such as Fab, Fab' and $F(ab')_2$ fragments can also be employed using methods known in the art such as those disclosed in PCT publication No. WO 92/22324; Mullinax et al., 1992, BioTechniques 12(6):864-869; Sawai et al., 1995, AJRI 34:26-34; and Better et al., 1988, Science 240:1041-1043.

[0346] In one aspect, to generate whole antibodies, PCR primers including variable heavy chain region or variable light chain region nucleotide sequences, a restriction site, and a flanking sequence to protect the restriction site can be used to amplify the variable heavy chain region or variable light chain region sequences from a template, e.g., scFv clones. Utilizing cloning techniques known to those of skill in the art, the PCR amplified variable heavy chain region can be cloned into vectors expressing a heavy chain constant region, and the PCR amplified variable light chain region can be cloned into vectors expressing a light chain constant region, e.g., human kappa or lambda constant regions. The variable heavy chain region and variable light chain region can also be cloned into one vector expressing the necessary constant regions. The heavy chain conversion vectors and light chain conversion vectors are then co-transfected into cell lines to generate stable or transient cell lines that express full-length antibodies, e.g., IgG, using techniques known to those of skill in the art.

[0347] For some uses, including in vivo use of antibodies in humans and in vitro detection assays, it can be preferable to use human, humanized or chimeric antibodies. Completely human antibodies are particularly desirable for therapeutic treatment of human subjects. Human antibodies can be made by a variety of methods known in the art including phage display methods described above using antibody libraries derived from human immunoglobulin sequences. See also U.S. Pat. Nos. 4,444,887 and 4,716,111; and International Publication Nos. WO 98/46645, WO 98/50433, WO 98/24893, WO 98/16654, WO 96/34096, WO 96/33735, and WO 91/10741.

[0348] Human antibodies can be produced using any method known in the art. For example, transgenic mice which are incapable of expressing functional endogenous immunoglobulins, but which can express human immunoglobulin genes, can be used. In particular, the human heavy and light chain immunoglobulin gene complexes can be introduced randomly or by homologous recombination into mouse embryonic stem cells. Alternatively, the human variable region, constant region, and diversity region can be introduced into mouse embryonic stem cells in addition to the human heavy and light chain genes. The mouse heavy and light chain immunoglobulin genes can be rendered non-functional separately or simultaneously with the introduction of human immunoglobulin loci by homologous recombination. In particular, homozygous deletion of the J_H region prevents endogenous antibody production. The modified embryonic stem cells are expanded and microinjected into blastocysts to produce chimeric mice. The chimeric mice are then bred to produce homozygous offspring which express human antibodies. The transgenic mice are immunized in the normal fashion with a selected antigen, e.g., all or a portion of an antigen (e.g., SARS-CoV-2 spike protein or a fragment thereof (e.g. RBD). Monoclonal antibodies directed against the antigen can be obtained from the immunized, transgenic mice using conventional hybridoma technology. The human immunoglobulin transgenes harbored by the transgenic mice rearrange during B cell differentiation, and subsequently undergo class switching and somatic mutation. Thus, using such a technique, it is possible to produce therapeutically useful IgG, IgA, IgM and IgE antibodies. For an overview of this technology for producing human antibodies, see Lonberg and Huszar, 1995, Int. Rev. Immunol. 13:65-93. For a detailed discussion of this technology for producing human antibodies and human monoclonal antibodies and protocols for producing such antibodies, see, e.g., PCT publication Nos. WO 98/24893, WO 96/34096, and WO 96/33735; and U.S. Pat. Nos. 5,413,923, 5,625,126, 5,633,425, 5,569,825, 5,661,016, 5,545,806, 5,814,318, and 5,939,598.

[0349] In some embodiments, human antibodies can be produced using mouse-human hybridomas. In some embodiments, human antibodies can be generated by inserting polynucleotides encoding human CDRs (e.g., VL CDRs and/or VH CDRs) of an antibody into an expression vector containing nucleotide sequences encoding human framework region sequences. In certain embodiments, such expression vectors further comprise nucleotide sequences encoding a constant region of a human light and/or heavy chain. In some embodiments, human antibodies can be

generated by inserting human CDRs (e.g., VL CDRs and/or VH CDRs) of an antibody obtained from a phage library into such human expression vectors.

[0350] In certain embodiments, a human antibody can be generated by selecting human CDR sequences that are homologous (or substantially homologous) to non-human CDR sequences of a non-human antibody and selecting human framework sequences that are homologous (or substantially homologous) to non-human framework sequences of a non-human antibody.

[0351] Single domain antibodies, for example, antibodies lacking the light chains, can be produced by methods well-known in the art. See Riechmann et al., 1999, J. Immunol. 231:25-38; Nuttall et al., 2000, Curr. Pharm. Biotechnol. 1(3):253-263; Muylderman, 2001, J. Biotechnol. 74(4):277302; U.S. Pat. No. 6,005,079; and International Publication Nos. WO 94/04678, WO 94/25591, and WO 01/44301.

[0352] Bispecific antibodies are antibodies that have binding specificities for at least two different epitopes. Exemplary bispecific antibodies may bind to two different epitopes of an antigen or to two different epitopes of two different antigens. In specific embodiments, a bispecific antibody has two distinct antigen-binding domains, wherein each domain specifically binds to a different antigen. Other such antibodies may bind a first antigen (e.g., SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD)) and further bind a second antigen. Bispecific antibodies can be prepared as full-length antibodies or antibody fragments (e.g., F(ab'): bispecific antibodies).

[0353] Methods for making bispecific antibodies are known in the art. (See, for example, Millstein et al., Nature, 305:537-539 (1983); Traunecker et al., EMBO J., 10:3655-3659 (1991); Suresh et al., Methods in Enzymology, 121: 210 (1986); Kostelny et al., J. Immunol., 148(5):1547-1553 (1992); Hollinger et al., Proc. Natl. Acad. Sci. USA, 90:6444-6448 (1993); Gruber et al., J. Immunol., 152:5368 (1994); U.S. Pat. Nos. 4,474,893; 4,714,681; 4,925,648; 5,573,920; 5,601,81; 95,731,168; 4,676,980; and 4,676,980, WO 94/04690; WO 91/00360; WO 92/200373; WO 93/17715; WO 92/08802; and EP 03089.)

[0354] Further, antibodies that bind to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) can, in turn, be utilized to generate anti-idiotype antibodies that "mimic" an antigen using techniques well known to those skilled in the art. (See, e.g., Greenspan & Bona, 1989, FASEB J. 7(5): 437-444; and Nissinoff, 1991, J. Immunol. 147(8):2429-2438).

[0355] Recombinant expression of an antibody described herein (e.g., a full-length antibody, heavy and/or light chain of an antibody, or a single chain antibody described herein) that binds to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), can for example, involve construction of vectors (e.g., expression vectors) containing a polynucleotide that encodes the antibody or fragments thereof (e.g., VL domain and/or VH domain). Once a polynucleotide encoding an antibody molecule, heavy and/or light chain of an antibody, or antigen-binding fragment thereof described herein has been obtained, a vector for the production of the antibody molecule can be produced by recombinant DNA technology using techniques well-known in the art. Methods for preparing a protein by expressing a polynucleotide containing an antibody encoding nucleotide sequence are described herein. Methods which are well known to those skilled in the art can be used to construct expression vectors containing antibody coding sequences and appropriate transcriptional and translational control signals. These methods include, for example, in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. Also provided are replicable vectors comprising a nucleotide sequence encoding an antibody molecule described herein, a heavy or light chain of an antibody, a heavy or light chain variable domain of an antibody or a fragment thereof, or a heavy or light chain CDR, operably linked to a promoter. Such vectors can, for example, include the nucleotide sequence encoding the constant region of the antibody molecule (see, e.g., International Publication Nos. WO 86/05807 and WO 89/01036; and U.S. Pat. No. 5,122,464) and the variable domain of the antibody can be cloned into such a vector for expression of the entire heavy, the entire light chain, or both the entire heavy and light chains.

[0356] An expression vector can be transferred to a cell (e.g., host cell) by conventional techniques and the resulting cells can then be cultured by conventional techniques to produce an antibody described herein or a fragment thereof. Thus, provided herein are host cells containing a polynucleotide encoding an antibody described herein or fragments thereof, or a heavy or light chain thereof, or antigen-binding fragment thereof, or a single chain antibody described herein, operably linked to a promoter for expression of such sequences in the host cell. In certain embodiments, e.g., for the expression of double-chained antibodies, vectors encoding both the heavy and light chains individually can be co-expressed in the host cell for expression of the entire immunoglobulin molecule, as detailed below. In certain embodiments, a host cell contains a vector comprising a polynucleotide encoding both the heavy chain and light chain of an antibody described herein, or a fragment thereof. In specific embodiments, a host cell contains two different vectors, a first vector comprising a polynucleotide encoding a heavy chain of an antibody described herein, or a fragment thereof, and a second vector comprising a polynucleotide encoding a light chain of an antibody described herein, or a fragment thereof. In other embodiments, a first host cell comprises a first vector comprising a polynucleotide encoding a heavy chain of an antibody described herein, or a fragment thereof, and a second host cell comprises a second vector comprising a polynucleotide encoding a light chain of an antibody described herein.

[0357] A variety of host-expression vector systems can be utilized to express antibody molecules described herein (see, e.g., U.S. Pat. No. 5,807,715). Such host-expression systems represent vehicles by which the coding sequences of interest can be produced and subsequently purified, but also represent cells which can, when transformed or transfected with the appropriate nucleotide coding sequences, express an antibody molecule described herein in situ. These include but are not limited to microorganisms such as bacteria (e.g., *E. coli* and *B. subtilis*) transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA expression vectors containing antibody coding sequences; yeast (e.g., *Saccharomyces, Pichia*) transformed with recombinant yeast expression vectors containing antibody coding sequences; insect cell systems infected with recombinant virus expression vectors (e.g., baculovirus) containing antibody coding sequences; plant cell systems (e.g., green algae such as *Chlamydomonas reinhardtii*) infected with recombinant virus expression vectors (e.g., cauliflower mosaic

virus, CaMV; tobacco mosaic virus, TMV) or transformed with recombinant plasmid expression vectors (e.g., Ti plasmid) containing antibody coding sequences; or mammalian cell systems (e.g., COS, CHO, BHK, MDCK, HEK 293, NS0, PER.C6, VERO, CRL7O3O, HsS78Bst, HeLa, and NIH 3T3 cells) harboring recombinant expression constructs containing promoters derived from the genome of mammalian cells (e.g., metallothionein promoter) or from mammalian viruses (e.g., the adenovirus late promoter; the vaccinia virus 7.5K promoter). In one embodiment, a mammalian expression vector is pOptiVEC™ or pcDNA3.3. Preferably, bacterial cells such as *Escherichia coli*, and more preferably, eukaryotic cells, especially for the expression of whole recombinant antibody molecule, are used for the expression of a recombinant antibody molecule. For example, mammalian cells such as Chinese hamster ovary (CHO) cells, in conjunction with a vector such as the major intermediate early gene promoter element from human cytomegalovirus is an effective expression system for antibodies (Foecking et al., 1986, Gene 45:101; and Cockett et al., 1990, Bio/Technology 8:2). In certain embodiments, antibodies described herein are produced by CHO cells or NS0 cells. In one embodiment, the expression of nucleotide sequences encoding antibodies described herein (or fragments thereof) which bind to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) is regulated by a constitutive promoter, inducible promoter or tissue specific promoter.

[0358] In bacterial systems, a number of expression vectors can be advantageously selected depending upon the use intended for the antibody molecule being expressed. For example, when a large quantity of such an antibody is to be produced, for the generation of pharmaceutical compositions of an antibody molecule, vectors which direct the expression of high levels of fusion protein products that are readily purified can be desirable. Such vectors include, but are not limited to, the *E. coli* expression vector pUR278 (Ruther et al., 1983, EMBO 12:1791), in which the antibody coding sequence can be ligated individually into the vector in frame with the lac Z coding region so that a fusion protein is produced; pIN vectors (Inouye & Inouye, 1985, Nucleic Acids Res. 13:3101-3109; Van Heeke & Schuster, 1989, J. Biol. Chem. 24:5503-5509); and the like. pGEX vectors can also be used to express foreign polypeptides as fusion proteins with glutathione 5-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption and binding to matrix glutathione agarose beads followed by elution in the presence of free glutathione. The pGEX vectors are designed to include thrombin or factor Xa protease cleavage sites so that the cloned target gene product can be released from the GST moiety.

[0359] In an insect system, *Autographa californica* nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes. The virus grows in *Spodoptera frugiperda* cells. The antibody coding sequence can be cloned individually into non-essential regions (for example the polyhedrin gene) of the virus and placed under control of an AcNPV promoter (for example the polyhedrin promoter).

[0360] In mammalian host cells, a number of viral-based expression systems can be utilized. In cases where an adenovirus is used as an expression vector, the antibody coding sequence of interest can be ligated to an adenovirus transcription/translation control complex, e.g., the late promoter and tripartite leader sequence. This chimeric gene can then be inserted in the adenovirus genome by in vitro or in vivo recombination. Insertion in a non-essential region of the viral genome (e.g., region E1 or E3) will result in a recombinant virus that is viable and capable of expressing the antibody molecule in infected hosts (e.g., see Logan & Shenk, 1984, Proc. Natl. Acad. Sci. USA 8 1:355-359). Specific initiation signals can also be required for efficient translation of inserted antibody coding sequences. These signals include the ATG initiation codon and adjacent sequences. Furthermore, the initiation codon must be in phase with the reading frame of the desired coding sequence to ensure translation of the entire insert. These exogenous translational control signals and initiation codons can be of a variety of origins, both natural and synthetic. The efficiency of expression can be enhanced by the inclusion of appropriate transcription enhancer elements, transcription terminators, etc. (see, e.g., Bittner et al., 1987, Methods in Enzymol. 153:51-544).

[0361] As used herein, the term "host cell" refers to any type of cell, e.g., a primary cell or a cell from a cell line. In specific embodiments, the term "host cell" refers a cell transfected with a polynucleotide and the progeny or potential progeny of such a cell. Progeny of such a cell may not be identical to the parent cell transfected with the polynucleotide due to mutations or environmental influences that may occur in succeeding generations or integration of the polynucleotide into the host cell genome.

[0362] In addition, a host cell strain can be chosen which modulates the expression of the inserted sequences or modifies and processes the gene product in the specific fashion desired. Such modifications (e.g., glycosylation) and processing (e.g., cleavage) of protein products can be important for the function of the protein. Different host cells have characteristic and specific mechanisms for the post-translational processing and modification of proteins and gene products. Appropriate cell lines or host systems can be chosen to ensure the correct modification and processing of the foreign protein expressed. To this end, eukaryotic host cells which possess the cellular machinery for proper processing of the primary transcript, glycosylation, and phosphorylation of the gene product can be used. Such mammalian host cells include but are not limited to CHO, VERO, BHK, Hela, COS, MDCK, HEK 293, NIH 3T3, W138, BT483, Hs578T, HTB2, BT2O and T47D, NS0 (a murine myeloma cell line that does not endogenously produce any immunoglobulin chains), CRL7O3O and HsS78Bst cells. In certain embodiments, humanized monoclonal antibodies described herein are produced in mammalian cells, such as CHO cells.

[0363] For long-term, high-yield production of recombinant proteins, stable expression is preferred. For example, cell lines that stably express the antibody molecule can be engineered. Rather than using expression vectors that contain viral origins of replication, host cells can be transformed with DNA controlled by appropriate expression control elements (e.g., promoter, enhancer, sequences, transcription terminators, polyadenylation sites, etc.), and a selectable marker. Following the introduction of the foreign DNA, engineered cells can be allowed to grow for 1-2 days in an enriched media, and then are switched to a selective media. The selectable marker in the recombinant plasmid confers resistance to the selection and allows cells to stably integrate the plasmid into their chromosomes and grow to form foci which in turn can be cloned and expanded into cell lines.

This method can advantageously be used to engineer cell lines which express the antibody molecule. Such engineered cell lines can be particularly useful in screening and evaluation of compositions that interact directly or indirectly with the antibody molecule.

[0364] A number of selection systems can be used, including but not limited to, the herpes simplex virus thymidine kinase (Wigler et al., 1977, Cell 11:223), hypoxanthineguanine phosphoribosyltransferase (Szybalska & Szybalski, 1992, Proc. Natl. Acad. Sci. USA 48:202), and adenine phosphoribosyltransferase (Lowy et al., 1980, Cell 22:8-17) genes can be employed in tk-, hgprt- or aprt-cells, respectively. Also, antimetabolite resistance can be used as the basis of selection for the following genes: dhfr, which confers resistance to methotrexate (Wigler et al., 1980, Natl. Acad. Sci. USA 77:357; O'Hare et al., 1981, Proc. Natl. Acad. Sci. USA 78:1527); gpt, which confers resistance to mycophenolic acid (Mulligan & Berg, 1981, Proc. Natl. Acad. Sci. USA 78:2072); neo, which confers resistance to the aminoglycoside G-418 (Wu and Wu, 1991, Biotherapy 3:87-95; Tolstoshev, 1993, Ann. Rev. Pharmacol. Toxicol. 32:573-596; Mulligan, 1993, Science 260:926-932; and Morgan and Anderson, 1993, Ann. Rev. Biochem. 62:191-217; May, 1993, TIB TECH 11(5):155-215); and hygro, which confers resistance to hygromycin (Santerre et al., 1984, Gene 30:147). Methods commonly known in the art of recombinant DNA technology can be routinely applied to select the desired recombinant clone, and such methods are described, for example, in Ausubel et al. (eds.), *Current Protocols in Molecular Biology*, John Wiley & Sons, N Y (1993); Kriegler, *Gene Transfer and Expression*, A Laboratory Manual, Stockton Press, N Y (1990); and in Chapters 12 and 13, Dracopoli et al. (eds.), *Current Protocols in Human Genetics*, John Wiley & Sons, N Y (1994); Colberre-Garapin et al., 1981, J. Mol. Biol. 150:1, which are incorporated by reference herein in their entireties.

[0365] The expression levels of an antibody molecule can be increased by vector amplification (for a review, see Bebbington and Hentschel, The use of vectors based on gene amplification for the expression of cloned genes in mammalian cells in DNA cloning, Vol. 3 (Academic Press, New York, 1987)). When a marker in the vector system expressing antibody is amplifiable, increase in the level of inhibitor present in culture of host cell will increase the number of copies of the marker gene. Since the amplified region is associated with the antibody gene, production of the antibody will also increase (Crouse et al., 1983, Mol. Cell. Biol. 3:257).

[0366] The host cell can be co-transfected with two or more expression vectors described herein, the first vector encoding a heavy chain derived polypeptide and the second vector encoding a light chain derived polypeptide. In one embodiment, a host cell comprises two expression vectors: one vector comprising a polynucleotide sequence comprising a nucleotide sequence encoding a heavy chain variable region of an antibody described herein and a second vector comprising a polynucleotide sequence comprising a nucleotide sequence encoding a light chain variable region of an antibody described herein.

[0367] Alternatively, a single vector can be used which encodes, and is capable of expressing, both heavy and light chain polypeptides. In such situations, the light chain should be placed before the heavy chain to avoid an excess of toxic free heavy chain (Proudfoot, 1986, Nature 322:52; and Kohler, 1980, Proc. Natl. Acad. Sci. USA 77:2197-2199). The coding sequences for the heavy and light chains can comprise cDNA or genomic DNA. The expression vector can be monocistronic or multicistronic. A multicistronic nucleic acid construct can encode 2, 3, 4, 5, 6, 7, 8, 9, 10 or more, or in the range of 2-5, 5-10 or 10-20 genes/nucleotide sequences. For example, a bicistronic nucleic acid construct can comprise in the following order a promoter, a first gene (e.g., heavy chain of an antibody described herein), and a second gene and (e.g., light chain of an antibody described herein). In such an expression vector, the transcription of both genes can be driven by the promoter, whereas the translation of the mRNA from the first gene can be by a cap-dependent scanning mechanism and the translation of the mRNA from the second gene can be by a cap-independent mechanism, e.g., by an IRES. Once an antibody molecule described herein has been produced by recombinant expression, it can be purified by any method known in the art for purification of an immunoglobulin molecule, for example, by chromatography (e.g., ion exchange, affinity, particularly by affinity for the specific antigen after Protein A, and sizing column chromatography), centrifugation, differential solubility, or by any other standard technique for the purification of proteins. Further, the antibodies described herein can be fused to heterologous polypeptide sequences described herein or otherwise known in the art to facilitate purification.

[0368] In some embodiments, an antibody (e.g., a monoclonal antibody, such as a humanized or chimeric antibody or an antigen-binding fragment thereof) described herein is isolated or purified. Generally, an isolated antibody is one that is substantially free of other antibodies with different antigenic specificities than the isolated antibody. For example, in one embodiment, a preparation of an antibody described herein is substantially free of cellular material and/or chemical precursors. The language "substantially free of cellular material" includes preparations of an antibody in which the antibody is separated from cellular components of the cells from which it is isolated or recombinantly produced. Thus, an antibody that is substantially free of cellular material includes preparations of antibody having less than about 30%, 20%, 10%, 5%, 2%, 1%, 0.5%, or 0.1% (by dry weight) of heterologous protein (also referred to herein as a "contaminating protein") and/or variants of an antibody, for example, different post-translational modified forms of an antibody or other different versions of an antibody (e.g., antibody fragments). When the antibody is recombinantly produced, it is also generally substantially free of culture medium, i.e., culture medium represents less than about 20%, 10%, 2%, 1%, 0.5%, or 0.1% of the volume of the protein preparation. When the antibody is produced by chemical synthesis, it is generally substantially free of chemical precursors or other chemicals, i.e., it is separated from chemical precursors or other chemicals that are involved in the synthesis of the protein. Accordingly, such preparations of the antibody have less than about 30%, 20%, 10%, 5% (by dry weight) of chemical precursors or compounds other than the antibody of interest. In one embodiment, antibodies described herein are isolated or purified.

[0369] 6.4 Compositions

[0370] Provided herein are compositions (e.g., pharmaceutical compositions) comprising an antibody having the desired degree of purity in a physiologically acceptable carrier, excipient or stabilizer (*Remington's Pharmaceutical*

Sciences (1990) Mack Publishing Co., Easton, PA). In one embodiment, a composition comprises an antibody described herein and an acceptable carrier or excipient. In some embodiments, a composition comprises two or more antibodies described herein an acceptable carrier or excipient. In one embodiment, the compositions comprise an antibody conjugated to a moiety such as described herein. Acceptable carriers, excipients, or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, histidine, and other organic acids; antioxidants; amino acids such as glycine, glutamine, asparagine, histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugars such as sucrose, mannitol, trehalose or sorbitol; salt-forming counter-ions such as sodium; metal complexes (e.g., Zn-protein complexes); and/or non-ionic surfactants such as TWEEN™, PLURONICS™ or polyethylene glycol (PEG).

[0371] In one embodiment, pharmaceutical compositions comprise an antibody, and optionally one or more additional prophylactic or therapeutic agents, in a pharmaceutically acceptable carrier. In one embodiment, pharmaceutical compositions comprise an effective amount of an antibody, and optionally one or more additional prophylactic of therapeutic agents, in a pharmaceutically acceptable carrier. In some embodiments, the antibody is the only active ingredient included in the pharmaceutical composition. In one embodiment, pharmaceutical compositions comprise an antibody conjugated to a moiety such as described herein, and optionally one or more additional prophylactic or therapeutic agents, in a pharmaceutically acceptable carrier. In some embodiments, the antibody conjugated to a moiety such as described herein is the only active ingredient included in the pharmaceutical composition. Pharmaceutical compositions described herein can be useful in the prevention and/or treatment of SARS-CoV-2 infection, or disease associated therewith. In one embodiment, a pharmaceutical compositions described herein can be useful in the prevention and/or treatment of COVID-19.

[0372] Pharmaceutically acceptable carriers used in parenteral preparations include aqueous vehicles, nonaqueous vehicles, antimicrobial agents, isotonic agents, buffers, antioxidants, local anesthetics, suspending and dispersing agents, emulsifying agents, sequestering or chelating agents and other pharmaceutically acceptable substances. Examples of aqueous vehicles include Sodium Chloride Injection, Ringers Injection, Isotonic Dextrose Injection, Sterile Water Injection, Dextrose and Lactated Ringers Injection. Nonaqueous parenteral vehicles include fixed oils of vegetable origin, cottonseed oil, corn oil, sesame oil and peanut oil. Antimicrobial agents in bacteriostatic or fungistatic concentrations can be added to parenteral preparations packaged in multiple-dose containers which include phenols or cresols, mercurials, benzyl alcohol, chlorobutanol, methyl and propyl p-hydroxybenzoic acid esters, thimerosal, benzalkonium chloride and benzethonium chloride. Isotonic agents include sodium chloride and dextrose. Buffers include phosphate and citrate. Antioxidants include sodium bisulfate. Local anesthetics include procaine hydrochloride. Suspending and dispersing agents include sodium carboxymethylcelluose, hydroxypropyl methylcellulose and polyvinylpyrrolidone. Emulsifying agents include Polysorbate 80 (TWEEN®80). A sequestering or chelating agent of metal ions includes EDTA. Pharmaceutical carriers also include ethyl alcohol, polyethylene glycol and propylene glycol for water miscible vehicles; and sodium hydroxide, hydrochloric acid, citric acid or lactic acid for pH adjustment.

[0373] A pharmaceutical composition may be formulated for any route of administration to a subject. Specific examples of routes of administration include intranasal, oral, pulmonary, transdermal, intradermal, parenteral, and mucosal. In one embodiment, the composition is formulated for intranasal or intramuscular administration. In one embodiment, the composition is formulation for intramuscular administration. In one embodiment, the composition is formulated for mucosal administration. In one embodiment, the composition is formulated for intranasal administration. For example, the composition may be formulated as an aersoal. Parenteral administration, characterized by either subcutaneous, intramuscular or intravenous injection, is also contemplated herein. Injectables can be prepared in conventional forms, either as liquid solutions or suspensions, solid forms suitable for solution or suspension in liquid prior to injection, or as emulsions. The injectables, solutions and emulsions also contain one or more excipients. Suitable excipients are, for example, water, saline, dextrose, glycerol or ethanol.

[0374] Topical mixtures comprising an antibody are prepared as described for the local and systemic administration. The resulting mixture can be a solution, suspension, emulsions or the like and can be formulated as creams, gels, ointments, emulsions, solutions, elixirs, lotions, suspensions, tinctures, pastes, foams, aerosols, irrigations, sprays, suppositories, bandages, dermal patches or any other formulations suitable for topical administration.

[0375] An antibody can be formulated as an aerosol for topical application, such as by inhalation (see, e.g., U.S. Pat. Nos. 4,044,126, 4,414,209, and 4,364,923, which describe aerosols for delivery of a steroid useful for treatment of inflammatory diseases, particularly asthma). These formulations for administration to the respiratory tract can be in the form of an aerosol or solution for a nebulizer, or as a microfine powder for insufflations, alone or in combination with an inert carrier such as lactose. In such a case, the particles of the formulation will, in one embodiment, have diameters of less than 50 microns, in one embodiment less than 10 microns.

[0376] In certain embodiments, a pharmaceutical composition comprising an antibody is a lyophilized powder, which can be reconstituted for administration as solutions, emulsions and other mixtures. It may also be reconstituted and formulated as solids or gels. The lyophilized powder is prepared by dissolving an antibody provided herein, or a pharmaceutically acceptable derivative thereof, in a suitable solvent. In some embodiments, the lyophilized powder is sterile. The solvent may contain an excipient that improves the stability or other pharmacological component of the powder or reconstituted solution, prepared from the powder. Excipients that may be used include, but are not limited to, dextrose, sorbitol, fructose, corn syrup, xylitol, glycerin, glucose, sucrose or other suitable agent. The solvent may also contain a buffer, such as citrate, sodium or potassium phosphate or other such buffer known to those of skill in the art at, in one embodiment, about neutral pH. Subsequent sterile filtration of the solution followed by lyophilization under standard conditions known to those of skill in the art

provides the desired formulation. In one embodiment, the resulting solution will be apportioned into vials for lyophilization. Each vial will contain a single dosage or multiple dosages of the compound. The lyophilized powder can be stored under appropriate conditions, such as at about 4° C. to room temperature. Reconstitution of this lyophilized powder with water for injection provides a formulation for use in parenteral administration. For reconstitution, the lyophilized powder is added to sterile water or other suitable carrier. The precise amount depends upon the selected compound. Such amount can be empirically determined.

[0377] An antibody or a nucleic acid sequence encoding an antibody can, for example, be formulated in liposomes. Liposomes containing the molecule of interest are prepared by methods known in the art, such as described in Epstein et al. (1985) *Proc. Natl. Acad. Sci. USA* 82:3688; Hwang et al. (1980) *Proc. Natl. Acad. Sci. USA* 77:4030; and U.S. Pat. Nos. 4,485,045 and 4,544,545. Liposomes with enhanced circulation time are disclosed in U.S. Pat. No. 5,013,556. In one embodiment, liposomal suspensions may also be suitable as pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art. For example, liposome formulations can be prepared as described in U.S. Pat. No. 4,522,811. Briefly, liposomes such as multilamellar vesicles (MLV's) may be formed by drying down egg phosphatidyl choline and brain phosphatidyl serine (7:3 molar ratio) on the inside of a flask. A solution of a compound comprising an antibody described herein in phosphate buffered saline lacking divalent cations (PBS) is added and the flask shaken until the lipid film is dispersed. The resulting vesicles are washed to remove unencapsulated compound, pelleted by centrifugation, and then resuspended in PBS.

[0378] An antibody can also be entrapped in a microcapsule prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsule and poly-(methylmethacylate) microcapsule, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles and nanocapsules) or in macroemulsions. Such techniques are disclosed in *Remington's Pharmaceutical Sciences* (1990) Mack Publishing Co., Easton, PA.

[0379] Sustained-release preparations can also be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers, which matrices are in the form of shaped articles, e.g., films, or microcapsule. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT™ (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(−)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods.

[0380] The compositions to be used for in vivo administration can be sterile. This is readily accomplished by filtration through, e.g., sterile filtration membranes.

[0381] In one embodiment, nucleic acids comprising sequences encoding an antibody described herein are administered to a subject by way of gene therapy. Gene therapy refers to therapy performed by the administration to a subject of an expressed or expressible nucleic acid. Encompassed herein are any of the methods for gene therapy available in the art. For general review of the methods of gene therapy, see Goldspiel et al., 1993, Clinical Pharmacy 12:488-505; Wu and Wu, 1991, Biotherapy 3:87-95; Tolstoshev, 1993, Ann. Rev. Pharmacol. Toxicol. 32:573-596; Mulligan, 1993, Science 260:926-932; and Morgan and Anderson, 1993, Ann. Rev. Biochem. 62:191-217; May, 1993, TIBTECH 11(5):155-215. For a review of methods of delivery of transgenes encoding antibodies, see, e.g., Deal, 2015, Curr. Opin. Immunol. 2015 August, 35:113-22; Deal, 2015, Curr Opin HIV AIDS. 2015 May, 10(3):190-7; Marschall, 2015, MAbs. 7(6):1010-35. In one embodiment, an mRNA encoding an antibody described herein is administered to a subject. Techniques known to one of skill in the art may be used to administer an mRNA encoding an antibody to a subject. For methods of delivery of mRNA encoding antibodies, see, e.g., U.S. Patent Application Publication No. US20130244282A1; U.S. Patent Application Publication No. US 2016/0158354A1; and International Patent Application No. WO2016014846A1, each of which is incorporated herein by reference in its entirety.

[0382] Methods commonly known in the art of recombinant DNA technology which can be used are described in Ausubel et al. (eds.), Current Protocols in Molecular Biology, John Wiley & Sons, N Y (1993); and Kriegler, Gene Transfer and Expression, A Laboratory Manual, Stockton Press, NY (1990).

[0383] 6.5 Prophylactic and Therapeutic Uses of Antibodies

[0384] In one aspect, provided herein are methods for preventing COVID-19 comprising administering an antibody described herein. In one embodiment, provided herein is a method for preventing COVID-19 in a subject comprising administering to the subject an effective amount of an antibody described herein. In one embodiment, provided herein is a method for preventing COVID-19 in a subject comprising administering to the subject a pharmaceutical composition comprising an effective amount of an antibody described herein. In one embodiment, the antibody is a protein or a protein conjugate. In one embodiment, the antibody is administered to the subjects as polynucleotide sequence comprising a nucleotide sequence encoding the antibody. In one embodiment, the antibody administered to the subject is a conjugated moiety such as described herein. In one embodiment, the administration of an effective amount of the antibody to the subject inhibits or reduces in the development or onset of COVID-19. In one embodiment, provided herein is a method for preventing COVID-19 in a subject comprising administering to the subject an effective amount of an antibody described herein and another therapy, such as known to one of skill in the art or described herein. In one embodiment, the administration of an effective amount of the antibody to the subject inhibits or reduces in the development or onset of COVID-19. In another embodiment, the administration of an effective amount of the antibody to the subject inhibits or reduces onset, development and/or severity of a symptom thereof (e.g., fever, myalgia, cough, difficulty breathing, tiredness) of COVID-19. In another embodiment, the administration of

an effective amount of the antibody inhibits or reduces in the recurrence of COVID-19 or a symptom associated therewith.

[0385] In some embodiments, the administration of an effective amount of an antibody to a subject results in one, two, three, four, or more of the following: (i) the reduction or inhibition of the spread of SARS-CoV-2 from one cell to another cell; (ii) the reduction or inhibition of the spread of SARS-CoV-2 from one organ or tissue to another organ or tissue; (iii) the reduction or inhibition of the spread of SARS-CoV-2 from one region of an organ or tissue to another region of the organ or tissue (e.g., the reduction in the spread of SARS-CoV-2 from the upper to lower respiratory tract); (iv) the prevention of COVID-19 after exposure to SARS-CoV-2; (v) the reduction or inhibition in SARS-CoV-2 infection and/or replication; and/or (vi) prevention of the onset or development of one or more symptoms associated with COVID-19 or SARS-CoV-2 infection.

[0386] In another aspect, provided herein are methods for treating a SARS-CoV-2 infection or COVID-19 comprising administering an antibody described herein. In one embodiment, provided herein is a method for treating SARS-CoV-2 infection or COVID-19 in a subject comprising administering to the subject an effective amount of an antibody described herein. In one embodiment, provided herein is a method for treating SARS-CoV-2 infection or COVD-19 in a subject comprising administering to the subject a pharmaceutical composition comprising an effective amount of an antibody described herein. In one embodiment, provided herein is a method for treating SARS-CoV-2 infection or COVID-19 comprising administering to the subject an effective amount of an antibody described herein and another therapy, such as known to one of skill in the art or described herein. In one embodiment, provided herein is a method for treating SARS-CoV-2 infection or COVID-19 in a subject comprising administering to the subject a pharmaceutical composition comprising an effective amount of an antibody described herein, and another therapy, such as known to one of skill in the art or described herein. In one embodiment, the antibody is administered as a polynucleotide sequence comprising a nucleotide sequence encoding the antibody. In one embodiment, the antibody that is administered to the subject is conjugated to a moiety such as described herein. In one embodiment, the administration of an effective amount of the antibody to the subject inhibits or reduces in the development of COVID-19. In another embodiment, the administration of an effective amount of the antibody to the subject inhibits or reduces onset, development and/or severity of a symptom thereof (e.g., fever, myalgia, cough, difficulty breathing, tiredness) of COVID-19. In another embodiment, the administration of an effective amount of the antibody inhibits or reduces duration of COVID-19 or a symptom associated therewith. In another embodiment, the administration of an effective amount of the antibody reduces organ failure associated with COVID-19. In another embodiment, the administration of an effective amount of the antibody reduces the hospitalization of the subject. In another embodiment, the administration of an effective amount of the antibody reduces the length of hospitalization of the subject. In another embodiment, the administration of an effective amount of the antibody increases the overall survival of subjects with COVID-19. In another embodiment, the administration of an effective amount of the antibody prevents the onset or progression of a secondary infection associated with SARS-CoV-2 infection.

[0387] In one embodiment, administration of an antibody (ies) to a subject reduces the incidence of hospitalization by at least 99%, at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 60%, at least 50%, at least 45%, at least 40%, at least 45%, at least 35%, at least 30%, at least 25%, at least 20%, or at least 10% relative to the incidence of hospitalization in the absence of administration of said antibody(ies).

[0388] In one embodiment, administration of an antibody (ies) to a subject reduces mortality by at least 99%, at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 60%, at least 50%, at least 45%, at least 40%, at least 45%, at least 35%, at least 30%, at least 25%, at least 20%, or at least 10% relative to the mortality in the absence of administration of said antibody(ies).

[0389] In one embodiment, administration of an antibody (ies) prevents or inhibits SARS-CoV-2 from binding to its host cell receptor (e.g., ACE-2) by at least 99%, at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 60%, at least 50%, at least 45%, at least 40%, at least 45%, at least 35%, at least 30%, at least 25%, at least 20%, or at least 10% relative to SARS-CoV-2 binding to its host cell receptor in the absence of said antibody(ies) or in the presence of a negative control in an assay known to one of skill in the art or described herein.

[0390] In one embodiment, administration of an antibody (ies) inhibits or reduces SARS-CoV-2 replication by at least 99%, at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 60%, at least 50%, at least 45%, at least 40%, at least 45%, at least 35%, at least 30%, at least 25%, at least 20%, or at least 10% relative to replication of SARS-CoV-2 in the absence of said antibody (ies) or in the presence of a negative control in an assay known to one of skill in the art or described herein. Inhibition of SARS-CoV-2 replication can be determined by detecting the SARS-CoV-2 titer in a biological specimen from a subject using methods known in the art (e.g., Northern blot analysis, RT-PCR, Western Blot analysis, etc.).

[0391] In one embodiment, administration of an antibody (ies) results in reduction of about 1-fold, about 1.5-fold, about 2-fold, about 3-fold, about 4-fold, about 5-fold, about 8-fold, about 10-fold, about 15-fold, about 20-fold, about 25-fold, about 30-fold, about 35-fold, about 40-fold, about 45-fold, about 50-fold, about 55-fold, about 60-fold, about 65-fold, about 70-fold, about 75-fold, about 80-fold, about 85-fold, about 90-fold, about 95-fold, about 100-fold, about 105 fold, about 110-fold, about 115-fold, about 120 fold, about 125-fold or higher in SARS-CoV-2 titer in the subject. The fold-reduction in SARS-CoV-2 titer may be as compared to a negative control, as compared to another treatment, or as compared to the titer in the patient prior to antibody administration.

[0392] In one embodiment, administration of an antibody (ies) results in a reduction of approximately 1 log or more, approximately 2 logs or more, approximately 3 logs or more, approximately 4 logs or more, approximately 5 logs or more, approximately 6 logs or more, approximately 7 logs or more, approximately 8 logs or more, approximately 9 logs or more, approximately 10 logs or more, 1 to 5 logs, 2 to 10 logs, 2 to 5 logs, or 2 to 10 logs in SARS-CoV-2 titer in the subject. The log-reduction in SARS-CoV-2 titer may be as compared

to a negative control, as compared to another treatment, or as compared to the titer in the patient prior to antibody administration.

[0393] In one embodiment, administration of an antibody (ies) inhibits or reduces SARS-CoV-2 infection of a subject by at least 99%, at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 60%, at least 50%, at least 45%, at least 40%, at least 45%, at least 35%, at least 30%, at least 25%, at least 20%, or at least 10% relative to SARS-CoV-2 infection of a subject in the absence of said antibody(ies) or in the presence of a negative control in an assay known to one of skill in the art or described herein.

[0394] In one embodiment, administration of an antibody (ies) inhibits or reduces the spread of SARS-CoV-2 in a subject by at least 99%, at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 60%, at least 50%, at least 45%, at least 40%, at least 45%, at least 35%, at least 30%, at least 25%, at least 20%, or at least 10% relative to the spread of SARS-CoV-2 in a subject in the absence of said an antibody(ies) or in the presence of a negative control in an assay known to one of skill in the art or described herein.

[0395] In one embodiment, administration of an antibody (ies) inhibits or reduces the spread of SARS-CoV-2 between a subject and at least one other subject by at least 99%, at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 60%, at least 50%, at least 45%, at least 40%, at least 45%, at least 35%, at least 30%, at least 25%, at least 20%, or at least 10% relative to the spread of SARS-CoV-2 between a subject and at least one other subject in the absence of said antibody(ies) or in the presence of a negative control in an assay known to one of skill in the art or described herein.

[0396] In one embodiment, administration of an antibody (ies) to a subject reduces the number of and/or the frequency of symptoms of in the subject (exemplary symptoms of a SARS-CoV-2 include, but are not limited to, body aches (especially joints and throat), fever, nausea, headaches, fatigue, sore throat, and difficulty breathing).

[0397] In one embodiment, administration of an antibody (ies) to a subject reduces the number of and/or the frequency of symptoms of COVID-19 in the subject (exemplary symptoms of COVID-19 include, but are not limited to, body aches (especially joints and throat), fever, nausea, headaches, fatigue, sore throat, and difficulty breathing).

[0398] An antibody(ies) may be administered alone or in combination with another/other type of therapy known in the art.

[0399] In specific embodiment, an antibody described herein may be used as any line of therapy, including, but not limited to, a first, second, third, fourth and/or fifth line of therapy. Encompassed herein are methods for administering one or more antibodies described herein to prevent the onset of a disease associated with SARS-CoV-2 infection and/or to treat or lessen the recurrence of a disease associated with SARS-CoV-2 infection.

[0400] In specific embodiment, an antibody described herein may be used as any line of therapy, including, but not limited to, a first, second, third, fourth and/or fifth line of therapy. Encompassed herein are methods for administering one or more antibodies described herein to prevent the onset of COVID-19 and/or to treat or lessen the recurrence of COVID-19.

[0401] Further encompassed herein are methods for preventing and/or treating a disease associated with SARS-CoV-2 infection (e.g., COVID-19) and/or a symptom relating thereto for which no other antiviral therapy is available.

[0402] 6.5.1 Routes of Administration and Dosage

[0403] An antibody (e.g., a monoclonal antibody, such as a chimeric or humanized antibody, or an antigen-binding fragment thereof) or composition described herein may be delivered to a subject by a variety of routes. In one embodiment, an antibody conjugated to a moiety such as described herein, or a polynucleotide encoding a sequence encoding an antibody may be administered to a subject by a variety of routes. These include, but are not limited to, intranasal, intratracheal, oral, intradermal, intramuscular, intraperitoneal, transdermal, intravenous, conjunctival and subcutaneous routes. Pulmonary administration can also be employed, e.g., by use of an inhaler or nebulizer, and formulation with an aerosolizing agent for use as a spray. In one embodiment, an antibody described herein is administered to a subject intranasally or intramuscularly.

[0404] The amount of an antibody (e.g., a monoclonal antibody, such as a chimeric or humanized antibody, or an antigen-binding fragment thereof), antibody conjugate or composition which will be effective in the treatment and/or prevention of SARS-CoV-2 infection, or a disease associated therewith (e.g., COVID-19) will depend on the nature of the disease. The precise dose to be employed in a composition will also depend on the route of administration, and the seriousness of the infection or disease caused by it, and should be decided according to the judgment of the practitioner and each subject's circumstances. For passive immunization with an antibody (e.g., a monoclonal antibody, such as a chimeric or humanized antibody, or an antigen-binding fragment thereof), the dosage ranges from about 0.0001 to 100 mg/kg, and more usually 0.01 to 5 mg/kg, of the patient body weight. Generally, human antibodies have a longer half-life within the human body than antibodies from other species due to the immune response to the foreign polypeptides. Thus, lower dosages of human antibodies and less frequent administration is often possible.

[0405] An exemplary treatment regime entails administration once per every two weeks or once a month or once every 3 to 6 months for a period of one year or over several years, or over several year-intervals. In some methods, two or more antibodies with different binding specificities are administered simultaneously to a subject. An antibody is usually administered on multiple occasions. Intervals between single dosages can be weekly, monthly, every 3 months, every 6 months or yearly. Intervals can also be irregular as indicated by measuring blood levels of antibody to the SARS-CoV-2 antigen in the patient.

[0406] In some embodiments, the plasma level of an antibody described herein in a patient is measured prior to administration of a subsequent dose of an antibody described herein, or a composition thereof. The plasma level of the antibody may be considered in determining the eligibility of a patient to receive a subsequent dose of an antibody described herein. For example, a patient's plasma level of an antibody described herein may suggest not administering an antibody described herein; alternatively, a patient's plasma level of an antibody described herein may suggest administering an antibody described herein at a particular dosage, at a particular frequency, and/or for a certain period of time.

[0407] In certain embodiments, the route of administration for a dose of an antibody described herein, or a composition thereof to a patient is intranasal, intramuscular, intravenous, or a combination thereof, but other routes described herein are also acceptable. Each dose may or may not be administered by an identical route of administration. In some embodiments, an antibody described herein, or composition thereof, may be administered via multiple routes of administration simultaneously or subsequently to other doses of the same or a different antibody described herein.

[0408] 6.5.2 Combination Therapy

[0409] In various embodiments, an antibody described herein or a nucleic acid encoding such an antibody may be administered to a subject in combination with one or more other therapies (e.g., antiviral or immunomodulatory therapies). In one embodiment, an antibody conjugated to a moiety such as described herein may be administered to a subject with one or more other therapies. In some embodiments, a pharmaceutical composition described herein may be administered to a subject in combination with one or more therapies. The one or more other therapies may be in the same composition or a different composition as an antibody described herein.

[0410] In some embodiments, the one or more other therapies that are supportive measures, such as pain relievers, anti-fever medications, or therapies that alleviate or assist with breathing. Specific examples of supportive measures include humidification of the air by an ultrasonic nebulizer, aerolized racemic epinephrine, oral dexamethasone, intravenous fluids, intubation, fever reducers (e.g., ibuprofen, acetometaphin), and antibiotic and/or antifungal therapy (i.e., to prevent or treat secondary bacterial and/or fungal infections).

[0411] In certain embodiments, the therapies are administered less than 5 minutes apart, less than 30 minutes apart, 1 hour apart, at about 1 hour apart, at about 1 to about 2 hours apart, at about 2 hours to about 3 hours apart, at about 3 hours to about 4 hours apart, at about 4 hours to about 5 hours apart, at about 5 hours to about 6 hours apart, at about 6 hours to about 7 hours apart, at about 7 hours to about 8 hours apart, at about 8 hours to about 9 hours apart, at about 9 hours to about 10 hours apart, at about 10 hours to about 11 hours apart, at about 11 hours to about 12 hours apart, at about 12 hours to 18 hours apart, 18 hours to 24 hours apart, 24 hours to 36 hours apart, 36 hours to 48 hours apart, 48 hours to 52 hours apart, 52 hours to 60 hours apart, 60 hours to 72 hours apart, 72 hours to 84 hours apart, 84 hours to 96 hours apart, or 96 hours to 120 hours part. In specific embodiments, two or more therapies are administered within the same patient visit. In some embodiments, two or more therapies are administered concurrently. The two or more therapies can be administered in the same composition or a different composition. Further, the two or more therapies can be administered by the same route of administration of a different route of administration.

[0412] 6.5.3 Patient Populations

[0413] As used herein, the terms "subject" and "patient" are used interchangeably to refer to an animal (e.g., birds, reptiles, and mammals). In one embodiment, a patient treated or prevented in accordance with the methods provided herein is a naïve subject, i.e., a subject that does not have COVID-19 or has not been and is not currently infected with SARS-CoV-2. In another embodiment, a patient treated or prevented in accordance with the methods provided herein is a subject that is at risk of acquiring SARS-CoV-2 infection. In another embodiment, a patient treated or prevented in accordance with the methods provided herein is a patient suffering from or expected to suffer from COVID-19. In another embodiment, a patient treated or prevented in accordance with the methods provided herein is a patient diagnosed with SARS-CoV-2 infection or COVID-19. In some embodiments, a patient treated or prevented in accordance with the methods provided herein is a patient infected with SARS-CoV-2 that does not manifest any symptoms of COVID-19. In certain embodiments, a patient treated or prevented in accordance with the methods provided herein is a patient infected with SARS-CoV-2 that manifests moderate to severe symptoms of COVID-19.

[0414] In another embodiment, a patient treated or prevented in accordance with the methods provided herein is a patient experiencing one or more symptoms of COVID-19. Symptoms of COVID-19 include, but are not limited to, body aches (especially joints and throat), fever, nausea, headaches, fatigue, sore throat, and difficulty breathing. In another embodiment, a patient treated or prevented in accordance with the methods provided herein is a patient with COVID-19 who does not manifest symptoms of the disease that are severe enough to require hospitalization.

[0415] In one embodiment, a patient treated or prevented in accordance with the methods provided herein is a human. In certain embodiments, a patient treated or prevented in accordance with the methods provided herein is a human infant. In some embodiments, a patient treated or prevented in accordance with the methods provided herein is a human toddler. In certain embodiments, a patient treated or prevented in accordance with the methods provided herein is a human child. In other embodiments, a patient treated or prevented in accordance with the methods provided herein is a human adult. In some embodiments, a patient treated or prevented in accordance with the methods provided herein is an elderly human. In certain embodiments, a patient treated or prevented in accordance with the methods provided herein is patient that is pregnant.

[0416] As used herein, the term "human adult" refers to a human that is 18 years or older. As used herein, the term "human child" refers to a human that is 1 year to 18 years old. As used herein, the term "human infant" refers to a newborn to 1 year old human. As used herein, the term "human toddler" refers to a human that is 1 years to 3 years old. As used herein, the term "elderly human" refers to a human that is 65 years old and older.

[0417] In some embodiments, a patient treated or prevented in accordance with the methods provided herein is any subject at increased risk of SARS-CoV-2 infection or COVID-19 (e.g., an immunocompromised or immunodeficient individual). In some embodiments, a patient treated or prevented in accordance with the methods provided herein is any subject in close contact with an individual with increased risk of SARS-CoV-2 infection or COVID-19 (e.g., immunocompromised or immunosuppressed individuals).

[0418] In some embodiments, a patient treated or prevented in accordance with the methods provided herein is a subject affected by any condition that increases susceptibility to SARS-CoV-2 infection or complications or COVID-19. In other embodiments, a patient treated or prevented in accordance with the methods provided herein is a subject in which SARS-CoV-2 infection has the potential to increase complications of another condition that the individual is

affected by, or for which they are at risk. In some embodiments, such conditions that increase susceptibility to SARS-CoV-2 complications or for which SARS-CoV-2 increases complications associated with the condition are, e.g., conditions that affect the lung, such as cystic fibrosis, asthma, chronic obstructive pulmonary disease, emphysema, or bacterial infections; cardiovascular disease; or diabetes. Other conditions that may increase SARS-CoV-2 complications include kidney disorders; blood disorders (including anemia or sickle cell disease); or weakened immune systems (including immunosuppression caused by medications, malignancies such as cancer, organ transplant, or HIV infection).

[0419] In some embodiments, a patient treated or prevented in accordance with the methods provided herein is a subject that resides in a group home, such as a nursing home or orphanage. In some embodiments, a patient treated or prevented in accordance with the methods provided herein is subject that works in, or spends a significant amount of time in, a group home, e.g., a nursing home or orphanage. In some embodiments, a patient treated or prevented in accordance with the methods provided herein is a health care worker (e.g., a doctor or nurse). In some embodiments, a patient treated or prevented in accordance with the methods provided herein resides in a dormitory (e.g., a college dormitory). In some embodiments, a patient treated or prevented in accordance with the methods provided herein is a member of the military. In some embodiments, a patient treated or prevented in accordance with the methods provided herein is a child that attends school or daycare.

[0420] In certain embodiments, patients treated or prevented in accordance with the methods provided herein are patients already being treated with antibiotics, antivirals, antifungals, or other biological therapy/immunotherapy.

[0421] 6.6 Diagnostic Uses

[0422] The antibodies described herein (e.g., a monoclonal antibody, such as a chimeric or humanized antibody, or an antigen-binding fragment thereof) can be used for diagnostic purposes to detect SARS-CoV-2 as well as detect, diagnose, or monitor a SARS-CoV-2 infection.

[0423] Provided herein are methods for the detection of SARS-CoV-2 infection comprising: (a) detecting the expression of SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) in a biological specimen (e.g., sputum, nasal drippings, cells or tissue samples) from a subject using an antibody described herein (e.g., a monoclonal antibody, such as a chimeric or humanized antibody, or an antigen-binding fragment thereof); and (b) comparing the level of the SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) with a control level, e.g., levels in a biological specimen from a subject not infected with SARS-CoV-2, wherein an increase in the assayed level of SARS-CoV-2 spike protein c or a fragment thereof (e.g., RBD) compared to the control level of the SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) is indicative of SARS-CoV-2 infection.

[0424] Provided herein is a diagnostic assay for diagnosing SARS-Co-2 infection comprising: (a) assaying for the level of SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) in a biological specimen from a subject using an antibody described herein (e.g., a monoclonal antibody, such as a chimeric or humanized antibody, or an antigen-binding fragment thereof); and (b) comparing the level of the SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) with a control level, e.g., levels in a biological specimen from a subject not infected with SARS-CoV-2, wherein an increase in the assayed SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) level compared to the control level of the SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) is indicative of SARS-CoV-2 infection. A more definitive diagnosis of SARS-CoV-2 infection may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the SARS-CoV-2 infection.

[0425] In one embodiment, provided herein is a method for detecting SARS-CoV-2, comprising: (a) contacting a biological sample (e.g., cells, sputum, nasal swab, mucous, etc.) with the antibody described herein; (b) detecting the binding of the antibody to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), wherein SARS-CoV-2 is detected if the level of binding of the antibody to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) is greater than the level of binding of the antibody to non-SARS-CoV-2 infected cells or a biological sample not infected with SARS-CoV-2. In one embodiment, the detection is done in vitro. In other embodiments, the detection is done in vivo. Techniques known to one of skill in the art may be used to detect the binding of the antibody to the SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD).

[0426] Antibodies described herein (e.g., a monoclonal antibody, such as a chimeric or humanized antibody, or an antigen-binding fragment thereof) can be used to assay SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) levels in a biological sample using classical immunohistological methods as described herein or as known to those of skill in the art (e.g., see Jalkanen et al., 1985, J. Cell. Biol. 101:976-985; and Jalkanen et al., 1987, J. Cell. Biol. 105:3087-3096). Antibody-based methods useful for detecting protein expression include immunoassays, such as the enzyme linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA). An antibody described herein or generated in accordance with the methods described herein may be labeled with a detectable label or a secondary antibody that binds to such an antibody may be labeled with a detectable label. Suitable antibody assay labels are known in the art and include enzyme labels, such as, glucose oxidase; radioisotopes, such as iodine (^{125}I, ^{121}I) carbon (^{14}C), sulfur (^{35}S), tritium (^{3}H), indium (^{121}In), and technetium (^{99}Tc); luminescent labels, such as luminol; and fluorescent labels, such as fluorescein and rhodamine, and biotin. See, above for examples of antibody conjugates that might be useful in the detection and diagnosis of SARS-CoV-2 infection.

[0427] In one embodiment, monitoring of SARS-CoV-2 infection is carried out by repeating the method for diagnosing the SARS-CoV-2 infection, for example, one day, two days, one week, two weeks, or one month after initial diagnosis.

[0428] 6.7 Biological Assays

[0429] An antibody described herein (e.g., a monoclonal antibody, such as a chimeric or humanized antibody, or an antigen-binding fragment thereof) may be characterized using any assay known to one of skill in the art or described herein. In one embodiment, an antibody described herein is characterized as described in Section 5, infra.

[0430] 6.7.1 Assays for Testing Antibody Activity

[0431] An antibody may be characterized in a variety of ways known to one of skill in the art (e.g., ELISA, biolayer interferometry, surface plasmon resonance display (BIAcore kinetic), Western blot, immunofluorescence, immunostaining, plaque reduction assays, and/or microneutralization

assays). In some embodiments, an antibody is assayed for its ability to bind to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD). In certain embodiments, an antibody is assayed for its ability to inhibit or reduce the interaction of SARS-CoV-2 with its host cell receptor (e.g., ACE-2) using techniques known to one of skill in the art. For example, the ability of an antibody to inhibit or reduce the interaction of SARS-CoV-2 spike protein with ACE-2 may be tested using techniques known to one of skill in the art.

[0432] The specificity or selectivity of an antibody for SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) and cross-reactivity with other antigens can be assessed by any method known in the art. Immunoassays which can be used to analyze specific binding and cross-reactivity include, but are not limited to, competitive and non-competitive assay systems using techniques such as Western blots, radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoprecipitation assays, precipitin reactions, gel diffusion precipitin reactions, immunodiffusion assays, agglutination assays, complement-fixation assays, immunoradiometric assays, fluorescent immunoassays, protein A immunoassays, to name but a few. Such assays are routine and well known in the art (see, e.g., Ausubel et al., eds., 1994, Current Protocols in Molecular Biology, Vol. 1, John Wiley & Sons, Inc., New York, which is incorporated by reference herein in its entirety).

[0433] The binding affinity of an antibody to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) and the off-rate of an antibody-antigen interaction can be determined by competitive binding assays. One example of a competitive binding assay is a radioimmunoassay comprising the incubation of labeled antigen (e.g., ^{3}H or ^{125}I) with the antibody of interest in the presence of increasing amounts of unlabeled antigen, and the detection of the antibody bound to the labeled antigen. The affinity of the antibody for a SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) and the binding off-rates can be determined from the data by Scatchard plot analysis. Competition with a second antibody can also be determined using radioimmunoassays. In this case, a a SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), or or SARS-CoV-2 is incubated with the test antibody conjugated to a detectable labeled (e.g., ^{3}H or ^{125}I) in the presence of increasing amounts of an unlabeled second antibody.

[0434] In some embodiments, surface plasmon resonance (e.g., BIAcore kinetic) analysis is used to determine the binding on and off rates of an antibody to SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD), or SARS-CoV-2.

[0435] In some embodiments, an antibody described herein is tested for its ability to neutralize SARS-CoV-2 or SARS-CoV-2 spike protein expressing pseudotyped viruses, such as described in the Section 5, infra.

[0436] 6.7.2 Cytotoxicity Assays

[0437] Many assays well-known in the art can be used to assess viability of cells (infected or uninfected) or cell lines following exposure to an antibody or composition thereof and, thus, determine the cytotoxicity of the antibody or composition thereof. For example, cell proliferation can be assayed by measuring Bromodeoxyuridine (BrdU) incorporation (See, e.g., Hoshino et al., 1986, Int. J. Cancer 38, 369; Campana et al., 1988, J. Immunol. Meth. 107:79), (3H) thymidine incorporation (See, e.g., Chen, J., 1996, Oncogene 13:1395-403; Jeoung, J., 1995, J. Biol. Chem. 270: 18367 73), by direct cell count, or by detecting changes in transcription, translation or activity of known genes such as proto-oncogenes (e.g., fos, myc) or cell cycle markers (Rb, cdc2, cyclin A, D1, D2, D3, E, etc). The levels of such protein and mRNA and activity can be determined by any method well known in the art. For example, protein can be quantitated by known immunodiagnostic methods such as ELISA, Western blotting or immunoprecipitation using antibodies, including commercially available antibodies. mRNA can be quantitated using methods that are well known and routine in the art, for example, using northern analysis, RNase protection, or polymerase chain reaction in connection with reverse transcription. Cell viability can be assessed by using trypan-blue staining or other cell death or viability markers known in the art. In one embodiment, the level of cellular ATP is measured to determined cell viability.

[0438] In specific embodiments, cell viability is measured in three-day and seven-day periods using an assay standard in the art, such as the CellTiter-Glo Assay Kit (Promega) which measures levels of intracellular ATP. A reduction in cellular ATP is indicative of a cytotoxic effect. In one embodiment, cell viability can be measured in the neutral red uptake assay. In other embodiments, visual observation for morphological changes may include enlargement, granularity, cells with ragged edges, a filmy appearance, rounding, detachment from the surface of the well, or other changes. These changes may be given a designation of T (100% toxic), PVH (partially toxic-very heavy—80%), PH (partially toxic-heavy—60%), P (partially toxic—40%), Ps (partially toxic-slight—20%), or 0 (no toxicity—0%), conforming to the degree of cytotoxicity seen. A 50% cell inhibitory (cytotoxic) concentration (IC_{50}) is determined by regression analysis of these data.

[0439] In one embodiment, the cells used in the cytotoxicity assay are animal cells, including primary cells and cell lines. In some embodiments, the cells are human cells. In certain embodiments, cytotoxicity is assessed in one or more of the following cell lines: U937, a human monocyte cell line; primary peripheral blood mononuclear cells (PBMC); Huh7, a human hepatoblastoma cell line; 293T, a human embryonic kidney cell line; and THP-1, monocytic cells. In certain embodiments, cytotoxicity is assessed in one or more of the following cell lines: MDCK, MEF, Huh 7.5, Detroit, or human tracheobronchial epithelial (HTBE) cells.

[0440] An antibody or composition thereof can be tested for in vivo toxicity in animal models. For example, animal models, described herein and/or others known in the art, used to test the activities of an antibody or composition thereof can also be used to determine the in vivo toxicity of these antibodies. For example, animals are administered a range of concentrations of an antibody. Subsequently, the animals are monitored over time for lethality, weight loss or failure to gain weight, and/or levels of serum markers that may be indicative of tissue damage (e.g., creatine phosphokinase level as an indicator of general tissue damage, level of glutamic oxalic acid transaminase or pyruvic acid transaminase as indicators for possible liver damage). These in vivo assays may also be adapted to test the toxicity of various administration mode and/or regimen in addition to dosages.

[0441] The toxicity and/or efficacy of an antibody or composition thereof can be determined by standard pharmaceutical procedures in cell cultures or experimental ani-

mals, e.g., for determining the LD_{50} (the dose lethal to 50% of the population) and the ED_{50} (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD_{50}/ED_{50}. An antibody or composition thereof that exhibits large therapeutic indices is preferred. While an antibody or composition thereof that exhibits toxic side effects may be used, care should be taken to design a delivery system that targets such agents to the site of affected tissue in order to minimize potential damage to uninfected cells and, thereby, reduce side effects.

[0442] The data obtained from the cell culture assays and animal studies can be used in formulating a range of dosage of an antibody or composition thereof for use in humans. The dosage of such antibodies lies preferably within a range of circulating concentrations that include the ED_{50} with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For an antibody or composition thereof used in a method described herein, the effective dose can be estimated initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range that includes the IC_{50} (i.e., the concentration of the antibody that achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma may be measured, for example, by high-performance liquid chromatography. Additional information concerning dosage determination is provided herein.

[0443] Further, any assays known to those skilled in the art can be used to evaluate the prophylactic and/or therapeutic utility of an antibody or composition thereof, for example, by measuring viral infection or a condition or symptoms associated therewith.

[0444] 6.7.3 In Vivo Assays

[0445] Antibodies and compositions thereof are preferably assayed in vivo for the desired therapeutic or prophylactic activity prior to use in humans. For example, in vivo assays can be used to determine whether it is preferable to administer an antibody or composition thereof and/or another therapy. For example, to assess the use of an antibody or composition thereof to prevent a disease associated with SARS-CoV-2 (e.g., COVID-19), the antibody or composition can be administered before the animal is infected with SARS-CoV-2. Alternatively, or in addition, an antibody or composition thereof can be administered to the animal at the same time that the animal is infected with SARS-CoV-2. To assess the use of an antibody or composition thereof to treat SARS-CoV-2 infection or a disease associated therewith (e.g., COVID-19), the antibody or composition may be administered after infecting the animal with SARS-CoV-2. In one embodiment, an antibody or composition thereof is administered to the animal more than one time.

[0446] In general, animals are infected with SARS-CoV-2 and concurrently or subsequently treated with an antibody or composition thereof, or placebo. Alternatively, animals are treated with an antibody or composition thereof or placebo and subsequently infected with SARS-CoV-2. Samples obtained from these animals (e.g., serum, urine, sputum, semen, saliva, plasma, or tissue sample) can be tested for viral replication via well known methods in the art, e.g., those that measure altered viral titers (as determined, e.g., by plaque formation), the production of viral proteins (as determined, e.g., by Western blot, ELISA, or flow cytometry analysis) or the production of viral nucleic acids (as determined, e.g., by RT-PCR or northern blot analysis). For quantitation of virus in tissue samples, tissue samples are homogenized in phosphate-buffered saline (PBS), and dilutions of clarified homogenates are adsorbed for a time period (e.g., 20 minutes or 1 hour) at 37° C. onto monolayers of cells (e.g., Vero, CEF or MDCK cells). In other assays, histopathologic evaluations are performed after infection, preferably evaluations of the organ(s) the virus is known to target for infection. Virus immunohistochemistry can be performed using a viral-specific monoclonal antibody.

[0447] The effect of an antibody or composition thereof on the infectious disease process or pathogenicity of a given virus can also be determined using in vivo assays in which the titer of the virus in an infected subject administered an antibody or composition thereof, the length of survival of an infected subject administered an antibody or composition thereof, the immune response in an infected subject administered an antibody or composition thereof, the number, duration and/or severity of the symptoms in an infected subject administered an antibody or composition thereof, and/or the time period before onset of one or more symptoms in an infected subject administered an antibody or composition thereof, is assessed. Techniques known to one of skill in the art can be used to measure such effects.

[0448] In yet other assays, histopathologic evaluations are performed after infection of an animal model subject. Nasal turbinates and trachea may be examined for epithelial changes and subepithelial inflammation. The lungs may be examined for bronchiolar epithelial changes and peribronchiolar inflammation in large, medium, and small or terminal bronchioles. The alveoli are also evaluated for inflammatory changes.

[0449] Virus immunohistochemistry may be performed using a viral-specific monoclonal antibody (e.g. spike-specific monoclonal antibodies).

[0450] In one embodiment, the ability of an antibody or composition thereof to treat SARS-CoV-2 infection or a disease associated therewith (e.g., COVID-19) is assessed by determining the ability of the antibody to confer passive immunity to a disease associated with SARS-CoV-2 infection (e.g., COVID-19) in a subject. The ability of an antibody described herein to confer passive immunity to a disease associated with SARS-CoV-2 infection (e.g., COVID-19) in a subject can be assessed using any methods known in the art.

[0451] 6.7.4 Assays in Humans

[0452] In one embodiment, an antibody or composition thereof that modulates replication of SARS-CoV-2 is assessed in infected human subjects. In accordance with this embodiment, an antibody or composition thereof is administered to the human subject, and the effect of the antibody and/or composition on viral replication is determined by, e.g., analyzing the level of the virus or viral nucleic acids in a biological sample (e.g., serum or plasma). An antibody or composition thereof that alters virus replication can be identified by comparing the level of virus replication in a subject or group of subjects treated with a control antibody to that in a subject or group of subjects treated with an antibody or composition thereof. Alternatively, alterations in viral replication can be identified by comparing the level of the virus replication in a subject or group of subjects before and after the administration of an antibody or composition

thereof. Techniques known to those of skill in the art can be used to obtain the biological sample and analyze the mRNA or protein expression.

[0453] In another embodiment, the effect of an antibody or composition thereof on the severity of one or more symptoms associated with SARS-CoV-2 infection/COVID-19 are assessed in an infected subject. In accordance with this embodiment, an antibody or composition thereof or a control antibody is administered to a human subject suffering from SARS-CoV-2 infection and the effect of the antibody or composition on one or more symptoms of the virus infection is determined. An antibody or composition thereof that reduces one or more symptoms can be identified by comparing the subjects treated with a control antibody to the subjects treated with the antibody or composition. Techniques known to physicians familiar with infectious diseases can be used to determine whether an antibody or composition thereof reduces one or more symptoms associated with a SARS-CoV-2 infection (e.g., COVID-19).

[0454] 6.8 Kits

[0455] In another aspect, provided herein is a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of a composition (e.g., a pharmaceutical compositions) described herein, such as one or more antibodies provided herein (e.g., a monoclonal antibody, such as a chimeric or humanized antibody, or an antigen-binding fragment thereof), one or more polynucleotides described herein, or one or more antibody conjugates described herein. Optionally associated with such container (s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration.

[0456] The kits encompassed herein can be used in the above methods. In one embodiment, a kit comprises an antibody described herein, preferably an isolated antibody, in one or more containers. An antibody described herein included in a kit may be attached to a solid support (e.g., a microtiter plate or bead). In one embodiment, the kits encompassed herein contain an isolated SARS-CoV2 antigen that the antibodies encompassed herein react with (e.g., the antibody binds to the antigen) as a control. In one embodiment, the kits provided herein further comprise a control antibody which does not react with SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) (such as a control IgG). In one embodiment, the kits provided herein contain a means for detecting the binding of an antibody to SARS-CoV-2 spike protein or a fragment thereof (e.g., the antibody may be conjugated to a detectable substrate such as a fluorescent compound, an enzymatic substrate, a radioactive compound, a luminescent compound, or another antibody that is conjugated to a detectable substrate (e.g., the antibody may be conjugated to a second antibody which recognizes/binds to the first antibody)). In certain embodiments, the kits comprise a second antibody which is labeled with a detectable substance and which binds to an antibody described herein. In specific embodiments, the kit may include a recombinantly produced or chemically synthesized SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD). The SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) provided in the kit may also be attached to a solid support. In a more specific embodiment, the detecting means of the above described kit includes a solid support to which SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) is attached. Such a kit may also include a non-attached reporter-labeled antibody. In this embodiment, binding of the antibody to the SARS-CoV-2 spike protein or a fragment thereof (e.g., RBD) can be detected by binding of the said reporter-labeled antibody.

Example 1: Production and Testing of Antibodies

[0457] The entry of SARS-CoV2 into cells requires the envelope S glycoprotein engagement with the human angiotensin-converting enzyme 2 gene (ACE2) cell surface protein. SARS-CoV2 S protein is a type I membrane protein with a large extracellular region. The S1 domain binds to ACE2 through its receptor-binding domain (RBD) leading to endocytosis of the virus. Similar to other viruses (e.g., influenza), monoclonal antibodies (mAbs) against regions of the S1 domain including the RBD can prevent infection by blocking virus binding. The S2 region of the spike is involved in fusion and is another target for monoclonal antibody therapeutics. This example describes unique monoclonal antibodies that neutralize the SARs-Cov2 virus in the low pM range.

[0458] Immunization: Harbour mice were immunized with either (1) full length spike or (2) a receptor binding domain (RBD) Fc fusion protein in adjuvant. Harbour mice use human VH and VL genes and rat constant region genes to make antibodies that can be rapidly converted to fully human by a simple cloning step. Multiple mice were fused, clones selected and the antibodies they produced tested by ELISA, Flow and inhibition of ACE2 binding.

[0459] Preliminary screening: The clones were screened in several assays that included binding to membrane bound whole spike on the cell surface (MFI/flow cytometry), binding to receptor binding domain (RBD) of spike protein (RBD ELISA), RBD/ACE2 competition assay (ACE2 inhibition), and pseudovirus neutralization assay (pseudovirus neutralization). In particular, the clones targeting SARS-CoV spike protein were subjected to a flow cytometry assay using HEK-293 cells expressing Spike protein. Clones that demonstrated a mean fluorescence intensity (MFI)>2×background were selected for further analysis. The heat map shows the diversity of mAb binding to the spike protein. The analysis of flow-positive clones using an ELISA in which SARS-CoV-2 RBD was the target protein revealed a significant number of clones that strongly bound to the RBD based on optical density. These clones were also evaluated using an RBD/ACE2 competition assay and calculated as % inhibition. Finally, the clones were subjected to a VsV-pseudovirus neutralization based on no antibody at 0% neutralization. See FIG. **1**.

[0460] Animal sera and mAb clones were selected if they bound to the surface of Expi293 cells expressing full length spike protein as measured by flow cytometry. In addition, binding to the RBD region was also measured by ELISA and analyzed by an RBD/ACE2 competition assay that measure the inhibition of RBD binding to ACE2 expressed on the surface of HEK-293 cells. In addition, the clones were subjected to inhibition of VSV-Spike pseudovirus infection based on the expression of GFP encoded in the pseudovirus. Briefly, the mAb was preincubated with the pseudovirus and analyzed for infection through measuring virus-infected cells or GFP fluorescence intensity.

[0461] The clones for further analysis were selected based on high binding for spike protein and RBD, ACE2 inhibi-

tion, and inhibition of SARs-CoV2/VSV-pseudo virus infectivity. These clones were further analyzed using a SARs-CoV2/VSV pseudo virus neutralization assay.

[0462] Neutralizing titer testing: Antibodies positive in all four of the above assays were tested further for neutralization titers (EC50s) of a SARs-CoV2 Spike/VSV pseudovirus particle infection of Vero E6 cells based on a dilution range. Dilutions of antibodies were premixed with the virus and blocking of infection was measured by the loss of GFP as measured by flow cytometry. The EC50 values were calculated based on concentration dependent inhibition (FIG. **2**) The EC50 values and ACE2 inhibition (Tables 3 and 4) was used as a selection criteria for sequencing and humanization.

[0463] Sequencing: Total RNA was extracted from the hybridomas and converted to cDNA. Antibody specific PCRs were performed to amplify the variable regions of the heavy and light chains. Purified PCR products were submitted for sanger sequencing (GeneWiz). Sequences were blasted using IMGT V-quest (www.imgt.org) to identify matching human variable gene family members, somatic mutation variances, and junctions (CDR3s). Antibodies were grouped together in families based on CDR3 identity, which determines antibody clonality. Clones that had completely identical sequences were considered exact copies and only one candidate was chosen to move forward from such identical clusters (FIG. **3**).

[0464] Addition of human constant regions: DNA for the variable regions of lead antibodies is synthesized from sequence information and cloned in frame into mammalian expression vectors containing human G1 and kappa constant regions (GenScript). DNA vectors is grown, prepped (mini/maxi) and used for transfection in mammalian cells for antibody production. To validate the antibodies, corresponding heavy/light pairs are transfected into Expi293 cells and supernatants collected for testing and purification (see section "purification and validation of fully human mAb").

[0465] Epitope mapping: Epitope mapping of neutralizing antibodies can be accomplished using site directed mutational analysis. By scanning the Spike/RBD and replacing certain amino acids with alanines, one epitope at a time can be disrupted. This procedure requires approximately 20 clones to be made, and then expressed in cells. Once produced the mutant spike expression plasmids is used to transfect Expi293 cells. Changes in binding are measured by flow cytometry using the 19 antibodies and comparing the binding to control spike expression.

[0466] Purification and validation of fully human mAbs: Expression vectors are transfected into Expi293 cells and supernatants collected for testing and purification. Antibodies are purified on protein A/G HiTrap columns using fast protein liquid chromatography (FPLC) on an AKTA Chromatography system (GE). In order to be certain that the specificity has not been altered by the process, purified, fully human antibodies are tested for binding to RBD by ELISA, to full length spike by flow cytometry and in the pseudovirus neutralization assay. In the PsV assay it is expected that the EC50 will not have changed from the pre-humanized versions.

[0467] Evaluation of ability of mAb to target immune cells to kill infected cells: The neutralizing mAbs are subjected to an Antibody-dependent cell-mediated cytotoxicity (ADCC) assay to evaluate the anti-SARS-CoV2 antibodies to recognize virus cells and induce immune cell killing. In general, HEK-293 cells expressing spike protein and SARS-CoV2 infected cells are included with increasing concentrations (0-25 μg/ml) of each antibody followed by the addition of ADCC target cell. After co-culture, Cyto-tox reagent (Promega) are used to quantitatively evaluate dead cells in the co-culture.

[0468] Neutralization experiments: Dilutions of mAb (500 ng/ml to 1 ng/ml) are mixed with a fixed amount of pseudovirus. Purified antibody alone or equal mixtures of two mAbs are performed and EC50 values determined. Complementary antibodies could show lower EC50 than either of the single mAbs or could provide protection from escape mutations. For identifying escape mutants, SARs-Cov2 spike pseudovirus assays are performed under selection pressure from one mAb, or a combination of mAbs. After 4 days in culture, virus is collected and used to infect a fresh well of Vero E6 cells, again under the selection of suboptimal concentrations of mAb. After another 4 days, virus is collected and subject to deep sequencing.

[0469] Affinity and binning analysis: Affinity (K_D) for purified antibodies is determined using bio-layer interferometry (BLI) on an Octet RED 96 with a tagged RBD only protein. Antibody pairs are also be binned against each other in similar format to determine if one antibody competes for binding of a second antibody, indicating either competing or non-competing epitope binding. Antibody pairs are chosen based on antibody family designations with pairs representing members of different families. Regeneron antibody pairs did not show a major improvement in neutralization when mixed together even though they bound to different sites. However, when analyzed for suppression of mutant escape such antibodies successfully block the appearance of mutant viruses.

[0470] Neutralization of live virus in BSL3 facility: EC50 of neutralization is performed as was done with the pseudovirus assay but under BSL3 conditions and with minor changes. Dilutions of antibodies (0-25 μg/ml) will be mixed and inoculated onto Vero E6 cells. 24 hours later the infected cells are washed and stained with 1C7, a monoclonal antibody specific for the nucleoprotein of the virus followed by an Alexa647 fluorophore tagged mouse IgG specific secondary antibody. The cell monolayers are fixed and fluorescence measured on a Celligo cytometer.

[0471] In vivo testing of mAb in hamster model of infection: The efficacy of the mAb is determined using a hamster model of SARsCoV2 infection. Animals are infected by intranasal inoculation with a predetermined dose of virus (100TCID50). One hour post infection the animals receive an intravenous administration of the antibodies to be tested. Two doses, 100 μg and 500 μg of each antibody are injected. Animal weights are monitored daily and on day 5 test animals are euthanized, lungs collected, homogenized and analyzed for viral titers by inoculation onto VeroE6 as described above. Experiments are done with individual lead antibodies and selected combinations of antibodies. Irrelevant human antibody serve as control.

[0472] Summary: The antibodies that utilize human V regions, neutralize SARsCoV2 in the pM range (Tables 3 and 4). All mAbs are of a rat IgG2a or 2b isotype. All mAbs have been sequenced (see Tables 1, 2, and 5-10) and show some degree of uniqueness with each other.

Example 2: Antibodies of Family E Bind to Different Epitopes than Antibodies of Families A and B

[0473] To determine epitope competition between families of antibodies, competitive ELISAs were performed on SARS-CoV RBD coated plates using supernatants (either undiluted (neat) or at a 1:10 dilution in sera free media) representing clones from each family. Rat IgG was used as an isotype control (1 μg/ml). Biotinylated purified antibody from family A (10D6) or B (16C5) was added after the supernatants and developed with streptavidin HRP. Representative clones included 19C4 (family A), 16C12 (family B), 2C1 (family D), 14G5 (family E), 7D2 (family F), and 10A3 (family G) (FIGS. **4**A and **4**B). Three family E clones (3E10, 14G5, and 14G11) were examined for competition with family A (FIG. **4**C) and B (FIG. **4**D) biotinylated monoclonals.

[0474] None of the family E antibodies competed with family A and B antibodies for epitope binding (FIG. **4**), indicating that family E antibodies bind to different epitopes from those epitopes bound by families A and B.

Example 3: Antibodies Neutralized WT Pseudovirus and Pseudovirus Variants

[0475] GFP expressing, VSV based pseudoviruses with either wildtype or major single variant mutation spike proteins N501Y (observed in the α (i.e., UK) mutant virus) and E484K (observed in the β (i.e., the South Africa) mutant virus) were mixed with purified human antibodies from each of the major antibody clonal families a concentration range from 5 μg/ml to 5 ng/ml. Prior to neutralization, hybridoma supernatants grown in SFM (sera free hybridoma media) (Invitrogen) were quantitated using an Octet Red96 by diluting supernatants 1:5 and 1:10 in sera free media and measured for binding against the Anti-Murine IgG Quantitation (AMQ) Biosensors (with cross reactivity to rat IgG Fc) on an Octet Red 96 BLI Instrument (SartoriusAG, Goettingen, Germany). Results were compared to in-lab derived purified rat IgG standards diluted in SFM in the range of 0.5-50 μg/ml. For neutralization, VsV-SARS-spike GFP-expressing reporter virus (PMCID: PMC8313705) was pre-incubated with mouse sera (1:100-1:3200), hybridoma supernatants (1:10-1:10,000), or purified human monoclonal antibodies (0.1 ng/ml-1 μg/ml) and incubated at 4° C. for 1 hr before the inoculum was added either to Vero E6 cells or to HEK-293 cells expressing Transmembrane Serine Protease-2 (PMCID: PMC8313705) overnight at 37° C., 5% CO_2. The cells were resuspended in cold FACS buffer and analyzed by flow cytometry (Intellicyte Corp.) for GFP fluorescence intensity. Cells with a high mean fluorescence intensity were identified using FlowJo software (Tree Star, Inc.) and graphed using GraphPad Prism to create a heat map based on MFI. A human isotype was used as a control (IgG1). Representative clones included 19C4 (family A), 16C12 (family B), 2C1 (family D), 14G5 (family E), 7D2 (family F), and 10A3 (family G).

[0476] All genetic clonal families of lead antibodies neutralized WT pseudovirus, and N501Y single mutation pseudovirus (FIG. **5**).

[0477] EC_{50} values for different antibodies and pseudovirus variants are shown in Table 11.

TABLE 11

Neutralization of different pseudovirus variants by selected antibodies. B1.1.7 is the UK alpha variant without the E484K mutation (VOC-20DEC-01).

		Pseudovirus Mutant Variants Neutralization (EC50 ng/ml)				
Genetic family	Clone name	J15 (WT)	484	501	B1.1.7	Inhibition of family B
Family I	5B6 (f3)	32.4	35.2	28.2	15.3	yes
Family E	13A12 (f3)	67.8	221	29	32.8	no
Family H	2G6 (f4)	157	1457	152	51.4	no

Example 4: ELISA Binding Analysis of Human Neutralizing mAbs to Wild Type-RBD, South African (SA)-RBD Variant, and N501Y-RBD Point Mutant

[0478] Fusion proteins representing the RBD domains of the SARS-CoV2 Spike protein from the wild type, the N501Y single mutant, or the South African (SA, E484K) variant were coated to ELISA plates and screened for binding as described in the materials and methods. Monoclonal antibodies representing each of the genetic families were added to coated ELISA plates at concentrations between 2 μg/ml to 2 ng/ml. Absorbance was read at 450 nm. All antibody families bound to WT and N501Y RBDs by ELISA (FIG. **6**).

Example 5: Anti-SARS-CoV2 RBD mAbs Block Virus Proliferation In Vivo

[0479] BALB/c mice were sensitized with Ad5-hACE2, treated with anti-RBD monoclonal antibodies, and challenged with SARS-CoV-2 (FIG. **7**A). Specifically, nine to twelve-week old female BALB/c mice were sensitized with Ad5-hACE2 via intranasal route at 2.5×10^8 PFU/animal five days prior to the challenge of SARS-CoV-2. Mice were transferred to BSL-3 facility 2 or 3 days before infection for acclimatization. One day before the challenge, each mouse received 200 μl of antibody (5H12, 10D6, 1D10, 16C5, or 19C4) at the designated amounts via intraperitoneal (IP) route. Two controls groups that received human IgG negative control or PBS were included. Twenty-four hours after the transfer, mice were challenged with 105 PFU of USA-WA1/2020 SARS-CoV-2 strain (day 0). The animals were sacrificed at day 2 post-challenge, when the virus replication peaks, to harvest lungs. Lung lobes from each animal were homogenized in 1 mL PBS. Plaque assays using Vero E6 cells were performed in the biosafety level 3 (BSL-3) facility following institutional guidelines to quantify infectious viral titers in the lung homogenates, in which plaque forming unit (PFU)/mL was used as the readout.

[0480] The panel of mAbs effectively and prophylactically blocked virus replication in the lungs in contrast to human IgG negative control and PBS, with almost no detectable titers in some groups (FIGS. **7**B and **7**C).

TABLE 1

Variable_Heavy Chain Sequences.
Antibodies are also referred to as SARS2-[antibody name] in the specification.
For example, SARS2-1C12_f3_H and 1C12_f3_H refer to the same antibody.

		Variable_Heavy Chain Nucleotide Sequence		Variable Heavy Chain Amino Acid Sequence	
Ab #	Name	SEQ ID NO	Sequence	SEQ ID NO	Sequence
1	1C12_f3_H	1	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGG GCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCA GTTATGATATCACCTGGGTGCGACAGGCCACTGGACAAGGGCTTGA GTGGATGGGATGGATGAGCCCTAACAGTGGTAACACAGGCTATAC ACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGAACACCTCCAT AAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACAC GGCCGTGTATTACTGTGCGAGATTCGGCTATGGTTCGGGGGCCCTC GACTACTACTACTACGGTTTGGACGTCTGGGGCCAAGGGACCACGG TCACCGTCTCCTCA	59	QVQLVQSGAEVKKPG ASVKVSCKASGYTFTS YDITWVRQATGQGLE WMGWMSPNSGNTGY TQKFQGRVTMTRNTSI STAYMELSSLRSEDTA VYYCARFGYGSGALD YYYYGLDVWGQGTTV TVSS
2	1D5_f3_H	2	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGG GCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCA GTTATGATATCACCTGGGTGCGACAGGCCACTGGACAAGGGCTTGA GTGGATGGGATGGATGAGCCCTAACAGTGGTAACACAGGCTATGC ACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGAACACCTCCAT AAGCACAGCCTACATGGAGCTGAACAGCCTGAGATCTGAGGACAC GGCCGTGTATTACTGTGCGAGATTCGGCTATGGTTCGGGGGCCCTC GACTACTACTACTACGGTTTGGACGTCTGGGGCCAAGGGACCACGG TCACCGTCTCCTCA	60	QVQLVQSGAEVKKPG ASVKVSCKASGYTFTS YDITWVRQATGQGLE WMGWMSPNSGNTGY AQKFQGRVTMTRNTSI STAYMELNSLRSEDTA VYYCARFGYGSGALD YYYYGLDVWGQGTTV TVSS
3	1D10_f3_H	3	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAAGTGAAGAAGCCTGGG GCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCA GTTATGATATCATCTGGGTGCGACAGGCCTCTGGACAAGGGCTTGA GTGGATGGGATGGATGAGCCCTAACAGCGGTAACACAGGCTATGC ACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGAACACCTCCAT AAACACAGCCTACATGGAGCTGAGTAGCCTGAGATCTGAGGACAC GGCCGTGTATTATTGTGCGAGATTCGGCTATGGTTCGGGGGCCCTC GACTACTACTATTACGGTTTGGACGTCTGGGGCCAAGGGACCACGG TCACCGTCTCCTCA	61	QVQLVQSGAEVKKPG ASVKVSCKASGYTFTS YDIIWVRQASGQGLE WMGWMSPNSGNTGY AQKFQGRVTMTRNTSI NTAYMELSSLRSEDTA VYYCARFGYGSGALD YYYYGLDVWGQGTTV TVSS
4	1E2_f3_H	4	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGG GCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCA GTTATGATATCACCTGGGTGCGACAGGCCACTGGACAAGGGCTTGA GTGGATGGGATGGATGAGCCCTAACAGTGGTAACACAGGCTATGC ACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGAACACCTCCAT AAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACAC GGCCGTGTATTACTGTGCGAGATTCGGCTATGGTTCGGGGGCCCTC GACTACTACTACTACGGTTTGGACGTCTGGGGCCAAGGGACCACGG TCACCGTCTCCTCA	62	QVQLVQSGAEVKKPG ASVKVSCKASGYTFTS YDITWVRQATGQGLE WMGWMSPNSGNTGY AQKFQGRVTMTRNTSI STAYMELSSLRSEDTA VYYCARFGYGSGALD YYYYGLDVWGQGTTV TVSS
5	1G9_f3_H	5	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGG GCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCA GTTATGATATCATTTGGGTGCGACAGGCCACTGGACAAGGGCTTGA GTGGATGGGATGGATGAGCCCTAACAGTGGTAACACAGGCTATGC ACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGAACACCTCCAT AAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACAC GGCCGTGTATTACTGTGCGAGATTCGGCTATGGTTCGGGGGCCCTC GACTACTACTACTACGGTTTGGACGTCTGGGGCCAAGGGACCACGG TCACCGTCTCCTCA	63	QVQLVQSGAEVKKPG ASVKVSCKASGYTFTS YDIIWVRQATGQGLE WMGWMSPNSGNTGY AQKFQGRVTMTRNTSI STAYMELSSLRSEDTA VYYCARFGYGSGALD YYYYGLDVWGQGTTV TVSS
6	5D7_f3_H	6	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGG ACCTCAGTGAAAGTCTCCTGCAAGACTTCTGGATACACCTTCACCA GTTATGATATCATCTGGGTGCGACAGGCCACTGGACAAGGGCTTGA GTGGATGGGATGGATGAGCCCTAAAAATGGTAACACAGGCTATGC ACAGAGGTTCCAGGGCAGAGTCACCATGACCAGGAACACCTCCAT AAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACAC GGCCGTGTATTACTGTGCGAGATTCGGCTATGGTTCGGGGGCCCTC GACTACTACTACTACGGTTTGGACGTCTGGGGCCAAGGGACCACGG TCACCGTCTCCTCA	64	QVQLVQSGAEVKKPG TSVKVSCKTSGYTFTS YDIIWVRQATGQGLE WMGWMSPKNGNTGY AQRFQGRVTMTRNTSI STAYMELSSLRSEDTA VYYCARFGYGSGALD YYYYGLDVWGQGTTV TVSS
7	5H12_f3_H	7	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGG ACCTCAGTGAAAGTCTCCTGCAAGACTTCTGGATACACCTTCCCCA GTTATGATATCATCTGGGTGCGACAGGCCACTGGACAAGGGCTTGA GTGGATGGGATGGATGAGCCCTAAAAATGGTAACACAGGCTTTGCA	65	QVQLVQSGAEVKKPG TSVKVSCKTSGYTFPS YDIIWVRQATGQGLE WMGWMSPKNGNTGF

TABLE 1-continued

Variable_Heavy Chain Sequences.
Antibodies are also referred to as SARS2-[antibody name] in the specification.
For example, SARS2-1C12_f3_H and 1C12_f3_H refer to the same antibody.

		Variable_Heavy Chain Nucleotide Sequence		Variable Heavy Chain Amino Acid Sequence	
Ab #	Name	SEQ ID NO	Sequence	SEQ ID NO	Sequence
			CAGAGGTTCCAGGGCAGAGTCACCATGACCAGGAACACCTCCATA AGCACAGCCTACATGGAACTGAGCAGCCTGAGATCTGAGGACACG GCCGTGTATTACTGTGCGAGATTCGGCTATGGGTCGGGGGCCCTCG GATATTACTACTACGGTTTGGACGTCTGGGGCCAAGGGACCACGGT CACCGTCTCCTCA		AQRFQGRVTMTRNTSI STAYMELSSLRSEDTA VYYCARFGYGSGALG YYYYGLDVWGQGTTV TVSS
8	7C10_f3_H	8	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGG GCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCA GTTATGATATCACCTGGGTGCGACAGGCCACTGGACAAGGGCTTGA GTGGATGGGGTGGATGAGCCCTAACAGTGGTAACACAGGCTATGC ACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGAACACCTCCAT AAGCACAGCCTACATGGAGCTGCGCAGCCTGAGGTCTGAGGACAC GGCCGTGTATTACTGTGCGAGATTCGGCTATGGTTCGGGGGCCCTC GACTACTACTACTACGGTTTGGACGTCTGGGGCCAAGGGACCACGG TCACCGTCTCCTCA	66	QVQLVQSGAEVKKPG ASVKVSCKASGYTFTS YDITWVRQATGQGLE WMGWMSPNSGNTGY AQKFQGRVTMTRNTSI STAYMELRSLRSEDTA VYYCARFGYGSGALD YYYYGLDVWGQGTTV TVSS
9	8H4_f3_H	9	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGG GCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCA GTTATGATATCACCTGGGTGCGACAGGCCACTGGACAAGGGCTTGA GTGGATGGGATGGATGAGCCCTAACAGTGGTAACACAGGCTATGC ACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGAACACCTCCAT AAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACAC GGCCGTGTATTACTGTGCGAGATTCGGCTATGGTTCGGGGGCCCTC GACTACTACTACTACGGTTTGGACGTCTGGGGCCAAGGGACCACGG TCACCGTCTCCTCA	67	QVQLVQSGAEVKKPG ASVKVSCKASGYTFTS YDITWVRQATGQGLE WMGWMSPNSGNTGY AQKFQGRVTMTRNTSI STAYMELSSLRSEDTA VYYCARFGYGSGALD YYYYGLDVWGQGTTV TVSS
10	9C6_f3_H	10	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGG GCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCA GTTATGATATCACCTGGGTGCGACAGGCCACTGGACAAGGGCTTGA GTGGATGGGATGGATGAGCCCTAAAAGTGGTAACACAGGCTATGC ACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGAACACCTCCAT AAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACAC GGCCGTGTATTACTGTGCGAGATTCGGCTATGGTTCGGGGGCCCTC GACTACTACTACTACGGTTTGGACGTCTGGGGCCAAGGGACCACGG TCACCGTCTCCTCA	68	QVQLVQSGAEVKKPG ASVKVSCKASGYTFTS YDITWVRQATGQGLE WMGWMSPKSGNTGY AQKFQGRVTMTRNTSI STAYMELSSLRSEDTA VYYCARFGYGSGALD YYYYGLDVWGQGTTV TVSS
11	10D6_f3_H	11	GAGGTGCAGTTGGTGGAGACTGGAGGAGGCTTGATCCAGCCTGGG GGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGGATCACCGTCAGTA GTAACTACATGAACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGG AGTGGGTCTCAGTTATTTATAGCGGTGGTAGCACATACTACGCAGA CTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAAC ACACTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCCG TGTATTACTGTGCGAGAGATTTAGAACTGGCTGGAGCTTTTGATATC TGGGGCCAAGGGACAATGGTCACCGTCTCTTTA	69	EVQLVETGGGLIQPGG SLRLSCAASGITVSSNY MNWVRQAPGKGLEW VSVIYSGGSTYYADSV KGRFTISRDNSKNTLY LQMNSLRAEDTAVYY CARDLELAGAFDIWG QGTMVTVSL
12	11D5_f3_H	12	GAGGTGCAGTTGGTGGAGACTGGAGGAGGCTTGATCCAGCCTGGG GGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGGATCACCGTCAGTA GTAACTACATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGG AGTGGGTCTCAGTTATTTATAGCGGTGGTAGCACATACTACGCAGA CTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCCG TGTATTACTGTGCGAGAGATTTAGCAGTGGCTGGAGCTTTTGATATC TGGGGCCAAGGGACAATGGTCACCGTCTCTTTA	70	EVQLVETGGGLIQPGG SLRLSCAASGITVSSNY MSWVRQAPGKGLEW VSVIYSGGSTYYADSV KGRFTISRDNSKNTLY LQMNSLRAEDTAVYY CARDLAVAGAFDIWG QGTMVTVSL
13	11G2_f3_H	13	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGG GCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCA GTTATGATATCACCTGGGTGCGACAGGCCACTGGACAAGGGCTTGA GTGGATGGGATGGATGAGCCCTAACAGTGGTAACACAGGCTATGC ACAGAAGTTCCAGGGCAGAGTCTCCATGACCAGGAACACCTCCATA AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACG GCCGTGTATTACTGTGCGAGATTCGGCTATGGTTCGGGGGCCCTCG ACTACTACTACTACGGTTTGGACGTCTGGGGCCAAGGGACCACGGT CACCGTCTCCTCA	71	QVQLVQSGAEVKKPG ASVKVSCKASGYTFTS YDITWVRQATGQGLE WMGWMSPNSGNTGY AQKFQGRVSMTRNTSI STAYMELSSLRSEDTA VYYCARFGYGSGALD YYYYGLDVWGQGTTV TVSS
14	11G7_f2_H	14	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCG GGGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCCATCAGCAG TAGTAACTGGTGGAGTTGGGTCCGCCAGCCCCCAGGGAAGGGGCTG	72	QVQLQESGPGLVKPSG TLSLTCAVSGGSISSSN WWSWVRQPPGKGLE

TABLE 1-continued

Variable_Heavy Chain Sequences.
Antibodies are also referred to as SARS2-[antibody name] in the specification.
For example, SARS2-1C12_f3_H and 1C12_f3_H refer to the same antibody.

		Variable_Heavy Chain Nucleotide Sequence		Variable Heavy Chain Amino Acid Sequence	
Ab #	Name	SEQ ID NO	Sequence	SEQ ID NO	Sequence
			GAGTGGATTGGGGAAATCTTTCATAGTGGGAGCACCAACTACAACC CGTCCCTCAAGAGTCGAGTCACCATATCAGTAGACAAGTCCAAGAA CCAGTTCTCCCTGAAGCTGAACTCTGTGACCGCCGCGGACACGGCC GTGTATTACTGTGCGAGATTCAGAAGGATAGTGGCTACGAGCTACT ATTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA		WIGEIFHSGSTNYNPSL KSRVTISVDKSKNQFS LKLNSVTAADTAVYY CARFRRIVATSYYFDY WGQGTLVTVSS
15	16C5_f3_H	15	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGG GCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCA GTTATGATATCATTTGGGTGCGACAGGCCACTGGACAAGGGCTTGA GTGGATGGGATGGATGAGCCCTAATAGTGGTAACACAGGCTATGCA CAGAAGTTCCAGGGCAGAGTCACCATGACCAGGAACACCTCCATA GGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACG GCCGTGTATTTCTGTGCGAGATTCGGCTATGGTTCGGGGGCCCTCG ACTACTACTACTACGGTTTGGACGTCTGGGGCCAAGGGACCACGGT CACCGTCTCCTCA	73	QVQLVQSGAEVKKPG ASVKVSCKASGYTFTS YDIIWVRQATGQGLE WMGWMSPNSGNTGY AQKFQGRVTMTRNTSI GTAYMELSSLRSEDTA VYFCARFGYGSGALD YYYYGLDVWGQGTTV TVSS
16	16C12_f3_H	16	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGG GCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCA GTTATGATATTATCTGGGTGCGACAGGCCACTGGACAAGGGCTTGA GTGGATGGGATGGATGAGCCCTAACAGTGGTAACACAGGCTATGC ACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGAACACCTCCAT AAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACAC GGCCGTGTATTACTGTGCGAGATTCGGCTATGGTTCGGGGGCCCTC GACTACTACTACTACGGTTTGGACGTCTGGGGCCAAGGGACCACGG TCACCGTCTCCTCA	74	QVQLVQSGAEVKKPG ASVKVSCKASGYTFTS YDIIWVRQATGQGLE WMGWMSPNSGNTGY AQKFQGRVTMTRNTSI STAYMELSSLRSEDTA VYYCARFGYGSGALD YYYYGLDVWGQGTTV TVSS
17	17A8_f3_H	17	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGG GCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCA GTTATGATATCATTTGGGTGCGACAGGCCACTGGACAAGGGCTTGA GTGGATGGGATGGATGAGCCCTAACAGTGGTAACACAGGCTATGC ACAGAAGTTCCAGGGCAGAGTCACCATGACCAAGAACACCTCCAT AAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACAC GGCCGTGTATTACTGTGCGAGATTCGGCTATGGTTCGGGGGCCCTC GACTACTACTACTACGGTTTGGACGTCTGGGGCCAAGGGACCACGG TCACCGTCTCCTCA	75	QVQLVQSGAEVKKPG ASVKVSCKASGYTFTS YDIIWVRQATGQGLE WMGWMSPNSGNTGY AQKFQGRVTMTKNTSI STAYMELSSLRSEDTA VYYCARFGYGSGALD YYYYGLDVWGQGTTV TVSS
18	17F2_f3_H	18	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAGGCCTGGG GCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCA GTTATGATATCACCTGGGTGCGACAGGCCACTGGACAAGGGCTTGA GTGGATGGGATGGATGAGCCCTGACAGTGGTAACACAGGCTATGC ACAGAGGTTCCAGGGCAGAGTCACCATGACCAGGAACACCTCCAT AAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACAC GGCCGTGTATTACTGTGCGAGATTCGGCTATGGTTCGGGGGCCCTC GACTACTACTACTACGGTTTGGACGTCTGGGGCCAAGGGACCACGG TCACCGTCTCCTCA	76	QVQLVQSGAEVKRPG ASVKVSCKASGYTFTS YDITWVRQATGQGLE WMGWMSPDSGNTGY AQRFQGRVTMTRNTSI STAYMELSSLRSEDTA VYYCARFGYGSGALD YYYYGLDVWGQGTTV TVSS
19	18E7_f3_H	19	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGG GCCTCAGTGACGGTCTCCTGCAAGGCTTCTGGATACACCTTTACCA GTTATGATATCATCTGGGTGCGACAGGCCACTGGACAAGGGCTTGA GTGGATGGGATGGATGAGCCCTAACAGTGGTAACACAGGCTATGC ACAGAGGTTCCAGGGCAGAGTCACCATGACCAGGAACACCTCCAT AAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACAC GGCCGTGTATTACTGTGCGAGATTCGGCTATGGTTCGGGGGCCCTC GACTACTACTACTACGGTTTGGACGTCTGGGGCCAAGGGACCACGG TCACCGTCTCCTCA	77	QVQLVQSGAEVKKPG ASVTVSCKASGYTFTS YDIIWVRQATGQGLE WMGWMSPNSGNTGY AQRFQGRVTMTRNTSI STAYMELSSLRSEDTA VYYCARFGYGSGALD YYYYGLDVWGQGTTV TVSS
20	19C4_f3_H	20	GAGGTGCAGTTGGTGGAGACTGGAGGAGGCTTGATCCAGCCTGGG GGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGGATCACCGTCAGTA GTAATTACATGAACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGG AGTGGGTCTCAGTTATTTATAGCGGTGGTAGCACATTCTACGCAGA CTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCCG TATATTACTGTGCGAGAGATTTAGAAGTGGCTGGAGGTTTTGATAT CTGGGGCCAAGGGACAATGGTCACCGTCTCTTTA	78	EVQLVETGGGLIQPGG SLRLSCAASGITVSSNY MNWVRQAPGKGLEW VSVIYSGGSTFYADSV KGRFTISRDNSKNTLY LQMNSLRAEDTAVYY CARDLEVAGGFDIWG QGTMVTVSL
21	2C1_f4_H	21	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCAGGA CGGTCCCTGAGACTCTCCTGTACAGCTTCTGGATTCACCTTTGGTGA	79	EVQLVESGGGLVQPGR SLRLSCTASGFTFGDY

TABLE 1-continued

Variable_Heavy Chain Sequences.
Antibodies are also referred to as SARS2-[antibody name] in the specification.
For example, SARS2-1C12_f3_H and 1C12_f3_H refer to the same antibody.

		Variable_Heavy Chain Nucleotide Sequence		Variable Heavy Chain Amino Acid Sequence	
Ab #	Name	SEQ ID NO	Sequence	SEQ ID NO	Sequence
			TTATACTTTGAGCTGGTTCCGCCAGGCTCCAGGGAAGGGGCTGGAA TGGGTAGGTTTCATTAGAAGCAAACCTTTTGGTGGGACAACACAAT ACGCCGCGTCTGTGAAAGGCAGATTCACCATCTCAAGGGATGATTC CAAAAGCATCGCCTATCTGCAAATGAACAGCCTGAAAACCGAGGA CACAGCCGTGTATTACTGTACTAGAGTGTCCGGGTATAGCAACATC TGGTTCTTTGCCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTC A		TLSWFRQAPGKGLEW VGFIRSKPFGGTTQYA ASVKGRFTISRDDSKSI AYLQMNSLKTEDTAV YYCTRVSGYSNIWFFA YWGQGTLVTVSS
22	4E3_f4_H	22	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGG AGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAG CTATGGCATGAACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGA GTGGGTGGCAGTTATTTGGTATGATGGAAATAATAAATACTATGCA GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGA ACACGTTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGG CTGTGTATTACTGTGCGAGAAAAGATTATTCGAAGACATTTTATGG ATACTACTTTGACTATTGGGGCCAGGGAACCCTGGTCACCGTCTCCT CA	80	QVQLVESGGGVVQPG RSLRLSCAASGFTFSSY GMNWVRQAPGKGLE WVAVIWYDGNNKYY ADSVKGRFTISRDNSK NTLYLQMNSLRAEDT AVYYCARKDYSKTFY GYYFDYWGQGTLVTV SS
23	7D2_f4_H	23	GAGGTGCAGCTGGTGGAGACTGGAGGAGGCTTGATCCAGCCTGGG GGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGGTTCACCGTCAGTA GCAACTACATGAACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGG AGTGGGTCTCAGTTATTTATAGCGGTGGTAGCACATTCTACGCAGA CTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCTACAAC ACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCCG TGTATTACTGTGCGAGAGATCTAGTCATCTACGGTATGGACGTCTG GGGCCAAGGGACCACGGTCACCGTCTCCTCA	81	EVQLVETGGGLIQPGG SLRLSCAASGFTVSSN YMNWVRQAPGKGLE WVSVIYSGGSTFY ADS VKGRFTISRDNSYNTL YLQMNSLRAEDTAVY YCARDLVIYGMDVWG QGTTVTVSS
24	9C5_f4_H	24	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGG AGGTCCCTGAGACTCTCCTGTGTAGCGTCTGGATTCACCTTCAGTAG CTATGGCATGAACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGA GTGGGTGGCAGTTATTTGGTATGATGGAAATAATAAATACTATGCA GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGA ACACGCTGTATCTGCAAATGAACAGTCTGAGAGCCGAGGACACGG CTGTGTATTACTGTGCGAGAAAAGATGGTTCGAAGACATATTATGG ATACTACTTTGACTATTGGGGCCAGGGAACCCTGGTCACCGTCTCCT CA	82	QVQLVESGGGVVQPG RSLRLSCVASGFTFSSY GMNWVRQAPGKGLE WVAVIWYDGNNKYY ADSVKGRFTISRDNSK NTLYLQMNSLRAEDT AVYYCARKDGSKTYY GYYFDYWGQGTLVTV SS
25	10A3_f4_H	25	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGG AGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAG TTATGGCATGAACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAG TGGGTGGCAATTATTTGGTATGATGGAAATAATACATACTATGTAG ACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAA CACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAAGACACGGCT GTGTATTACTGTGCGAGAAAAAGATGGTTCGAAGACATATTATGGAT ACTACTTTGACTATTGGGGCCAGGGAACCCTGGTCACCGTCTCCTC A	83	QVQLVESGGGVVQPG RSLRLSCAASGFTFSSY GMNWVRQAPGKGLE WVAIIWYDGNNTYYV DSVKGRFTISRDNSKN TLYLQMNSLRAEDTA VYYCARKDGSKTYYG YYFDYWGQGTLVTVS S
26	14G5_f4_H	26	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCG GGGACCCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCCATCAGCAG TAATAACTGGTGGAGTTGGGTCCGCCAGCCCCCAGGGAAGGGGCTG GTGTGGATTGGGGAAATCTTGCATGGTGAGATCACCAACTACAACC CGTCCCTCAAGAGTCGAGTCACCATATCAATAGACAAGTCCAAGAA CCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCCGCGGACACGGCC GTGTATTACTGTGCGAGAGATGCGAATTTCTATGGTTCGGGGAGTT CTTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA	84	QVQLQESGPGLVKPSG TLSLTCAVSGGSISSNN WWSWVRQPPGKGLV WIGEILHGEITNYNPSL KSRVTISIDKSKNQFSL KLSSVTAADTAVYYC ARDANFYGSGSSYFDY WGQGTLVTVSS
27	13A12_f3_H	27	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCG GGGACCCTGTCCCTCACCTGCGCTGTCTCAGGTGGCTCCATCTACAG TAGTAACTGCTGGAGTTGGGTCCGCCAGCCCCCAGGGAAGGGGCTG GAGTGGATTGGGGAAATCTATCATAGTGGGGGCACCAACTACAACC CGTCCCTCAAGAGTCGAGTCACCATATCATTAGACAAGTCCAAGAA CAGGTTCTCCCTGAGGCTGAGCTCTGTGACCGCCGCGGACACGGCC GTGTATTACTGTGCGAGAGATCAAGATTACTATGGTTCGGGGAGTT CCCTCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA	85	QVQLQESGPGLVKPSG TLSLTCAVSGGSIYSSN CWSWVRQPPGKGLEW IGEIYHSGGTNYNPSLK SRVTISLDKSKNRFSLR LSSVTAADTAVYYCA RDQDYYGSGSSLFDY WGQGTLVTVSS
28	5B6_f3_H	28	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTAAAGCCTGGG GGGTCCCTTAGACTCTCCTGTGCAGCCTCTGGATTCACTTTCAGTAA	86	EVQLVESGGGLVKPG GSLRLSCAASGFTFSN

TABLE 1-continued

Variable_Heavy Chain Sequences.
Antibodies are also referred to as SARS2-[antibody name] in the specification.
For example, SARS2-1C12 f3 H and 1C12 f3 H refer to the same antibody.

		Variable Heavy Chain Nucleotide Sequence		Variable Heavy Chain Amino Acid Sequence	
Ab #	Name	SEQ ID NO	Sequence	SEQ ID NO	Sequence
			CGCCTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGA		AWMSWVRQAPGKGL
			GTGGGTTGGCCGTTTTAAAAGCAAAACTGATGGTGGGACAACAGAC		EWVGRFKSKTDGGTT
			TACGCTGCACCCGTGAAAGGCAGATTCACCATCTCAAGAGATGATT		DYAAPVKGRFTISRDD
			CAAAAAACACGCTGTATCTGCAAATGAACAGCCTGAAAACCGAGG		SKNTLYLQMNSLKTED
			ACACAGCCGTGTATTACTGTACCACCAGCAGTGGCTACTGGGGCCA		TAVYYCTTSSGYWGQ
			GGGAACCCTGGTCACCGTCTCCTCA		GTLVTVSS
29	2G6_f4_H	29	CAGGTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGG	87	QVQLQQWGAGLLKPS
			AGACCCTGTCCCTCACCTGCACTATCTATGGTGGGTCCTTCAGTGTT		ETLSLTCTIYGGSFSVY
			TACTACTGGAACTGGATCCGCCAGCCCCCAGAGAAGGGGCTGGAGT		YWNWIRQPPEKGLEWI
			GGATTGGGGAAATCAATCATAGTGGAAACACCAACTACAACCCGTC		GEINHSGNTNYNPSLK
			CCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAA		SRVTISVDTSKNQFSLK
			TTCTCCCTGAAGCTGAGCTCTGTGACCGCCGCGGACACGGCTGTGT		LSSVTAADTAVYYCA
			ATTACTGTGCGAGGTATTACTATGATGGTAATGGTTATTACCCCTGG		RYYYDGNGYYPWGQ
			GGCCAGGGAACCCTGGTCACCGTCTCCTCA		GTLVTVSS

TABLE 2

Variable Light Chain Sequences.

		VariABLE Light Chain Nucleotide Sequence		Variable Light Chain Amino Acid Sequence	
Ab #	Name	SEQ ID NO	Sequence	SEQ ID NO	Sequence
1	1C12_f3_K	30	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG	88	EIVLTQSPGTLSLSPGE
			GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGGAGC		RATLSCRASQSVRSSH
			AGTCACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGC		LAWYQQKPGQAPRLL
			TCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGG		IYGASSRATGIPDRFS
			TTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAG		GSGSGTDFTLTISRLEP
			ACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATAATA		EDFAVYYCQQYNNSP
			ACTCACCGATCACCTTCGGCCAAGGGACACGACTGGAGATTAAA		ITFGQGTRLEIK
2	1D5_f3_K	31	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG	89	EIVLTQSPGTLSLSPG
			GGACAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGGAGC		DRATLSCRASQSVRSS
			AGTCACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGC		HLAWYQQKPGQAPR
			TCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGG		LLIYGASSRATGIPDR
			TTCAGTGGCAGTGGGTCTGGGACAGACTTCTCTCTCACCATCAGCAG		FSGSGSGTDFSLTISRL
			ACTGGAGCCTGAGGATTTTGCAGTGTATTACTGTCAGCAGTTTGGTA		EPEDFAVYYCQQFGS
			GCTCACCGATCACCTTCGGCCAAGGGACACGGCTGGAGATTAAA		SPITFGQGTRLEIK
3	1D10_f3_K	32	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG	90	EIVLTQSPGTLSLSPGE
			GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGC		RATLSCRASQSVSSSH
			AGCCACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGC		LAWYQQKPGQAPRLL
			TCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGG		IYGASSRATGIPDRFS
			TTCAGTGGCAGTGGGTCTGGAACAGACTTCACTCTCACCATCAGCAG		GSGSGTDFTLTISRLEP
			ACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATAATA		EDFAVYYCQQYNSSPI
			GCTCACCGATCACCTTCGGCCAAGGGACACGACTGGAGATTAAA		TFGQGTRLEIK
4	1E2_f3_K	33	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG	91	EIVLTQSPGTLSLSPGE
			GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGGAGC		RATLSCRASQSVRSSH
			AGTCACTTTGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCT		FAWYQQKPGQAPRLL
			CCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGT		IYGASSRATGIPDRFS
			TCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAG		GSGSGTDFTLTISRLEP
			ACTGGAGCCTGAAGATTTTGCAGTGTGTTACTGTCAGCAGTATGGTA		EDFAVCYCQQYGSSPI
			GCTCACCGATCACCTTCGGCCAAGGGACACGACTGGAGATTAAA		TFGQGTRLEIK
5	1G9_f3_K	34	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG	92	EIVLTQSPGTLSLSPGE
			GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGGAGC		RATLSCRASQSVRSSH
			AGTCACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGC		LAWYQQKPGQAPRLL
			TCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGG		IYGASSRATGIPDRFS

TABLE 2-continued

Variable Light Chain Sequences.

Ab #	Name	VariABLE Light Chain Nucleotide Sequence SEQ ID NO	Sequence	Variable Light Chain Amino Acid Sequence SEQ ID NO	Sequence
			TTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAG		GSGSGTDFTLTISRLEP
			ACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTA		EDFAVYYCQQYGSSPI
			GCTCACCGATCACCTTCGGCCAAGGGACACGACTGGAGATTAAA		TFGQGTRLEIK
6	5D7_f3_K	35	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG	93	EIVLTQSPGTLSLSPGE
			GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGGAGC		RATLSCRASQSVRSSH
			AGTCACTTAGCCTGGTACCGGCAGAAACCTGGCCAGGCTCCCAGGC		LAWYRQKPGQAPRLL
			TCCTCATCTATGGTGCCTCCAGCAGGGCCACTGGCATCCCAGACAGG		IYGASSRATGIPDRFS
			TTCAGTGGCCGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAG		GRGSGTDFTLTISRLE
			ACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATAATA		PEDFAVYYCQQYNISP
			TCTCACCGATCACCTTCGGCCAAGGGACACGACTGGAGATTAAA		ITFGQGTRLEIK
7	5H12_f3_K	36	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG	94	EIVLTQSPGTLSLSPGE
			GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGGAGC		RATLSCRASQSVRSSH
			AGTCACTTAGCCTGGTACCGGCAGAAACCTGGCCAGGCTCCCAGGC		LAWYRQKPGQAPRLL
			TCCTCATCTATGGTGCCTCCAGCAGGGCCACTGGCATCCCAGACAGG		IYGASSRATGIPDRFS
			TTCAGTGGCCGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAG		GRGSGTDFTLTISRLE
			ACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATAATT		PEDFAVYYCQQYNFS
			TCTCACCGATCACCTTCGGCCAAGGGACACGACTGGAGATTAAA		PITFGQGTRLEIK
8	7C10_f3_K	37	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG	95	EIVLTQSPGTLSLSPGE
			GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGGAGC		RATLSCRASQSVRSSH
			AGTCACTTAGCCTGGTCCCAGCAGAAACCTGGCCAGGCTCCCAGGC		LAWSQQKPGQAPRLL
			TCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGG		IYGASSRATGIPDRFS
			TTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAG		GSGSGTDFTLTISRLEP
			ACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTTTGGTA		EDFAVYYCQQFGSSPI
			GCTCACCGATCACCTTCGGCCAAGGGACACGACTGGAGATTAAA		TFGQGTRLEIK
9	8H4_f3_K	38	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG	96	EIVLTQSPGTLSLSPGE
			GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGGAGC		RATLSCRASQSVRSSH
			AGTCACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGC		LAWYQQKPGQAPRLL
			TCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGG		IYGASSRATGIPDRFS
			TTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAG		GSGSGTDFTLTISRLEP
			ACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTTTGGTA		EDFAVYYCQQFGSSPI
			GCTCACCGATCACCTTCGGCCAAGGGACACGACTGGAGATTAAG		TFGQGTRLEIK
10	9C6_f3_K	39	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG	97	EIVLTQSPGTLSLSPGE
			GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGGAGC		RATLSCRASQSVRSSH
			AGTCACTTAGCCTGGTACCGGCAGAAACCTGGCCAGGCTCCCAGGC		LAWYRQKPGQAPRLL
			TCCTCATCTATGGTGCCTCCAGCAGGGCCACTGGCATCCCAGACAGG		IYGASSRATGIPDRFS
			TTCAGTGGCCGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAG		GRGSGTDFTLTISRLE
			ACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATAATA		PEDFAVYYCQQYNSS
			GCTCACCGATCACCTTCGGCCAAGGGACACGACTGGAGATAAAA		PITFGQGTRLEIK
11	10D6_f3_K	40	GACATCCAGTTGACCCAGTCTCCATCCTTCCTGTCTGCATCTGTAGG	98	DIQLTQSPSFLSASVG
			AGACAGAGTCACCATCACTTGCCGGGCCAGTCAGGGCATTAGCAGT		DRVTITCRASQGISSY
			TATTTAGCCTGGTATCAGCAAAAACCAGGGAAAGCCCCTAAGGTCC		LAWYQQKPGKAPKV
			TGATCTATGCTGCATCCACTTTGCAAAGTGGGGTCCCATCAAGGTTC		LIYAASTLQSGVPSRF
			AGCGGCAGTGGATCTGGGACAGAATTCACTCTCACAATCAGCAGCC		SGSGSGTEFTLTISSLQ
			TGCAGCCTGAAGATTTTGCAACTTATTACTGTCAACAGCTTAATAGT		PEDFATYYCQQLNSY
			TACCCTCCGTCCACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA		PPSTFGQGTKLEIK
12	11D5_f3_K	41	GACATCCAGTTGACCCAGTCTCCATCCTTCCTGTCTGCATCTGTAGG	99	DIQLTQSPSFLSASVG
			AGACAGAGTCACCATCACTTGCCGGGCCAGTCAGGGCATTAGCAGT		DRVTITCRASQGISSY
			TATTTAGCCTGGTATCAGCAAAAACCAGGGAAAGCCCCTAAGGTCC		LAWYQQKPGKAPKV
			TGATCTATGCTGCATCCACTTTGCAAAGTGGGGTCCCATCAAGGTTC		LIYAASTLQSGVPSRF
			AGCGGCAGTGGATCTGGGACAGAATTCACTCTCACAATCAGCAGCC		SGSGSGTEFTLTISSLQ
			TGCAGCCTGAAGATTTTGCAACTTATTACTGTCAACAGCTTAATAGT		PEDFATYYCQQLNSY
			TACCCTCCGTCCACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA		PPSTFGQGTKLEIK
13	11G2_f3_K	42	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG	100	EIVLTQSPGTLSLSPGE
			GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGGAAC		RATLSCRASQSVRNS
			AGTCACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGC		HLAWYQQKPGQAPR
			TCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGG		LLIYGASSRATGIPDR
			TTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAG		FSGSGSGTDFTLTISRL
			ACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTTTGGTA		EPEDFAVYYCQQFGS
			GCTCACCGATCACCTTCGGCCAAGGGACACGACTGGAGATTAAA		SPITFGQGTRLEIK

TABLE 2-continued

Variable Light Chain Sequences.

Ab #	Name	VariABLE Light Chain Nucleotide Sequence SEQ ID NO	Sequence	Variable Light Chain Amino Acid Sequence SEQ ID NO	Sequence
14	11G7_f2_K	43	GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGG AGAGCCGGCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCATA GTAATGGATACAACTATTTGGATTGGTACCTGCAGAAGCCAGGGCA GTCTCCACAGCTCCTGATCTATTTGGGTTCTAATCGGGCCTCCGGGG TCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTG AAAATCAGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCA TGCAAGCTCTACAAACTCCTCTCACTTTCGGCGGAGGGACCAAGGTG GAGATCAAA	101	DIVMTQSPLSLPVTPG EPASISCRSSQSLLHSN GYNYLDWYLQKPGQ SPQLLIYLGSNRASGV PDRFSGSGSGTDFTLK ISRVEAEDVGVYYCM QALQTPLTFGGGTKV EIK
15	16C5_f3_K	44	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGGAGC AGTCACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGC TCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGG TTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAG ACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATAATA ACTCACCGATCACCTTCGGCCAAGGGACACGACTGGAGATTAAA	102	EIVLTQSPGTLSLSPGE RATLSCRASQSVRSSH LAWYQQKPGQAPRLL IYGASSRATGIPDRFS GSGSGTDFTLTISRLEP EDFAVYYCQQYNNSP ITFGQGTRLEIK
16	16C12_f3_K	45	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGGAGC AGTCACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGC TCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGG TTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAG ACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTA GCTCACCGATCACCTTCGGCCAAGGGACACGACTGGAGATTAAA	103	EIVLTQSPGTLSLSPGE RATLSCRASQSVRSSH LAWYQQKPGQAPRLL IYGASSRATGIPDRFS GSGSGTDFTLTISRLEP EDFAVYYCQQYGSSPI TFGQGTRLEIK
17	17A8_f3_K	46	GAAACTGTGTTGACGCAGTCTCCAGGCACTCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGGAGC AGTCACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGC TCCTCATCTATGGTGCATCCAGTAGGGCCACTGGCATCCCAGACAGG TTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAG ACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTA GCTCACCGATCACCTTCGGCCAAGGGACACGACTGGAGATTAAA	104	ETVLTQSPGTLSLSPG ERATLSCRASQSVRSS HLAWYQQKPGQAPR LLIYGASSRATGIPDR FSGSGSGTDFTLTISRL EPEDFAVYYCQQYGS SPITFGQGTRLEIK
18	17F2_f3_K	47	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGGAGC AGTCACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGC TCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGG TTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAG ACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATAATA GCTCACCGATCACCTTCGGCCAAGGGACACGACTGGAGATAAAA	105	EIVLTQSPGTLSLSPGE RATLSCRASQSVRSSH LAWYQQKPGQAPRLL IYGASSRATGIPDRFS GSGSGTDFTLTISRLEP EDFAVYYCQQYNSSPI TFGQGTRLEIK
19	18E7_f3_K	48	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGGAGC AGTCACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGC TCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGG TTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAG ACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTA GCTCACCGATCACCTTCGGCCAAGGGACACGACTGGAGATTAAA	106	EIVLTQSPGTLSLSPGE RATLSCRASQSVRSSH LAWYQQKPGQAPRLL IYGASSRATGIPDRFS GSGSGTDFTLTISRLEP EDFAVYYCQQYGSSPI TFGQGTRLEIK
20	19C4_f3_K	49	GACATCCAGTTGACCCAGTCTCCATCCTTCCTGTCTGCATCTGTAGG AGACAGAGTCACCATCACTTGCCGGGCCAGTCAGGGCATTAGCAGT TATTTAGCCTGGTATCAGCAAAAACCAGGGAAAGCCCCTAAGGTCC TGATCTATGCTGCATCCACTTTGCAAAGTGGGGTCCCATCAAGGTTC AGCGGCAGTGGATCTGGGACAAAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTTGCAACTTATTACTGTCAACAGCTTAATAGT TTCCCTCCGTCCACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA	107	DIQLTQSPSFLSASVG DRVTITCRASQGISSY LAWYQQKPGKAPKV LIYAASTLQSGVPSRF SGSGSGTKFTLTISSLQ PEDFATYYCQQLNSFP PSTFGQGTKLEIK
21	2C1_f4_K	50	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCATC AACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCC TCATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTC AGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCGTCAGCAGCC TGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTATAATAAC TGGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA	108	EIVMTQSPATLSVSPG ERATLSCRASQSVSIN LAWYQQKPGQAPRLL IYGASTRATGIPARFS GSGSGTEFTLTVSSLQ SEDFAVYYCQQYNN WWTFGQGTKVEIK
22	4E3_f4_K	51	GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGG AGACAGAGTCACCATCACTTGCCGGGCAAGTCAGAGCATTCACAGC TTTTTAAATTGGTATCAGCAGAAACCAGGGAAACCCCCTAAGCTCCT	109	DIQMTQSPSSLSASVG DRVTITCRASQSIHSFL NWYQQKPGKPPKLLI

TABLE 2-continued

Variable Light Chain Sequences.

		VariABLE Light Chain Nucleotide Sequence		Variable Light Chain Amino Acid Sequence	
Ab #	Name	SEQ ID NO	Sequence	SEQ ID NO	Sequence
			GATCTATGCTGCATCCAGTTTGCCAAGTGGGCTCCCATCAAGGTTCA		YAASSLPSGLPSRFSG
			GTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTG		SGSGTDFTLTISSLQPE
			CAACCTGAAGATTTTGCAACTTACTACTGTCAACAGAGTTACATTAC		DFATYYCQQSYITPPT
			CCCTCCGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA		FGQGTKVEIK
23	7D2_f4_K	52	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGG	110	EIVMTQSPATLSVSPG
			GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGC		ERATLSCRASQSVSSN
			AACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCC		LAWYQQKPGQAPRLL
			TCATCTATGGTGCATCCACCAGGGCCACTGGTGTCCCAGCCAGGTTC		IYGASTRATGVPARFS
			AGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCC		GSGSGTEFTLTISSLQS
			TGCAGTCTGAAGATTTTGCAGTTTATTTCTGTCAGCAGTATAATAAC		EDFAVYFCQQYNNW
			TGGCCCCCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA		PPFGGGTKVEIK
24	9C5_f4_K	53	GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGG	111	DIQMTQSPSSLSASVG
			AGACAGAGTCACCATCACTTGCCGGGCAAGTCAGAGCATTCACAGC		DRVTITCRASQSIHSFL
			TTTTTAAATTGGTATCAGCAGAAACCAGGGAAACCCCCTAAGCTCCT		NWYQQKPGKPPKLLI
			GATCTATACTACATCCAGTTTGCAAAGTGGGCTCCCATCAAGGTTCA		YTTSSLQSGLPSRFSG
			GTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTG		SGSGTDFTLTISSLQPE
			CAACCTGAAGATTTTGCAACTTACTACTGTCAACAGAGTTACATTAC		DFATYYCQQSYITPPT
			CCCTCCGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA		FGQGTKVEIK
25	10A3_f4_K	54	GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGG	112	DIQMTQSPSSLSASVG
			AGACAGAGTCACCATCACTTGCCGGGCAAGTCAGAGCATTCACAGC		DRVTITCRASQSIHSFL
			TTTTTAAATTGGTATCAGCAGAAACCAGGGAAACCCCCTAACCTCCT		NWYQQKPGKPPNLLI
			GATCTATGCTGCATCCAGTTTGCAAAGTGGGCTCCCATCAAGGTTCA		YAASSLQSGLPSRFSG
			GTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTG		SGSGTDFTLTISSLQPE
			CAACCTGAAGATTTTGCAACTTACTACTGTCAACAGAGTTACATTAC		DFATYYCQQSYITPPT
			CCCTCCGACGTTCGGCCATGGGACCAAGGTGGAAATCAAA		FGHGTKVEIK
26	14G5_f4_K	55	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGG	113	EIVMTQSPATLSVSPG
			GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGC		ERATLSCRASQSVSSN
			AACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCC		LAWYQQKPGQAPRLL
			TCATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTC		IYGASTRATGIPARFS
			AGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCC		GSGSGTEFTLTISSLQS
			TGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTATAATAAC		EDFAVYYCQQYNNW
			TGGCCTCCGACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA		PPTFGQGTKLEIK
27	13A12_f3_K	56	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGG	114	EIVMTQSPATLSVSPG
			GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGC		ERATLSCRASQSVSSN
			AACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCC		LAWYQQKPGQAPRLL
			TCATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTC		IYGASTRATGIPARFS
			AGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCC		GSGSGTEFTLTISSLQS
			TGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTATGATAAC		EDFAVYYCQQYDNW
			TGGCCTCTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA		PLTFGGGTKVEIK
28	5B6_f3_K	57	GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGG	115	DIQMTQSPSSLSASVG
			AGACAGAGTCACCATCACTTGCCGGGCGAGTCAGGGCATTAGCAAT		DRVTITCRASQGISNY
			TATTTAGCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCT		LAWYQQKPGKVPKL
			GATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTTCA		LIYAASTLQSGVPSRF
			GTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG		SGSGSGTDFTLTISSLQ
			CAGCCTGAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGC		PEDVATYYCQKYNSA
			CCCTCACACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA		PHTFGQGTKLEIK
29	2G6_f4_K	58	GACATCCAGTTGACCCAGTCTCCATCCTTCCTGTCTGCATCTGTAGG	116	DIQLTQSPSFLSASVG
			AGACAGAGTCACCATCACTTGCCGGGCCAGTCAGGGCATTAGCAGT		DRVTITCRASQGISSY
			TATTTAGCCTGGTATCAGCAAAAACCAGGGAAAGCCCCTAAGCTCC		LAWYQQKPGKAPKL
			TGATCTATGCTGCATCCACTTTGCAAAGTGGGGTCCCATCAAGGTTC		LIYAASTLQSGVPSRF
			AGCGGCAGTGGATCTGGGACAGAATTCACTCTCACAATCAGCAGCC		SGSGSGTEFTLTISSLQ
			TGCAGTCTGAAGATTTTGCAATTTATTACTGTCAACAGCTTAATAGT		SEDFAIYYCQQLNSYP
			TACCCGCTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA		LTFGGGTKVEIK

TABLE 3

Summary of anti-SARS-CoV-2 Monoclonal Antibody Function.

Antibody #	Clone	EC50 (pM)	ACE2 Inhibition (%)
	1B1	90	07
	1B9	240	95
1	1C12	75	88
3	1D10	47	95
2	1D5	49	94
4	1E2	218	86
5	1G9	145	96
	2E10	573	98
	3E1	362	99
	3E6	195	95
	3E7	8175	91
	4B12	139	99
	4D3	6800	91
	4H11	6800	91
	5B11	6800	95
6	5D7	284	97
7	5H12	377	100
	5H3	127	99
	5H5	94	83
	6D12	6800	93
8	7C10	152	85
	7F3	5075	99
	8A1	96	95
	8E11	65	91
9	8H4	100	93
10	9C6	105	85
	9D10	262	93
	9C6	105	85
	9D10	262	93
	10A8	68	88
11	10D6	1016	81
	11B5	2240	89
12	11D5	440	66
13	11G2	74	90
	12A12	6800	98
	13B4	1199	87
	15C2	6800	56
16	16C12	59	87
15	16C5	107	94
	16G5	5139	77

TABLE 3-continued

Summary of anti-SARS-CoV-2 Monoclonal Antibody Function.

Antibody #	Clone	EC50 (pM)	ACE2 Inhibition (%)
	16H4	239	70
17	17A8	59	98
	17E4	256	72
18	17F2	151	65
	18B6	968	59
19	18E7	62	82
	19B3	128	91
20	19C4	492	89

TABLE 4

Summary of anti-SARS-CoV-2 Monoclonal Antibody Function.

Antibody #	Clone name	ACE2 binding [% inhibition]	Inhibition: EC50 [pM]
1	1C12	88	75
2	1D5	94	94
3	1D10	95	47
4	1E2	86	218
5	1G9	96	145
6	5D7	97	284
7	5H12	100	377
8	7C10	85	152
9	8H4	93	100
10	9C6	85	105
11	10D6	81	1016
12	11D5	66	440
13	11G2	90	109
15	16C5	94	107
16	16C12	87	59
17	17A8	98	59
18	17F2	65	151
19	18E7	82	62
20	19C4	89	492
	19B3	91	123

TABLE 5

Heavy Chain CDR Sequences (Nucleic Acid Sequences).

		Variable Heavy Chain Nucleotide Sequence					
		CDR1-IMGT		CDR2-IMGT		CDR3-IMGT	
Ab #	Name	SEQ ID NO	Sequence	SEQ ID NO	Sequence	SEQ ID NO	Sequence
1	1C12_f3_H	117	GGATACACCTTCAC CAGTTATGAT	146	ATGAGCCCTAAC AGTGGTAACACA	175	GCGAGATTCGGCTATGGTTCGGG GGCCCTCGACTACTACTACTACG GTTTGGACGTC
2	1D5_f3_H	118	GGATACACCTTCAC CAGTTATGAT	147	ATGAGCCCTAAC AGTGGTAACACA	176	GCGAGATTCGGCTATGGTTCGGG GGCCCTCGACTACTACTACTACG GTTTGGACGTC
3	1D10_f3_H	119	GGATACACCTTCAC CAGTTATGAT	148	ATGAGCCCTAAC AGCGGTAACACA	177	GCGAGATTCGGCTATGGTTCGGG GGCCCTCGACTACTACTATTACG GTTTGGACGTC
4	1E2_f3_H	120	GGATACACCTTCAC CAGTTATGAT	149	ATGAGCCCTAAC AGTGGTAACACA	178	GCGAGATTCGGCTATGGTTCGGG GGCCCTCGACTACTACTACTACG GTTTGGACGTC

TABLE 5-continued

Heavy Chain CDR Sequences (Nucleic Acid Sequences).

		Variable Heavy Chain Nucleotide Sequence					
		CDR1-IMGT		CDR2-IMGT		CDR3-IMGT	
Ab #	Name	SEQ ID NO	Sequence	SEQ ID NO	Sequence	SEQ ID NO	Sequence
5	1G9_f3_H	121	GGATACACCTTCAC CAGTTATGAT	150	ATGAGCCCTAAC AGTGGTAACACA	179	GCGAGATTCGGCTATGGTTCGGG GGCCCTCGACTACTACTACTACG GTTTGGACGTC
6	5D7_f3_H	122	GGATACACCTTCAC CAGTTATGAT	151	ATGAGCCCTAAA AATGGTAACACA	180	GCGAGATTCGGCTATGGTTCGGG GGCCCTCGACTACTACTACTACG GTTTGGACGTC
7	5H12_f3_H	123	GGATACACCTTCCC CAGTTATGAT	152	ATGAGCCCTAAA AATGGTAACACA	181	GCGAGATTCGGCTATGGGTCGGG GGCCCTCGGATATTACTACTACG GTTTGGACGTC
8	7C10_f3_H	124	GGATACACCTTCAC CAGTTATGAT	153	ATGAGCCCTAAC AGTGGTAACACA	182	GCGAGATTCGGCTATGGTTCGGG GGCCCTCGACTACTACTACTACG GTTTGGACGTC
9	8H4_f3_H	125	GGATACACCTTCAC CAGTTATGAT	154	ATGAGCCCTAAC AGTGGTAACACA	183	GCGAGATTCGGCTATGGTTCGGG GGCCCTCGACTACTACTACTACG GTTTGGACGTC
10	9C6_f3_H	126	GGATACACCTTCAC CAGTTATGAT	155	ATGAGCCCTAAA AGTGGTAACACA	184	GCGAGATTCGGCTATGGTTCGGG GGCCCTCGACTACTACTACTACG GTTTGGACGTC
11	10D6_f3_H	127	GGGATCACCGTCAG TAGTAACTAC	156	ATTTATAGCGGT GGTAGCACA	185	GCGAGAGATTTAGAACTGGCTGG AGCTTTTGATATC
12	11D5_f3_H	128	GGGATCACCGTCAG TAGTAACTAC	157	ATTTATAGCGGT GGTAGCACA	186	GCGAGAGATTTAGCAGTGGCTGG AGCTTTTGATATC
13	11G2_f3_H	129	GGATACACCTTCAC CAGTTATGAT	158	ATGAGCCCTAAC AGTGGTAACACA	187	GCGAGATTCGGCTATGGTTCGGG GGCCCTCGACTACTACTACTACG GTTTGGACGTC
14	11G7_f2_H	130	GGTGGCTCCATCAG CAGTAGTAACTGG	159	ATCTTTCATAGT GGGAGCACC	188	GCGAGATTCAGAAGGATAGTGGC TACGAGCTACTATTTTGACTAC
15	16C5_f3_H	131	GGATACACCTTCAC CAGTTATGAT	160	ATGAGCCCTAAT AGTGGTAACACA	189	GCGAGATTCGGCTATGGTTCGGG GGCCCTCGACTACTACTACTACG GTTTGGACGTC
16	16C12_f3_H	132	GGATACACCTTCAC CAGTTATGAT	161	ATGAGCCCTAAC AGTGGTAACACA	190	GCGAGATTCGGCTATGGTTCGGG GGCCCTCGACTACTACTACTACG GTTTGGACGTC
17	17A8_f3_H	133	GGATACACCTTCAC CAGTTATGAT	162	ATGAGCCCTAAC AGTGGTAACACA	191	GCGAGATTCGGCTATGGTTCGGG GGCCCTCGACTACTACTACTACG GTTTGGACGTC
18	17F2_f3_H	134	GGATACACCTTCAC CAGTTATGAT	163	ATGAGCCCTGAC AGTGGTAACACA	192	GCGAGATTCGGCTATGGTTCGGG GGCCCTCGACTACTACTACTACG GTTTGGACGTC
19	18E7_f3_H	135	GGATACACCTTTAC CAGTTATGAT	164	ATGAGCCCTAAC AGTGGTAACACA	193	GCGAGATTCGGCTATGGTTCGGG GGCCCTCGACTACTACTACTACG GTTTGGACGTC
20	19C4_f3_H	136	GGGATCACCGTCAG TAGTAATTAC	165	ATTTATAGCGGT GGTAGCACA	194	GCGAGAGATTTAGAAGTGGCTGG AGGTTTTGATATC
21	2C1_f4_H	137	GGATTCACCTTTGG TGATTATACT	166	ATTAGAAGCAAA CCTTTTGGTGGG ACAACA	195	ACTAGAGTGTCCGGGTATAGCAA CATCTGGTTCTTTGCCTAC
22	4E3_f4_H	138	GGATTCACCTTCAG TAGCTATGGC	167	ATTTGGTATGAT GGAAATAATAAA	196	GCGAGAAAAGATTATTCGAAGAC ATTTTATGGATACTACTTTGACTA T

TABLE 5-continued

Heavy Chain CDR Sequences (Nucleic Acid Sequences).

		Variable Heavy Chain Nucleotide Sequence					
		CDR1-IMGT		CDR2-IMGT		CDR3-IMGT	
Ab #	Name	SEQ ID NO	Sequence	SEQ ID NO	Sequence	SEQ ID NO	Sequence
23	7D2_f4_H	139	GGGTTCACCGTCAGTAGCAACTAC	168	ATTTATAGCGGTGGTAGCACA	197	GCGAGAGATCTAGTCATCTACGGTATGGACGTC
24	9C5_f4_H	140	GGATTCACCTTCAGTAGCTATGGC	169	ATTTGGTATGATGGAAATAATAAA	198	GCGAGAAAAGATGGTTCGAAGACATATTATGGATACTACTTTGACTAT
25	10A3_f4_H	141	GGATTCACCTTCAGTAGTTATGGC	170	ATTTGGTATGATGGAAATAATACA	199	GCGAGAAAAGATGGTTCGAAGACATATTATGGATACTACTTTGACTAT
26	14G5_f4_H	142	GGTGGCTCCATCAGCAGTAATAACTGG	171	ATCTTGCATGGTGAGATCACC	200	GCGAGAGATGCGAATTTCTATGGTTCGGGGAGTTCTTACTTTGACTAC
27	13A12_f3_H	143	GGTGGCTCCATCTACAGTAGTAACTGC	172	ATCTATCATAGTGGGGGCACC	201	GCGAGAGATCAAGATTACTATGGTTCGGGGAGTTCCCTCTTTGACTAC
28	5B6_f3_H	144	GGATTCACTTTCAGTAACGCCTGG	173	TTTAAAAGCAAAACTGATGGTGGGACAACA	202	ACCACCAGCAGTGGCTAC
29	2G6_f4_H	145	GGTGGGTCCTTCAGTGTTTACTAC	174	ATCAATCATAGTGGAAACACC	203	GCGAGGTATTACTATGATGGTAATGGTTATTACCCC

TABLE 6

Heavy Chain CDR Sequences (Amino Acid Sequences).

		Variable Heavy Chain Amino Acid Sequence					
		CDR1-IMGT		CDR2-IMGT		CDR3-IMGT	
Ab #	Name	SEQ ID NO	Sequence	SEQ ID NO	Sequence	SEQ ID NO	Sequence
1	1C12_f3_H	204	GYTFTSYD	233	MSPNSGNT	262	ARFGYGSGALDYYYYGLDV
2	1D5_f3_H	205	GYTFTSYD	234	MSPNSGNT	263	ARFGYGSGALDYYYYGLDV
3	1D10_f3_H	206	GYTFTSYD	235	MSPNSGNT	264	ARFGYGSGALDYYYYGLDV
4	1E2_f3_H	207	GYTFTSYD	236	MSPNSGNT	265	ARFGYGSGALDYYYYGLDV
5	1G9_f3_H	208	GYTFTSYD	237	MSPNSGNT	266	ARFGYGSGALDYYYYGLDV
6	5D7_f3_H	209	GYTFTSYD	238	MSPKNGNT	267	ARFGYGSGALDYYYYGLDV
7	5H12_f3_H	210	GYTFPSYD	239	MSPKNGNT	268	ARFGYGSGALGYYYYGLDV
8	7C10_f3_H	211	GYTFTSYD	240	MSPNSGNT	269	ARFGYGSGALDYYYYGLDV
9	8H4_f3_H	212	GYTFTSYD	241	MSPNSGNT	270	ARFGYGSGALDYYYYGLDV
10	9C6_f3_H	213	GYTFTSYD	242	MSPKSGNT	271	ARFGYGSGALDYYYYGLDV
11	10D6_f3_H	214	GITVSSNY	243	IYSGGST	272	ARDLELAGAFDI
12	11D5_f3_H	215	GITVSSNY	244	IYSGGST	273	ARDLAVAGAFDI
13	11G2_f3_H	216	GYTFTSYD	245	MSPNSGNT	274	ARFGYGSGALDYYYYGLDV
14	11G7_f2_H	217	GGSISSSNW	246	IFHSGST	275	ARFRRIVATSYYFDY

TABLE 6-continued

Heavy Chain CDR Sequences (Amino Acid Sequences).

		Variable Heavy Chain Amino Acid Sequence					
		CDR1-IMGT		CDR2-IMGT		CDR3-IMGT	
Ab #	Name	SEQ ID NO	Sequence	SEQ ID NO	Sequence	SEQ ID NO	Sequence
15	16C5_f3_H	218	GYTFTSYD	247	MSPNSGNT	276	ARFGYGSGALDYYYYGLDV
16	16C12_f3_H	219	GYTFTSYD	248	MSPNSGNT	277	ARFGYGSGALDYYYYGLDV
17	17A8_f3_H	220	GYTFTSYD	249	MSPNSGNT	278	ARFGYGSGALDYYYYGLDV
18	17F2_f3_H	221	GYTFTSYD	250	MSPDSGNT	279	ARFGYGSGALDYYYYGLDV
19	18E7_f3_H	222	GYTFTSYD	251	MSPNSGNT	280	ARFGYGSGALDYYYYGLDV
20	19C4_f3_H	223	GITVSSNY	252	IYSGGST	281	ARDLEVAGGFDI
21	2C1_f4_H	224	GFTFGDYT	253	IRSKPFGGTT	282	TRVSGYSNIWFFAY
22	4E3_f4_H	225	GFTFSSYG	254	IWYDGNNK	283	ARKDYSKTFYGYYFDY
23	7D2_f4_H	226	GFTVSSNY	255	IYSGGST	284	ARDLVIYGMDV
24	9C5_f4_H	227	GFTFSSYG	256	IWYDGNNK	285	ARKDGSKTYYGYYFDY
25	10A3_f4_H	228	GFTFSSYG	257	IWYDGNNT	286	ARKDGSKTYYGYYFDY
26	14G5_f4_H	229	GGSISSNNW	258	ILHGEIT	287	ARDANFYGSGSSYFDY
27	13A12_f3_H	230	GGSIYSSNC	259	IYHSGGT	288	ARDQDYYGSGSSLFDY
28	5B6_f3_H	231	GFTFSNAW	260	FKSKTDGGTT	289	TTSSGY
29	2G6_f4_H	232	GGSFSVYY	261	INHSGNT	290	ARYYYDGNGYYP

TABLE 7

Light Chain CDR Sequences (Nucleic Acid Sequences)

		Variable Light Chain Nucleotide Sequence					
		CDR1-IMGT		CDR2-IMGT		CDR3-IMGT	
Ab #	Name	SEQ ID NO	Sequence	SEQ ID NO	Sequence	SEQ ID NO	Sequence
1	1C12_f3_K	291	CAGAGTGTTAGGAG CAGTCAC	320	GGTGCATCC	349	CAGCAGTATAATAACTCACCGAT CACC
2	1D5_f3_K	292	CAGAGTGTTAGGAG CAGTCAC	321	GGTGCATCC	350	CAGCAGTTTGGTAGCTCACCGAT CACC
3	1D10_f3_K	293	CAGAGTGTTAGCAG CAGCCAC	322	GGTGCATCC	35	CAGCAGTATAATAGCTCACCGAT CACC
4	1E2_f3_K	294	CAGAGTGTTAGGAG CAGTCAC	323	GGTGCATCC	352	CAGCAGTATGGTAGCTCACCGAT CACC
5	1G9_f3_K	295	CAGAGTGTTAGGAG CAGTCAC	324	GGTGCATCC	353	CAGCAGTATGGTAGCTCACCGAT CACC
6	5D7_f3_K	296	CAGAGTGTTAGGAG CAGTCAC	325	GGTGCCTCC	354	CAGCAGTATAATATCTCACCGAT CACC
7	5H12_f3_K	297	CAGAGTGTTAGGAG CAGTCAC	326	GGTGCCTCC	355	CAGCAGTATAATTTCTCACCGAT CACC
8	7C10_f3_K	298	CAGAGTGTTAGGAG CAGTCAC	327	GGTGCATCC	356	CAGCAGTTTGGTAGCTCACCGAT CACC

TABLE 7-continued

Light Chain CDR Sequences (Nucleic Acid Sequences)

		Variable Light Chain Nucleotide Sequence					
		CDR1-IMGT		CDR2-IMGT		CDR3-IMGT	
Ab #	Name	SEQ ID NO	Sequence	SEQ ID NO	Sequence	SEQ ID NO	Sequence
9	8H4_f3_K	299	CAGAGTGTTAGGAG CAGTCAC	328	GGTGCATCC	357	CAGCAGTTTGGTAGCTCACCGAT CACC
10	9C6_f3_K	300	CAGAGTGTTAGGAG CAGTCAC	329	GGTGCCTCC	358	CAGCAGTATAATAGCTCACCGAT CACC
11	10D6_f3_K	301	CAGGGCATTAGCAG TTAT	330	GCTGCATCC	359	CAACAGCTTAATAGTTACCCTCC GTCCACT
12	11D5_f3_K	302	CAGGGCATTAGCAG TTAT	331	GCTGCATCC	360	CAACAGCTTAATAGTTACCCTCC GTCCACT
13	11G2_f3_K	303	CAGAGTGTTAGGAA CAGTCAC	332	GGTGCATCC	36	CAGCAGTTTGGTAGCTCACCGAT CACC
14	11G7_f2_K	304	CAGAGCCTCCTGCA TAGTAATGGATACA ACTAT	333	TTGGGTTCT	362	ATGCAAGCTCTACAAACTCCTCT CACT
15	16C5_f3_K	305	CAGAGTGTTAGGAG CAGTCAC	334	GGTGCATCC	363	CAGCAGTATAATAACTCACCGAT CACC
16	16C12_f3_K	306	CAGAGTGTTAGGAG CAGTCAC	335	GGTGCATCC	364	CAGCAGTATGGTAGCTCACCGAT CACC
17	17A8_f3_K	307	CAGAGTGTTAGGAG CAGTCAC	336	GGTGCATCC	365	CAGCAGTATGGTAGCTCACCGAT CACC
18	17F2_f3_K	308	CAGAGTGTTAGGAG CAGTCAC	337	GGTGCATCC	366	CAGCAGTATAATAGCTCACCGAT CACC
19	18E7_f3_K	309	CAGAGTGTTAGGAG CAGTCAC	338	GGTGCATCC	367	CAGCAGTATGGTAGCTCACCGAT CACC
20	19C4_f3_K	310	CAGGGCATTAGCAG TTAT	339	GCTGCATCC	368	CAACAGCTTAATAGTTTCCCTCC GTCCACT
21	2C1_f4_K	311	CAGAGTGTTAGCAT CAAC	340	GGTGCATCC	369	CAGCAGTATAATAACTGGTGGAC G
22	4E3_f4_K	312	CAGAGCATTCACAG CTTT	341	GCTGCATCC	370	CAACAGAGTTACATTACCCCTCC GACG
23	7D2_f4_K	313	CAGAGTGTTAGCAG CAAC	342	GGTGCATCC	371	CAGCAGTATAATAACTGGCCCCC T
24	9C5_f4_K	314	CAGAGCATTCACAG CTTT	343	ACTACATCC	372	CAACAGAGTTACATTACCCCTCC GACG
25	10A3_f4_K	315	CAGAGCATTCACAG CTTT	344	GCTGCATCC	373	CAACAGAGTTACATTACCCCTCC GACG
26	14G5_f4_K	316	CAGAGTGTTAGCAG CAAC	345	GGTGCATCC	374	CAGCAGTATAATAACTGGCCTCC GACT
27	13A12_f3_K	317	CAGAGTGTTAGCAG CAAC	346	GGTGCATCC	375	CAGCAGTATGATAACTGGCCTCT CACT
28	5B6_f3_K	318	CAGGGCATTAGCAA TTAT	347	GCTGCATCC	376	CAAAAGTATAACAGTGCCCCTCA CACT
29	2G6_f4_K	319	CAGGGCATTAGCAG TTAT	348	GCTGCATCC	377	CAACAGCTTAATAGTTACCCGCT CACT

TABLE 8

Light Chain CDR Sequences (Amino Acid Sequences)

		Variable Light Chain Amino Acid Sequence					
		CDR1-IMGT		CDR2-IMGT		CDR3-IMGT	
Ab #	Name	SEQ ID NO	Sequence	SEQ ID NO	Sequence	SEQ ID NO	Sequence
1	1C12_f3_K	378	QSVRSSH	n/a	GAS	407	QQYNNSPIT
2	1D5_f3_K	379	QSVRSSH	n/a	GAS	408	QQFGSSPIT
3	1D10_f3_K	380	QSVSSSH	n/a	GAS	409	QQYNSSPIT
4	1E2_f3_K	381	QSVRSSH	n/a	GAS	410	QQYGSSPIT
5	1G9_f3_K	382	QSVRSSH	n/a	GAS	411	QQYGSSPIT
6	5D7_f3_K	383	QSVRSSH	n/a	GAS	412	QQYNISPIT
7	5H12_f3_K	384	QSVRSSH	n/a	GAS	413	QQYNFSPIT
8	7C10_f3_K	385	QSVRSSH	n/a	GAS	414	QQFGSSPIT
9	8H4_f3_K	386	QSVRSSH	n/a	GAS	415	QQFGSSPIT
10	9C6_f3_K	387	QSVRSSH	n/a	GAS	416	QQYNSSPIT
11	10D6_f3_K	388	QGISSY	n/a	AAS	417	QQLNSYPPST
12	11D5_f3_K	389	QGISSY	n/a	AAS	418	QQLNSYPPST
13	11G2_f3_K	390	QSVRNSH	n/a	GAS	419	QQFGSSPIT
14	11G7_f2_K	391	QSLLHSNGYNY	n/a	LGS	420	MQALQTPLT
15	16C5_f3_K	392	QSVRSSH	n/a	GAS	421	QQYNNSPIT
16	16C12_f3_K	393	QSVRSSH	n/a	GAS	422	QQYGSSPIT
17	17A8_f3_K	394	QSVRSSH	n/a	GAS	423	QQYGSSPIT
18	17F2_f3_K	395	QSVRSSH	n/a	GAS	424	QQYNSSPIT
19	18E7_f3_K	396	QSVRSSH	n/a	GAS	425	QQYGSSPIT
20	19C4_f3_K	397	QGISSY	n/a	AAS	426	QQLNSFPPST
21	2C1_f4_K	398	QSVSIN	n/a	GAS	427	QQYNNWWT
22	4E3_f4_K	399	QSIHSF	n/a	AAS	428	QQSYITPPT
23	7D2_f4_K	400	QSVSSN	n/a	GAS	429	QQYNNWPP
24	9C5_f4_K	401	QSIHSF	n/a	TTS	430	QQSYITPPT
25	10A3_f4_K	402	QSIHSF	n/a	AAS	431	QQSYITPPT
26	14G5_f4_K	403	QSVSSN	n/a	GAS	432	QQYNNWPPT
27	13A12_f3_K	404	QSVSSN	n/a	GAS	433	QQYDNWPLT
28	5B6_f3_K	405	QGISNY	n/a	AAS	434	QKYNSAPHT
29	2G6_f4_K	406	QGISSY	n/a	AAS	435	QQLNSYPLT

TABLE 9

Summary of Antibody Sequences (Nucleic Acid Sequences)

Antibody #	Antibody name	VH SEQ ID NO	CDR1H-IMGT SEQ ID NO	CDR2H-IMGT SEQ ID NO	CDR3H-IMGT SEQ ID NO	VL SEQ ID NO	CDR1L-IMGT SEQ ID NO	CDR2L-IMGT SEQ ID NO	CDR3L-IMGT SEQ ID NO
1	1C12_f3	1	117	146	175	30	291	320	349
2	1D5_f3	2	118	147	176	31	292	321	350
3	1D10_f3	3	119	148	177	32	293	322	351
4	1E2_f3	4	120	149	178	33	294	323	352
5	1G9_f3	5	121	150	179	34	295	324	353
6	5D7_f3	6	122	151	180	35	296	325	354
7	5H12_f3	7	123	152	181	36	297	326	355
8	7C10_f3	8	124	153	182	37	298	327	356
9	8H4_f3	9	125	154	183	38	299	328	357
10	9C6_f3	10	126	155	184	39	300	329	358
11	10D6_f3	11	127	156	185	40	301	330	359
12	11D5_f3	12	128	157	186	41	302	331	360
13	11G2_f3	13	129	158	187	42	303	332	361
14	11G7_f2	14	130	159	188	43	304	333	362
15	16C5_f3	15	131	160	189	44	305	334	363
16	16C12_f3	16	132	161	190	45	306	335	364
17	17A8_f3	17	133	162	191	46	307	336	365
18	17F2_f3	18	134	163	192	47	308	337	366
19	18E7_f3	19	135	164	193	48	309	338	367
20	19C4_f3	20	136	165	194	49	310	339	368
21	2C1_f4	21	137	166	195	50	311	340	369
22	4E3_f4	22	138	167	196	51	312	341	370
23	7D2_f4	23	139	168	197	52	313	342	371
24	9C5_f4	24	140	169	198	53	314	343	372
25	10A3_f4	25	141	170	199	54	315	344	373
26	14G5_f4	26	142	171	200	55	316	345	374
27	13A12_f3	27	143	172	201	56	317	346	375
28	5B6_f3	28	144	173	202	57	318	347	376
29	2G6_f4	29	145	174	203	58	319	348	377

TABLE 10

Summary of Antibody Sequences (Amino Acid Sequences)

Antibody #	Antibody name	VH SEQ ID NO	CDR1H-IMGT SEQ ID NO	CDR2H-IMGT SEQ ID NO	CDR3H-IMGT SEQ ID NO	VL SEQ ID NO	CDR1L-IMGT SEQ ID NO	CDR2L-IMGT Sequence	CDR3L-IMGT SEQ ID NO
1	1C12_f3	59	204	233	262	88	378	GAS	407
2	1D5_f3	60	205	234	263	89	379	GAS	408
3	1D10_f3	61	206	235	264	90	380	GAS	409
4	1E2_f3	62	207	236	265	91	381	GAS	410
5	1G9_f3	63	208	237	266	92	382	GAS	411
6	5D7_f3	64	209	238	267	93	383	GAS	412
7	5H12_f3	65	210	239	268	94	384	GAS	413
8	7C10_f3	66	211	240	269	95	385	GAS	414
9	8H4_f3	67	212	241	270	96	386	GAS	415
10	9C6_f3	68	213	242	271	97	387	GAS	416
11	10D6_f3	69	214	243	272	98	388	AAS	417
12	11D5_f3	70	215	244	273	99	389	AAS	418
13	11G2_f3	71	216	245	274	100	390	GAS	419
14	11G7_f2	72	217	246	275	101	391	LGS	420
15	16C5_f3	73	218	247	276	102	392	GAS	421
16	16C12_f3	74	219	248	277	103	393	GAS	422
17	17A8_f3	75	220	249	278	104	394	GAS	423
18	17F2_f3	76	221	250	279	105	395	GAS	424
19	18E7_f3	77	222	251	280	106	396	GAS	425
20	19C4_f3	78	223	252	28	107	397	AAS	426
21	2C1_f4	79	224	253	282	108	398	GAS	427
22	4E3_f4	80	225	254	283	109	399	AAS	428
23	7D2_f4	81	226	255	284	110	400	GAS	429
24	9C5_f4	82	227	256	285	111	401	TTS	430
25	10A3_f4	83	228	257	286	112	402	AAS	431

TABLE 10-continued

Summary of Antibody Sequences (Amino Acid Sequences)

Antibody #	Antibody name	VH SEQ ID NO	CDR1H-IMGT SEQ ID NO	CDR2H-IMGT SEQ ID NO	CDR3H-IMGT SEQ ID NO	VL SEQ ID NO	CDR1L-IMGT SEQ ID NO	CDR2L-IMGT Sequence	CDR3L-IMGT SEQ ID NO
26	14G5_f4	84	229	258	287	113	403	GAS	432
27	13A12_f3	85	230	259	288	114	404	GAS	433
28	5B6_f3	86	231	260	289	115	405	AAS	434
29	2G6_f4	87	232	261	290	116	406	AAS	435

[0481] The foregoing is not to be limited in scope by the specific embodiments described herein. Indeed, various modifications of the antibodies and methods provided herein and their equivalents, in addition to those described herein will become apparent to those skilled in the art from the foregoing description and accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

[0482] All references cited herein are incorporated herein by reference in their entireties and for all purposes to the same extent as if each individual publication or patent or patent application was specifically and individually indicated to be incorporated by reference in its entirety for all purposes.

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acacagaagt tccagggcag agtcaccatg accaggaaca cctccataag cacagcctac 240

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tctggacaag ggcttgagtg gatgggatgg atgagcccta acagcggtaa cacaggctat 180

gcacagaagt tccagggcag agtcaccatg accaggaaca cctccataaa cacagcctac 240

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actggacaag ggcttgagtg gatgggatgg atgagcccta acagtggtaa cacaggctat 180

gcacagaagt tccagggcag agtcaccatg accaggaaca cctccataag cacagcctac 240

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<223> OTHER INFORMATION: 1G9_f3 variable heavy chain

<400> SEQUENCE: 5

caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

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tcctgcaagg cttctggata caccttcacc agttatgata tcatttgggt gcgacaggcc 120

actggacaag ggcttgagtg gatgggatgg atgagcccta acagtggtaa cacaggctat 180

gcacagaagt tccagggcag agtcaccatg accaggaaca cctccataag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagattcggc 300

tatggttcgg gggccctcga ctactactac tacggtttgg acgtctgggg ccaagggacc 360

acggtcaccg tctcctca 378

<210> SEQ ID NO 6
<211> LENGTH: 378
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 5D7_f3 variable heavy chain

<400> SEQUENCE: 6

caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggacctc agtgaaagtc 60

tcctgcaaga cttctggata caccttcacc agttatgata tcatctgggt gcgacaggcc 120

actggacaag ggcttgagtg gatgggatgg atgagcccta aaaatggtaa cacaggctat 180

gcacagaggt tccagggcag agtcaccatg accaggaaca cctccataag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagattcggc 300

tatggttcgg gggccctcga ctactactac tacggtttgg acgtctgggg ccaagggacc 360

acggtcaccg tctcctca 378

<210> SEQ ID NO 7
<211> LENGTH: 378
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 5H12_f3 variable heavy chain

<400> SEQUENCE: 7

caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggacctc agtgaaagtc 60

tcctgcaaga cttctggata caccttcccc agttatgata tcatctgggt gcgacaggcc 120

actggacaag ggcttgagtg gatgggatgg atgagcccta aaaatggtaa cacaggcttt 180

gcacagaggt tccagggcag agtcaccatg accaggaaca cctccataag cacagcctac 240

atggaactga gcagcctgag atctgaggac acggccgtgt attactgtgc gagattcggc 300

tatgggtcgg gggccctcgg atattactac tacggtttgg acgtctgggg ccaagggacc 360

acggtcaccg tctcctca 378

<210> SEQ ID NO 8
<211> LENGTH: 378
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 7C10_f3 variable heavy chain

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<400> SEQUENCE: 8

caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata caccttcacc agttatgata tcacctgggt gcgacaggcc 120

actggacaag ggcttgagtg gatggggtgg atgagcccta acagtggtaa cacaggctat 180

gcacagaagt tccagggcag agtcaccatg accaggaaca cctccataag cacagcctac 240

atggagctgc gcagcctgag gtctgaggac acggccgtgt attactgtgc gagattcggc 300

tatggttcgg gggccctcga ctactactac tacggtttgg acgtctgggg ccaagggacc 360

acggtcaccg tctcctca 378

<210> SEQ ID NO 9
<211> LENGTH: 378
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 8H4_f3 variable heavy chain

<400> SEQUENCE: 9

caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata caccttcacc agttatgata tcacctgggt gcgacaggcc 120

actggacaag ggcttgagtg gatgggatgg atgagcccta acagtggtaa cacaggctat 180

gcacagaagt tccagggcag agtcaccatg accaggaaca cctccataag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagattcggc 300

tatggttcgg gggccctcga ctactactac tacggtttgg acgtctgggg ccaagggacc 360

acggtcaccg tctcctca 378

<210> SEQ ID NO 10
<211> LENGTH: 378
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 9C6_f3 variable heavy chain

<400> SEQUENCE: 10

caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata caccttcacc agttatgata tcacctgggt gcgacaggcc 120

actggacaag ggcttgagtg gatgggatgg atgagcccta aaagtggtaa cacaggctat 180

gcacagaagt tccagggcag agtcaccatg accaggaaca cctccataag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagattcggc 300

tatggttcgg gggccctcga ctactactac tacggtttgg acgtctgggg ccaagggacc 360

acggtcaccg tctcctca 378

<210> SEQ ID NO 11
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 10D6_f3 variable heavy chain

<400> SEQUENCE: 11

gaggtgcagt tggtggagac tggaggaggc ttgatccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggat caccgtcagt agtaactaca tgaactgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac atactacgca 180

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac actgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgcgag agatttagaa 300

ctggctggag cttttgatat ctggggccaa gggacaatgg tcaccgtctc ttta 354

<210> SEQ ID NO 12
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 11D5_f3 variable heavy chain

<400> SEQUENCE: 12

gaggtgcagt tggtggagac tggaggaggc ttgatccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggat caccgtcagt agtaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac atactacgca 180

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgcgag agatttagca 300

gtggctggag cttttgatat ctggggccaa gggacaatgg tcaccgtctc ttta 354

<210> SEQ ID NO 13
<211> LENGTH: 378
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 11G2_f3 variable heavy chain

<400> SEQUENCE: 13

caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata caccttcacc agttatgata tcacctgggt gcgacaggcc 120

actggacaag ggcttgagtg gatgggatgg atgagcccta acagtggtaa cacaggctat 180

gcacagaagt tccagggcag agtctccatg accaggaaca cctccataag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagattcggc 300

tatggttcgg gggccctcga ctactactac tacggtttgg acgtctgggg ccaagggacc 360

acggtcaccg tctcctca 378

<210> SEQ ID NO 14
<211> LENGTH: 366
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 11G7_f2 variable heavy chain

<400> SEQUENCE: 14

caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggggac cctgtccctc 60

acctgcgctg tctctggtgg ctccatcagc agtagtaact ggtggagttg ggtccgccag 120

cccccaggga aggggctgga gtggattggg gaaatctttc atagtgggag caccaactac 180

aacccgtccc tcaagagtcg agtcaccata tcagtagaca agtccaagaa ccagttctcc 240

ctgaagctga actctgtgac cgccgcggac acggccgtgt attactgtgc gagattcaga 300

aggatagtgg ctacgagcta ctattttgac tactggggcc agggaaccct ggtcaccgtc 360

tcctca 366

<210> SEQ ID NO 15
<211> LENGTH: 378
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 16C5_f3 variable heavy chain

<400> SEQUENCE: 15

caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata caccttcacc agttatgata tcatttgggt gcgacaggcc 120

actggacaag ggcttgagtg gatgggatgg atgagcccta atagtggtaa cacaggctat 180

gcacagaagt tccagggcag agtcaccatg accaggaaca cctccatagg cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt atttctgtgc gagattcggc 300

tatggttcgg gggccctcga ctactactac tacggtttgg acgtctgggg ccaagggacc 360

acggtcaccg tctcctca 378

<210> SEQ ID NO 16
<211> LENGTH: 378
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 16C12_f3 variable heavy chain

<400> SEQUENCE: 16

caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata caccttcacc agttatgata ttatctgggt gcgacaggcc 120

actggacaag ggcttgagtg gatgggatgg atgagcccta acagtggtaa cacaggctat 180

gcacagaagt tccagggcag agtcaccatg accaggaaca cctccataag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagattcggc 300

tatggttcgg gggccctcga ctactactac tacggtttgg acgtctgggg ccaagggacc 360

acggtcaccg tctcctca 378

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<210> SEQ ID NO 17
<211> LENGTH: 378
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 17A8_f3 variable heavy chain

<400> SEQUENCE: 17

caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata caccttcacc agttatgata tcatttgggt gcgacaggcc 120

actggacaag ggcttgagtg gatgggatgg atgagcccta acagtggtaa cacaggctat 180

gcacagaagt tccagggcag agtcaccatg accaagaaca cctccataag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagattcggc 300

tatggttcgg gggccctcga ctactactac tacggtttgg acgtctgggg ccaagggacc 360

acggtcaccg tctcctca 378

<210> SEQ ID NO 18
<211> LENGTH: 378
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 17F2_f3 variable heavy chain

<400> SEQUENCE: 18

caggtgcagc tggtgcagtc tggggctgag gtgaagaggc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata caccttcacc agttatgata tcacctgggt gcgacaggcc 120

actggacaag ggcttgagtg gatgggatgg atgagccctg acagtggtaa cacaggctat 180

gcacagaggt tccagggcag agtcaccatg accaggaaca cctccataag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagattcggc 300

tatggttcgg gggccctcga ctactactac tacggtttgg acgtctgggg ccaagggacc 360

acggtcaccg tctcctca 378

<210> SEQ ID NO 19
<211> LENGTH: 378
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 18E7_f3 variable heavy chain

<400> SEQUENCE: 19

caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgacggtc 60

tcctgcaagg cttctggata caccttttacc agttatgata tcatctgggt gcgacaggcc 120

actggacaag ggcttgagtg gatgggatgg atgagcccta acagtggtaa cacaggctat 180

gcacagaggt tccagggcag agtcaccatg accaggaaca cctccataag cacagcctac 240

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atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagattcggc 300

tatggttcgg gggccctcga ctactactac tacggtttgg acgtctgggg ccaagggacc 360

acggtcaccg tctcctca 378

<210> SEQ ID NO 20
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 19C4_f3 variable heavy chain

<400> SEQUENCE: 20

gaggtgcagt tggtggagac tggaggaggc ttgatccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggat caccgtcagt agtaattaca tgaactgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca 180

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gccgtatatt actgtgcgag agatttagaa 300

gtggctggag gttttgatat ctggggccaa gggacaatgg tcaccgtctc ttta 354

<210> SEQ ID NO 21
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 2C1_f4 variable heavy chain

<400> SEQUENCE: 21

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc caggacggtc cctgagactc 60

tcctgtacag cttctggatt caccttttggt gattatactt tgagctggtt ccgccaggct 120

ccagggaagg ggctggaatg ggtaggtttc attagaagca aacctttttgg tgggacaaca 180

caatacgccg cgtctgtgaa aggcagattc accatctcaa gggatgattc caaaagcatc 240

gcctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtatta ctgtactaga 300

gtgtccgggt atagcaacat ctggttcttt gcctactggg gccagggaac cctggtcacc 360

gtctcctca 369

<210> SEQ ID NO 22
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 4E3_f4 variable heavy chain

<400> SEQUENCE: 22

caggtgcaac tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctggatt caccttcagt agctatggca tgaactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atttggtatg atggaaataa taaatactat 180

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gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgttgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagaaaagat 300

tattcgaaga cattttatgg atactacttt gactattggg gccagggaac cctggtcacc 360

gtctcctca 369

<210> SEQ ID NO 23
<211> LENGTH: 351
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 7D2_f4 variable heavy chain

<400> SEQUENCE: 23

gaggtgcagc tggtggagac tggaggaggc ttgatccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggtt caccgtcagt agcaactaca tgaactgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca 180

gactccgtga agggccgatt caccatctcc agagacaatt cctacaacac gctgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgcgag agatctagtc 300

atctacggta tggacgtctg gggccaaggg accacggtca ccgtctcctc a 351

<210> SEQ ID NO 24
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 9C5_f4 variable heavy chain

<400> SEQUENCE: 24

caggtgcaac tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgtag cgtctggatt caccttcagt agctatggca tgaactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atttggtatg atggaaataa taaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagtctgag agccgaggac acggctgtgt attactgtgc gagaaaagat 300

ggttcgaaga catattatgg atactacttt gactattggg gccagggaac cctggtcacc 360

gtctcctca 369

<210> SEQ ID NO 25
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 10A3_f4 variable heavy chain

<400> SEQUENCE: 25

caggtgcaac tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

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tcctgtgcag cgtctggatt caccttcagt agttatggca tgaactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcaatt atttggtatg atggaaataa tacatactat 180

gtagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaagac acggctgtgt attactgtgc gagaaaagat 300

ggttcgaaga catattatgg atactacttt gactattggg gccagggaac cctggtcacc 360

gtctcctca 369

<210> SEQ ID NO 26
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 14G5_f4 variable heavy chain

<400> SEQUENCE: 26

caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggggac cctgtccctc 60

acctgcgctg tctctggtgg ctccatcagc agtaataact ggtggagttg ggtccgccag 120

cccccaggga aggggctggt gtggattggg gaaatcttgc atggtgagat caccaactac 180

aacccgtccc tcaagagtcg agtcaccata tcaatagaca agtccaagaa ccagttctcc 240

ctgaagctga gctctgtgac cgccgcggac acggccgtgt attactgtgc gagagatgcg 300

aatttctatg gttcggggag ttcttacttt gactactggg gccagggaac cctggtcacc 360

gtctcctca 369

<210> SEQ ID NO 27
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 13A12_f3 variable heavy chain

<400> SEQUENCE: 27

caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggggac cctgtccctc 60

acctgcgctg tctcaggtgg ctccatctac agtagtaact gctggagttg ggtccgccag 120

cccccaggga aggggctgga gtggattggg gaaatctatc atagtggggg caccaactac 180

aacccgtccc tcaagagtcg agtcaccata tcattagaca agtccaagaa caggttctcc 240

ctgaggctga gctctgtgac cgccgcggac acggccgtgt attactgtgc gagagatcaa 300

gattactatg gttcggggag ttccctcttt gactactggg gccagggaac cctggtcacc 360

gtctcctca 369

<210> SEQ ID NO 28
<211> LENGTH: 345
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 5B6_f3 variable heavy chain

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<400> SEQUENCE: 28

gaggtgcagc tggtggagtc tgggggaggc ttggtaaagc ctgggggtc ccttagactc 60

tcctgtgcag cctctggatt cactttcagt aacgcctgga tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggttggccgt tttaaaagca aaactgatgg tgggacaaca 180

gactacgctg cacccgtgaa aggcagattc accatctcaa gagatgattc aaaaaacacg 240

ctgtatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtatta ctgtaccacc 300

agcagtggct actggggcca gggaaccctg gtcaccgtct cctca 345

<210> SEQ ID NO 29
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 2G6_f4 variable heavy chain

<400> SEQUENCE: 29

caggtgcagc tacagcagtg gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60

acctgcacta tctatggtgg gtccttcagt gtttactact ggaactggat ccgccagccc 120

ccagagaagg ggctggagtg gattggggaa atcaatcata gtggaaacac caactacaac 180

ccgtccctca agagtcgagt caccatatca gtagacacgt ccaagaacca attctccctg 240

aagctgagct ctgtgaccgc cgcggacacg gctgtgtatt actgtgcgag gtattactat 300

gatggtaatg gttattaccc ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> SEQ ID NO 30
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 1C12_f3 variable light chain

<400> SEQUENCE: 30

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagg agcagtcact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtataata actcaccgat caccttcggc 300

caagggacac gactggagat taaa 324

<210> SEQ ID NO 31
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 1D5_f3 variable light chain

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<400> SEQUENCE: 31

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga cagagccacc 60

ctctcctgca gggccagtca gagtgttagg agcagtcact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttctctc tcaccatcag cagactggag 240

cctgaggatt ttgcagtgta ttactgtcag cagtttggta gctcaccgat caccttcggc 300

caagggacac ggctggagat taaa 324

<210> SEQ ID NO 32
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 1D10_f3 variable light chain

<400> SEQUENCE: 32

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagccact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctggaaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtataata gctcaccgat caccttcggc 300

caagggacac gactggagat taaa 324

<210> SEQ ID NO 33
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 1E2_f3 variable light chain

<400> SEQUENCE: 33

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagg agcagtcact ttgcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcaccgat caccttcggc 300

caagggacac gactggagat taaa 324

<210> SEQ ID NO 34
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 1G9_f3 variable light chain

<400> SEQUENCE: 34

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gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagg agcagtcact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccgat caccttcggc 300

caagggacac gactggagat taaa 324

<210> SEQ ID NO 35
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 5D7_f3 variable light chain

<400> SEQUENCE: 35

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagg agcagtcact tagcctggta ccggcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcctcca gcagggccac tggcatccca 180

gacaggttca gtggccgtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtataata tctcaccgat caccttcggc 300

caagggacac gactggagat taaa 324

<210> SEQ ID NO 36
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 5H12_f3 variable light chain

<400> SEQUENCE: 36

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagg agcagtcact tagcctggta ccggcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcctcca gcagggccac tggcatccca 180

gacaggttca gtggccgtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtataatt tctcaccgat caccttcggc 300

caagggacac gactggagat taaa 324

<210> SEQ ID NO 37
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 7C10_f3 variable light chain

<400> SEQUENCE: 37

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gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagg agcagtcact tagcctggtc ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtttggta gctcaccgat caccttcggc 300

caagggacac gactggagat taaa 324

<210> SEQ ID NO 38
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 8H4_f3 variable light chain

<400> SEQUENCE: 38

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagg agcagtcact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtttggta gctcaccgat caccttcggc 300

caagggacac gactggagat taag 324

<210> SEQ ID NO 39
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 9C6_f3 variable light chain

<400> SEQUENCE: 39

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagg agcagtcact tagcctggta ccggcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcctcca gcagggccac tggcatccca 180

gacaggttca gtggccgtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtataata gctcaccgat caccttcggc 300

caagggacac gactggagat aaaa 324

<210> SEQ ID NO 40
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 10D6_f3 variable light chain

<400> SEQUENCE: 40

gacatccagt tgacccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc 60

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atcacttgcc gggccagtca gggcattagc agttatttag cctggtatca gcaaaaacca 120

gggaaagccc ctaaggtcct gatctatgct gcatccactt tgcaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtcaacag cttaatagtt accctccgtc cacttttggc 300

caggggacca agctggagat caaa 324

<210> SEQ ID NO 41
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 11D5_f3 variable light chain

<400> SEQUENCE: 41

gacatccagt tgacccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggccagtca gggcattagc agttatttag cctggtatca gcaaaaacca 120

gggaaagccc ctaaggtcct gatctatgct gcatccactt tgcaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtcaacag cttaatagtt accctccgtc cacttttggc 300

caggggacca agctggagat caaa 324

<210> SEQ ID NO 42
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 11G2_f3 variable light chain

<400> SEQUENCE: 42

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagg aacagtcact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtttggta gctcaccgat caccttcggc 300

caagggacac gactggagat taaa 324

<210> SEQ ID NO 43
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 11G7_f2 variable light chain

<400> SEQUENCE: 43

gatattgtga tgactcagtc tccactctcc ctgcccgtca cccctggaga gccggcctcc 60

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atctcctgca ggtctagtca gagcctcctg catagtaatg gatacaacta tttggattgg 120

tacctgcaga agccagggca gtctccacag ctcctgatct atttgggttc taatcgggcc 180

tccggggtcc ctgacaggtt cagtggcagt ggatcaggca cagattttac actgaaaatc 240

agcagagtgg aggctgagga tgttggggtt tattactgca tgcaagctct acaaactcct 300

ctcactttcg gcggagggac caaggtggag atcaaa 336

<210> SEQ ID NO 44
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 16C5_f3 variable light chain

<400> SEQUENCE: 44

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagg agcagtcact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtataata actcaccgat caccttcggc 300

caagggacac gactggagat taaa 324

<210> SEQ ID NO 45
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 16C12_f3 variable light chain

<400> SEQUENCE: 45

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagg agcagtcact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccgat caccttcggc 300

caagggacac gactggagat taaa 324

<210> SEQ ID NO 46
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 17A8_f3 variable light chain

<400> SEQUENCE: 46

gaaactgtgt tgacgcagtc tccaggcact ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagg agcagtcact tagcctggta ccagcagaaa 120

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cctggccagg ctcccaggct cctcatctat ggtgcatcca gtagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccgat caccttcggc 300

caagggacac gactggagat taaa 324

<210> SEQ ID NO 47
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 17F2_f3 variable light chain

<400> SEQUENCE: 47

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagg agcagtcact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtataata gctcaccgat caccttcggc 300

caagggacac gactggagat aaaa 324

<210> SEQ ID NO 48
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 18E7_f3 variable light chain

<400> SEQUENCE: 48

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagg agcagtcact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccgat caccttcggc 300

caagggacac gactggagat taaa 324

<210> SEQ ID NO 49
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 19C4_f3 variable light chain

<400> SEQUENCE: 49

gacatccagt tgacccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggccagtca gggcattagc agttatttag cctggtatca gcaaaaacca 120

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gggaaagccc ctaaggtcct gatctatgct gcatccactt tgcaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacaaaa ttcactctca caatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtcaacag cttaatagtt tccctccgtc cacttttggc 300

caggggacca agctggagat caaa 324

<210> SEQ ID NO 50
<211> LENGTH: 318
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 2C1_f4 variable light chain

<400> SEQUENCE: 50

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc atcaacttag cctggtacca gcagaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccgtcagcag cctgcagtct 240

gaagattttg cagtttatta ctgtcagcag tataataact ggtggacgtt cggccaaggg 300

accaaggtgg aaatcaaa 318

<210> SEQ ID NO 51
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 4E3_f4 variable light chain

<400> SEQUENCE: 51

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattcac agctttttaa attggtatca gcagaaacca 120

gggaaacccc ctaagctcct gatctatgct gcatccagtt tgccaagtgg gctcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacatta cccctccgac gttcggccaa 300

gggaccaagg tggaaatcaa a 321

<210> SEQ ID NO 52
<211> LENGTH: 318
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 7D2_f4 variable light chain

<400> SEQUENCE: 52

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcaacttag cctggtacca gcagaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tgtcccagcc 180

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aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240

gaagattttg cagtttattt ctgtcagcag tataataact ggcccccttt cggcggaggg 300

accaaggtgg agatcaaa 318

<210> SEQ ID NO 53
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 9C5_f4 variable light chain

<400> SEQUENCE: 53

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattcac agctttttaa attggtatca gcagaaacca 120

gggaaacccc ctaagctcct gatctatact acatccagtt tgcaaagtgg gctcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacatta cccctccgac gttcggccaa 300

gggaccaagg tggaaatcaa a 321

<210> SEQ ID NO 54
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 10A3_f4 variable light chain

<400> SEQUENCE: 54

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattcac agctttttaa attggtatca gcagaaacca 120

gggaaacccc ctaacctcct gatctatgct gcatccagtt tgcaaagtgg gctcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacatta cccctccgac gttcggccat 300

gggaccaagg tggaaatcaa a 321

<210> SEQ ID NO 55
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 14G5_f4 variable light chain

<400> SEQUENCE: 55

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcaacttag cctggtacca gcagaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc 180

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aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240

gaagattttg cagtttatta ctgtcagcag tataataact ggcctccgac ttttggccag 300

gggaccaagc tggagatcaa a 321

<210> SEQ ID NO 56
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 13A12_f3 variable light chain

<400> SEQUENCE: 56

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcaacttag cctggtacca gcagaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240

gaagattttg cagtttatta ctgtcagcag tatgataact ggcctctcac tttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> SEQ ID NO 57
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 5B6_f3 variable light chain

<400> SEQUENCE: 57

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcgagtca gggcattagc aattatttag cctggtatca gcagaaacca 120

gggaaagttc ctaagctcct gatctatgct gcatccactt tgcaatcagg ggtcccatct 180

cggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagatgttg caacttatta ctgtcaaaag tataacagtg cccctcacac ttttggccag 300

gggaccaagc tggagatcaa a 321

<210> SEQ ID NO 58
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 2G6_f4 variable light chain

<400> SEQUENCE: 58

gacatccagt tgacccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggccagtca gggcattagc agttatttag cctggtatca gcaaaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccactt tgcaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagtct 240

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gaagattttg caatttatta ctgtcaacag cttaatagtt acccgctcac tttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> SEQ ID NO 59
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 1C12_f3 variable heavy chain

<400> SEQUENCE: 59

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Asp Ile Thr Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Met Ser Pro Asn Ser Gly Asn Thr Gly Tyr Thr Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asn Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Phe Gly Tyr Gly Ser Gly Ala Leu Asp Tyr Tyr Tyr Tyr Gly
100 105 110

Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> SEQ ID NO 60
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 1D5_f3 variable heavy chain

<400> SEQUENCE: 60

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Asp Ile Thr Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Met Ser Pro Asn Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asn Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Asn Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Phe Gly Tyr Gly Ser Gly Ala Leu Asp Tyr Tyr Tyr Tyr Gly
100 105 110

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Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> SEQ ID NO 61
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 1D10_f3 variable heavy chain

<400> SEQUENCE: 61

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Asp Ile Ile Trp Val Arg Gln Ala Ser Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Met Ser Pro Asn Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asn Thr Ser Ile Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Phe Gly Tyr Gly Ser Gly Ala Leu Asp Tyr Tyr Tyr Tyr Gly
100 105 110

Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> SEQ ID NO 62
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 1E2_f3 variable heavy chain

<400> SEQUENCE: 62

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Asp Ile Thr Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Met Ser Pro Asn Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asn Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Phe Gly Tyr Gly Ser Gly Ala Leu Asp Tyr Tyr Tyr Tyr Gly
100 105 110

Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

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<210> SEQ ID NO 63
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 1G9_f3 variable heavy chain

<400> SEQUENCE: 63

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Asp Ile Ile Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Met Ser Pro Asn Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asn Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Phe Gly Tyr Gly Ser Gly Ala Leu Asp Tyr Tyr Tyr Tyr Gly
100 105 110

Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> SEQ ID NO 64
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 5D7_f3 variable heavy chain

<400> SEQUENCE: 64

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Thr
1 5 10 15

Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Asp Ile Ile Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Met Ser Pro Lys Asn Gly Asn Thr Gly Tyr Ala Gln Arg Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asn Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Phe Gly Tyr Gly Ser Gly Ala Leu Asp Tyr Tyr Tyr Tyr Gly
100 105 110

Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

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<210> SEQ ID NO 65
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 5H12_f3 variable heavy chain

<400> SEQUENCE: 65

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Thr
1 5 10 15

Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Thr Phe Pro Ser Tyr
20 25 30

Asp Ile Ile Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Met Ser Pro Lys Asn Gly Asn Thr Gly Phe Ala Gln Arg Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asn Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Phe Gly Tyr Gly Ser Gly Ala Leu Gly Tyr Tyr Tyr Tyr Gly
100 105 110

Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> SEQ ID NO 66
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 7C10_f3 variable heavy chain

<400> SEQUENCE: 66

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Asp Ile Thr Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Met Ser Pro Asn Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asn Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Phe Gly Tyr Gly Ser Gly Ala Leu Asp Tyr Tyr Tyr Tyr Gly
100 105 110

Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> SEQ ID NO 67
<211> LENGTH: 126

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 8H4_f3 variable heavy chain

<400> SEQUENCE: 67

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Asp Ile Thr Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Met Ser Pro Asn Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asn Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Phe Gly Tyr Gly Ser Gly Ala Leu Asp Tyr Tyr Tyr Tyr Gly
100 105 110

Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> SEQ ID NO 68
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 9C6_f3 variable heavy chain

<400> SEQUENCE: 68

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Asp Ile Thr Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Met Ser Pro Lys Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asn Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Phe Gly Tyr Gly Ser Gly Ala Leu Asp Tyr Tyr Tyr Tyr Gly
100 105 110

Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> SEQ ID NO 69
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 10D6_f3 variable heavy chain

<400> SEQUENCE: 69

Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Ile Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ile Thr Val Ser Ser Asn
20 25 30

Tyr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Leu Glu Leu Ala Gly Ala Phe Asp Ile Trp Gly Gln Gly Thr
100 105 110

Met Val Thr Val Ser Leu
115

<210> SEQ ID NO 70
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 11D5_f3 variable heavy chain

<400> SEQUENCE: 70

Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Ile Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ile Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Leu Ala Val Ala Gly Ala Phe Asp Ile Trp Gly Gln Gly Thr
100 105 110

Met Val Thr Val Ser Leu
115

<210> SEQ ID NO 71
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 11G2_f3 variable heavy chain

<400> SEQUENCE: 71

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Asp Ile Thr Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Met Ser Pro Asn Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Ser Met Thr Arg Asn Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Phe Gly Tyr Gly Ser Gly Ala Leu Asp Tyr Tyr Tyr Tyr Gly
100 105 110

Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> SEQ ID NO 72
<211> LENGTH: 122
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 11G7_f2 variable heavy chain

<400> SEQUENCE: 72

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gly
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Ser Ser Ser
20 25 30

Asn Trp Trp Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
35 40 45

Ile Gly Glu Ile Phe His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Val Thr Ile Ser Val Asp Lys Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Phe Arg Arg Ile Val Ala Thr Ser Tyr Tyr Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 73
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polypeptide
<220> FEATURE:

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<223> OTHER INFORMATION: 16C5_f3 variable heavy chain

<400> SEQUENCE: 73

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Asp Ile Ile Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Met Ser Pro Asn Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asn Thr Ser Ile Gly Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg Phe Gly Tyr Gly Ser Gly Ala Leu Asp Tyr Tyr Tyr Tyr Gly
100 105 110

Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> SEQ ID NO 74
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 16C12_f3 variable heavy chain

<400> SEQUENCE: 74

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Asp Ile Ile Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Met Ser Pro Asn Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asn Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Phe Gly Tyr Gly Ser Gly Ala Leu Asp Tyr Tyr Tyr Tyr Gly
100 105 110

Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> SEQ ID NO 75
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 17A8_f3 variable heavy chain

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<400> SEQUENCE: 75

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Asp Ile Ile Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Met Ser Pro Asn Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Lys Asn Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Phe Gly Tyr Gly Ser Gly Ala Leu Asp Tyr Tyr Tyr Tyr Gly
100 105 110

Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> SEQ ID NO 76
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 17F2_f3 variable heavy chain

<400> SEQUENCE: 76

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Arg Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Asp Ile Thr Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Met Ser Pro Asp Ser Gly Asn Thr Gly Tyr Ala Gln Arg Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asn Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Phe Gly Tyr Gly Ser Gly Ala Leu Asp Tyr Tyr Tyr Tyr Gly
100 105 110

Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> SEQ ID NO 77
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 18E7_f3 variable heavy chain

<400> SEQUENCE: 77

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Thr Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30

Asp Ile Ile Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Trp Met Ser Pro Asn Ser Gly Asn Thr Gly Tyr Ala Gln Arg Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asn Thr Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Phe Gly Tyr Gly Ser Gly Ala Leu Asp Tyr Tyr Tyr Tyr Gly
            100                 105                 110

Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125


<210> SEQ ID NO 78
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 19C4_f3 variable heavy chain

<400> SEQUENCE: 78

Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Ile Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ile Thr Val Ser Ser Asn
            20                  25                  30

Tyr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
    50                  55                  60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65                  70                  75                  80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Leu Glu Val Ala Gly Gly Phe Asp Ile Trp Gly Gln Gly Thr
            100                 105                 110

Met Val Thr Val Ser Leu
        115


<210> SEQ ID NO 79
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 2C1_f4 variable heavy chain

<400> SEQUENCE: 79

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15
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```
Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Gly Asp Tyr
            20                  25                  30

Thr Leu Ser Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Phe Ile Arg Ser Lys Pro Phe Gly Gly Thr Thr Gln Tyr Ala Ala
    50                  55                  60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
65                  70                  75                  80

Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Tyr Cys Thr Arg Val Ser Gly Tyr Ser Asn Ile Trp Phe Phe Ala Tyr
            100                 105                 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> SEQ ID NO 80
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 4E3_f4 variable heavy chain

<400> SEQUENCE: 80

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Val Ile Trp Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Lys Asp Tyr Ser Lys Thr Phe Tyr Gly Tyr Tyr Phe Asp Tyr
            100                 105                 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> SEQ ID NO 81
<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 7D2_f4 variable heavy chain

<400> SEQUENCE: 81

Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Ile Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Ser Asn
```

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```
            20                  25                  30

Tyr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
    50                  55                  60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Tyr Asn Thr Leu Tyr Leu
65                  70                  75                  80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Leu Val Ile Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr
            100                 105                 110

Val Thr Val Ser Ser
        115


<210> SEQ ID NO 82
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 9C5_f4 variable heavy chain

<400> SEQUENCE: 82

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Val Ile Trp Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Lys Asp Gly Ser Lys Thr Tyr Tyr Gly Tyr Tyr Phe Asp Tyr
            100                 105                 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> SEQ ID NO 83
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 10A3_f4 variable heavy chain

<400> SEQUENCE: 83

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30
```

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```
Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Ile Ile Trp Tyr Asp Gly Asn Asn Thr Tyr Tyr Val Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Lys Asp Gly Ser Lys Thr Tyr Tyr Gly Tyr Tyr Phe Asp Tyr
            100                 105                 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> SEQ ID NO 84
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 14G5_f4 variable heavy chain

<400> SEQUENCE: 84

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gly
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Ser Ser Asn
            20                  25                  30

Asn Trp Trp Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Val Trp
        35                  40                  45

Ile Gly Glu Ile Leu His Gly Glu Ile Thr Asn Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Arg Val Thr Ile Ser Ile Asp Lys Ser Lys Asn Gln Phe Ser
65                  70                  75                  80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Ala Asn Phe Tyr Gly Ser Gly Ser Ser Tyr Phe Asp Tyr
            100                 105                 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> SEQ ID NO 85
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 13A12_f3 variable heavy chain

<400> SEQUENCE: 85

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gly
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Tyr Ser Ser
            20                  25                  30

Asn Cys Trp Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45
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Ile Gly Glu Ile Tyr His Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Val Thr Ile Ser Leu Asp Lys Ser Lys Asn Arg Phe Ser
65 70 75 80

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gln Asp Tyr Tyr Gly Ser Gly Ser Ser Leu Phe Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 86
<211> LENGTH: 115
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 5B6_f3 variable heavy chain

<400> SEQUENCE: 86

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Ala
20 25 30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Arg Phe Lys Ser Lys Thr Asp Gly Gly Thr Thr Asp Tyr Ala Ala
50 55 60

Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Thr Thr Ser Ser Gly Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> SEQ ID NO 87
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 2G6_f4 variable heavy chain

<400> SEQUENCE: 87

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ile Tyr Gly Gly Ser Phe Ser Val Tyr
20 25 30

Tyr Trp Asn Trp Ile Arg Gln Pro Pro Glu Lys Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn His Ser Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys

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    50                  55                  60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65                  70                  75                  80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Tyr Tyr Tyr Asp Gly Asn Gly Tyr Tyr Pro Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser
        115


<210> SEQ ID NO 88
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 1C12_f3 variable light chain

<400> SEQUENCE: 88

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser
            20                  25                  30

His Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Asn Ser Pro
                85                  90                  95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100                 105


<210> SEQ ID NO 89
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 1D5_f3 variable light chain

<400> SEQUENCE: 89

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15

Asp Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser
            20                  25                  30

His Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80
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Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe Gly Ser Ser Pro
                85                  90                  95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100                 105


<210> SEQ ID NO 90
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 1D10_f3 variable light chain

<400> SEQUENCE: 90

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
            20                  25                  30

His Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Ser Ser Pro
                85                  90                  95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100                 105


<210> SEQ ID NO 91
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 1E2_f3 variable light chain

<400> SEQUENCE: 91

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser
            20                  25                  30

His Phe Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80

Pro Glu Asp Phe Ala Val Cys Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100                 105


<210> SEQ ID NO 92
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<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 1G9_f3 variable light chain

<400> SEQUENCE: 92

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser
20 25 30

His Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> SEQ ID NO 93
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 5D7_f3 variable light chain

<400> SEQUENCE: 93

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser
20 25 30

His Leu Ala Trp Tyr Arg Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Arg Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Ile Ser Pro
85 90 95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> SEQ ID NO 94
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 5H12_f3 variable light chain

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<400> SEQUENCE: 94

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser
20 25 30

His Leu Ala Trp Tyr Arg Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Arg Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Phe Ser Pro
85 90 95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> SEQ ID NO 95
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 7C10_f3 variable light chain

<400> SEQUENCE: 95

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser
20 25 30

His Leu Ala Trp Ser Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe Gly Ser Ser Pro
85 90 95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> SEQ ID NO 96
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 8H4_f3 variable light chain

<400> SEQUENCE: 96

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser
20 25 30

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His Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe Gly Ser Ser Pro
                85                  90                  95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100                 105


<210> SEQ ID NO 97
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 9C6_f3 variable light chain

<400> SEQUENCE: 97

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser
            20                  25                  30

His Leu Ala Trp Tyr Arg Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

Gly Arg Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Ser Ser Pro
                85                  90                  95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100                 105


<210> SEQ ID NO 98
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 10D6_f3 variable light chain

<400> SEQUENCE: 98

Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Tyr
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
        35                  40                  45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
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65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Asn Ser Tyr Pro Pro
85 90 95

Ser Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> SEQ ID NO 99
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 11D5_f3 variable light chain

<400> SEQUENCE: 99

Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Asn Ser Tyr Pro Pro
85 90 95

Ser Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> SEQ ID NO 100
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 11G2_f3 variable light chain

<400> SEQUENCE: 100

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Asn Ser
20 25 30

His Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe Gly Ser Ser Pro
85 90 95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

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<210> SEQ ID NO 101
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 11G7_f2 variable light chain

<400> SEQUENCE: 101

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
85 90 95

Leu Gln Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> SEQ ID NO 102
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 16C5_f3 variable light chain

<400> SEQUENCE: 102

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser
20 25 30

His Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Asn Ser Pro
85 90 95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> SEQ ID NO 103
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide

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<220> FEATURE:
<223> OTHER INFORMATION: 16C12_f3 variable light chain

<400> SEQUENCE: 103

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser
20 25 30

His Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> SEQ ID NO 104
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 17A8_f3 variable light chain

<400> SEQUENCE: 104

Glu Thr Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser
20 25 30

His Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> SEQ ID NO 105
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 17F2_f3 variable light chain

<400> SEQUENCE: 105

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser
            20                  25                  30

His Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Ser Ser Pro
                85                  90                  95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100                 105


<210> SEQ ID NO 106
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 18E7_f3 variable light chain

<400> SEQUENCE: 106

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser
            20                  25                  30

His Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100                 105


<210> SEQ ID NO 107
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 19C4_f3 variable light chain

<400> SEQUENCE: 107

Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Tyr
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
        35                  40                  45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
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Ser Gly Ser Gly Thr Lys Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Asn Ser Phe Pro Pro
                85                  90                  95

Ser Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105


<210> SEQ ID NO 108
<211> LENGTH: 106
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 2C1_f4 variable light chain

<400> SEQUENCE: 108

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1               5                   10                  15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ile Asn
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35                  40                  45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Val Ser Ser Leu Gln Ser
65                  70                  75                  80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Asn Trp Trp Thr
                85                  90                  95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105


<210> SEQ ID NO 109
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 4E3_f4 variable light chain

<400> SEQUENCE: 109

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile His Ser Phe
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Pro Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Ala Ala Ser Ser Leu Pro Ser Gly Leu Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ile Thr Pro Pro
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
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            100                 105


<210> SEQ ID NO 110
<211> LENGTH: 106
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 7D2_f4 variable light chain

<400> SEQUENCE: 110

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1               5                   10                  15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35                  40                  45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Val Pro Ala Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65                  70                  75                  80

Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Tyr Asn Asn Trp Pro Pro
                85                  90                  95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105


<210> SEQ ID NO 111
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 9C5_f4 variable light chain

<400> SEQUENCE: 111

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile His Ser Phe
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Pro Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Thr Thr Ser Ser Leu Gln Ser Gly Leu Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ile Thr Pro Pro
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105


<210> SEQ ID NO 112
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 10A3_f4 variable light chain

<400> SEQUENCE: 112

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile His Ser Phe
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Pro Pro Asn Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Leu Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ile Thr Pro Pro
85 90 95

Thr Phe Gly His Gly Thr Lys Val Glu Ile Lys
100 105

<210> SEQ ID NO 113
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 14G5_f4 variable light chain

<400> SEQUENCE: 113

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Asn Trp Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> SEQ ID NO 114
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 13A12_f3 variable light chain

<400> SEQUENCE: 114

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly

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1               5                   10                  15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35                  40                  45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65                  70                  75                  80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asp Asn Trp Pro Leu
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105


<210> SEQ ID NO 115
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 5B6_f3 variable light chain

<400> SEQUENCE: 115

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Asn Ser Ala Pro His
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105


<210> SEQ ID NO 116
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<223> OTHER INFORMATION: 2G6_f4 variable light chain

<400> SEQUENCE: 116

Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Tyr
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45
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Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Gln Leu Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> SEQ ID NO 117
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 1C12_f3 CDR1H

<400> SEQUENCE: 117

ggatacacct tcaccagtta tgat 24

<210> SEQ ID NO 118
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 1D5_f3 CDR1H

<400> SEQUENCE: 118

ggatacacct tcaccagtta tgat 24

<210> SEQ ID NO 119
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 1D10_f3 CDR1H

<400> SEQUENCE: 119

ggatacacct tcaccagtta tgat 24

<210> SEQ ID NO 120
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 1E2_f3 CDR1H

<400> SEQUENCE: 120

ggatacacct tcaccagtta tgat 24

<210> SEQ ID NO 121
<211> LENGTH: 24
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 1G9_f3 CDR1H

<400> SEQUENCE: 121

ggatacacct tcaccagtta tgat 24

<210> SEQ ID NO 122
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 5D7_f3 CDR1H

<400> SEQUENCE: 122

ggatacacct tcaccagtta tgat 24

<210> SEQ ID NO 123
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 5H12_f3 CDR1H

<400> SEQUENCE: 123

ggatacacct tccccagtta tgat 24

<210> SEQ ID NO 124
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 7C10_f3 CDR1H

<400> SEQUENCE: 124

ggatacacct tcaccagtta tgat 24

<210> SEQ ID NO 125
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 8H4_f3 CDR1H

<400> SEQUENCE: 125

ggatacacct tcaccagtta tgat 24

<210> SEQ ID NO 126
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 9C6_f3 CDR1H

<400> SEQUENCE: 126

ggatacacct tcaccagtta tgat 24

<210> SEQ ID NO 127
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 10D6_f3 CDR1H

<400> SEQUENCE: 127

gggatcaccg tcagtagtaa ctac 24

<210> SEQ ID NO 128
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 11D5_f3 CDR1H

<400> SEQUENCE: 128

gggatcaccg tcagtagtaa ctac 24

<210> SEQ ID NO 129
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 11G2_f3 CDR1H

<400> SEQUENCE: 129

ggatacacct tcaccagtta tgat 24

<210> SEQ ID NO 130
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 11G7_f2 CDR1H

<400> SEQUENCE: 130

ggtggctcca tcagcagtag taactgg 27

<210> SEQ ID NO 131
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 16C5_f3 CDR1H

<400> SEQUENCE: 131

ggatacacct tcaccagtta tgat 24

<210> SEQ ID NO 132
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 16C12_f3 CDR1H

<400> SEQUENCE: 132

ggatacacct tcaccagtta tgat 24

<210> SEQ ID NO 133
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 17A8_f3 CDR1H

<400> SEQUENCE: 133

ggatacacct tcaccagtta tgat 24

<210> SEQ ID NO 134
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 17F2_f3 CDR1H

<400> SEQUENCE: 134

ggatacacct tcaccagtta tgat 24

<210> SEQ ID NO 135
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 18E7_f3 CDR1H

<400> SEQUENCE: 135

ggatacacct ttaccagtta tgat 24

<210> SEQ ID NO 136
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 19C4_f3 CDR1H

<400> SEQUENCE: 136

gggatcaccg tcagtagtaa ttac 24

<210> SEQ ID NO 137
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 2C1_f4 CDR1H

<400> SEQUENCE: 137

ggattcacct ttggtgatta tact 24

<210> SEQ ID NO 138
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 4E3_f4 CDR1H

<400> SEQUENCE: 138

ggattcacct tcagtagcta tggc 24

<210> SEQ ID NO 139
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 7D2_f4 CDR1H

<400> SEQUENCE: 139

gggttcaccg tcagtagcaa ctac 24

<210> SEQ ID NO 140
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 9C5_f4 CDR1H

<400> SEQUENCE: 140

ggattcacct tcagtagcta tggc 24

<210> SEQ ID NO 141
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
oligonucleotide

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<220> FEATURE:
<223> OTHER INFORMATION: 10A3_f4 CDR1H

<400> SEQUENCE: 141

ggattcacct tcagtagtta tggc 24

<210> SEQ ID NO 142
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 14G5_f4 CDR1H

<400> SEQUENCE: 142

ggtggctcca tcagcagtaa taactgg 27

<210> SEQ ID NO 143
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 13A12_f3 CDR1H

<400> SEQUENCE: 143

ggtggctcca tctacagtag taactgc 27

<210> SEQ ID NO 144
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 5B6_f3 CDR1H

<400> SEQUENCE: 144

ggattcactt tcagtaacgc ctgg 24

<210> SEQ ID NO 145
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 2G6_f4 CDR1H

<400> SEQUENCE: 145

ggtgggtcct tcagtgttta ctac 24

<210> SEQ ID NO 146
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:

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<223> OTHER INFORMATION: 1C12_f3 CDR2H

<400> SEQUENCE: 146

atgagcccta acagtggtaa caca 24

<210> SEQ ID NO 147
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 1D5_f3 CDR2H

<400> SEQUENCE: 147

atgagcccta acagtggtaa caca 24

<210> SEQ ID NO 148
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 1D10_f3 CDR2H

<400> SEQUENCE: 148

atgagcccta acagcggtaa caca 24

<210> SEQ ID NO 149
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 1E2_f3 CDR2H

<400> SEQUENCE: 149

atgagcccta acagtggtaa caca 24

<210> SEQ ID NO 150
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 1G9_f3 CDR2H

<400> SEQUENCE: 150

atgagcccta acagtggtaa caca 24

<210> SEQ ID NO 151
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 5D7_f3 CDR2H

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<400> SEQUENCE: 151

atgagcccta aaaatggtaa caca 24

<210> SEQ ID NO 152
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 5H12_f3 CDR2H

<400> SEQUENCE: 152

atgagcccta aaaatggtaa caca 24

<210> SEQ ID NO 153
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 7C10_f3 CDR2H

<400> SEQUENCE: 153

atgagcccta acagtggtaa caca 24

<210> SEQ ID NO 154
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 8H4_f3 CDR2H

<400> SEQUENCE: 154

atgagcccta acagtggtaa caca 24

<210> SEQ ID NO 155
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 9C6_f3 CDR2H

<400> SEQUENCE: 155

atgagcccta aaagtggtaa caca 24

<210> SEQ ID NO 156
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 10D6_f3 CDR2H

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<400> SEQUENCE: 156

atttatagcg gtggtagcac a 21

<210> SEQ ID NO 157
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 11D5_f3 CDR2H

<400> SEQUENCE: 157

atttatagcg gtggtagcac a 21

<210> SEQ ID NO 158
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 11G2_f3 CDR2H

<400> SEQUENCE: 158

atgagcccta acagtggtaa caca 24

<210> SEQ ID NO 159
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 11G7_f2 CDR2H

<400> SEQUENCE: 159

atctttcata gtgggagcac c 21

<210> SEQ ID NO 160
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 16C5_f3 CDR2H

<400> SEQUENCE: 160

atgagcccta atagtggtaa caca 24

<210> SEQ ID NO 161
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 16C12_f3 CDR2H

<400> SEQUENCE: 161

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atgagcccta acagtggtaa caca 24

<210> SEQ ID NO 162
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 17A8_f3 CDR2H

<400> SEQUENCE: 162

atgagcccta acagtggtaa caca 24

<210> SEQ ID NO 163
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 17F2_f3 CDR2H

<400> SEQUENCE: 163

atgagccctg acagtggtaa caca 24

<210> SEQ ID NO 164
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 18E7_f3 CDR2H

<400> SEQUENCE: 164

atgagcccta acagtggtaa caca 24

<210> SEQ ID NO 165
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 19C4_f3 CDR2H

<400> SEQUENCE: 165

atttatagcg gtggtagcac a 21

<210> SEQ ID NO 166
<211> LENGTH: 30
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 2C1_f4 CDR2H

<400> SEQUENCE: 166

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attagaagca aacctttgg tgggacaaca 30

<210> SEQ ID NO 167
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 4E3_f4 CDR2H

<400> SEQUENCE: 167

atttggtatg atggaaataa taaa 24

<210> SEQ ID NO 168
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 7D2_f4 CDR2H

<400> SEQUENCE: 168

atttatagcg gtggtagcac a 21

<210> SEQ ID NO 169
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 9C5_f4 CDR2H

<400> SEQUENCE: 169

atttggtatg atggaaataa taaa 24

<210> SEQ ID NO 170
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 10A3_f4 CDR2H

<400> SEQUENCE: 170

atttggtatg atggaaataa taca 24

<210> SEQ ID NO 171
<211> LENGTH: 21
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 14G5_f4 CDR2H

<400> SEQUENCE: 171

atcttgcatg gtgagatcac c 21

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<210> SEQ ID NO 172
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 13A12_f3 CDR2H

<400> SEQUENCE: 172

atctatcata gtgggggcac c 21

<210> SEQ ID NO 173
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 5B6_f3 CDR2H

<400> SEQUENCE: 173

tttaaaagca aaactgatgg tgggacaaca 30

<210> SEQ ID NO 174
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 2G6_f4 CDR2H

<400> SEQUENCE: 174

atcaatcata gtggaaacac c 21

<210> SEQ ID NO 175
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 1C12_f3 CDR3H

<400> SEQUENCE: 175

gcgagattcg gctatggttc gggggccctc gactactact actacggttt ggacgtc 57

<210> SEQ ID NO 176
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<400> SEQUENCE: 176

gcgagattcg gctatggttc gggggccctc gactactact actacggttt ggacgtc 57

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<210> SEQ ID NO 177
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 1D10_f3 CDR3H

<400> SEQUENCE: 177

gcgagattcg gctatggttc gggggccctc gactactact attacggttt ggacgtc 57

<210> SEQ ID NO 178
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 1E2_f3 CDR3H

<400> SEQUENCE: 178

gcgagattcg gctatggttc gggggccctc gactactact actacggttt ggacgtc 57

<210> SEQ ID NO 179
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 1G9_f3 CDR3H

<400> SEQUENCE: 179

gcgagattcg gctatggttc gggggccctc gactactact actacggttt ggacgtc 57

<210> SEQ ID NO 180
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 5D7_f3 CDR3H

<400> SEQUENCE: 180

gcgagattcg gctatggttc gggggccctc gactactact actacggttt ggacgtc 57

<210> SEQ ID NO 181
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 5H12_f3 CDR3H

<400> SEQUENCE: 181

gcgagattcg gctatgggtc gggggccctc ggatattact actacggttt ggacgtc 57

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<210> SEQ ID NO 182
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 7C10_f3 CDR3H

<400> SEQUENCE: 182

gcgagattcg gctatggttc gggggccctc gactactact actacggttt ggacgtc 57

<210> SEQ ID NO 183
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 8H4_f3 CDR3H

<400> SEQUENCE: 183

gcgagattcg gctatggttc gggggccctc gactactact actacggttt ggacgtc 57

<210> SEQ ID NO 184
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 9C6_f3 CDR3H

<400> SEQUENCE: 184

gcgagattcg gctatggttc gggggccctc gactactact actacggttt ggacgtc 57

<210> SEQ ID NO 185
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 10D6_f3 CDR3H

<400> SEQUENCE: 185

gcgagagatt tagaactggc tggagctttt gatatc 36

<210> SEQ ID NO 186
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 11D5_f3 CDR3H

<400> SEQUENCE: 186

gcgagagatt tagcagtggc tggagctttt gatatc 36

<210> SEQ ID NO 187

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<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 11G2_f3 CDR3H

<400> SEQUENCE: 187

gcgagattcg gctatggttc gggggccctc gactactact actacggttt ggacgtc 57

<210> SEQ ID NO 188
<211> LENGTH: 45
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 11G7_f2 CDR3H

<400> SEQUENCE: 188

gcgagattca gaaggatagt ggctacgagc tactattttg actac 45

<210> SEQ ID NO 189
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 16C5_f3 CDR3H

<400> SEQUENCE: 189

gcgagattcg gctatggttc gggggccctc gactactact actacggttt ggacgtc 57

<210> SEQ ID NO 190
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 16C12_f3 CDR3H

<400> SEQUENCE: 190

gcgagattcg gctatggttc gggggccctc gactactact actacggttt ggacgtc 57

<210> SEQ ID NO 191
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 17A8_f3 CDR3H

<400> SEQUENCE: 191

gcgagattcg gctatggttc gggggccctc gactactact actacggttt ggacgtc 57

<210> SEQ ID NO 192
<211> LENGTH: 57

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 17F2_f3 CDR3H

<400> SEQUENCE: 192

gcgagattcg gctatggttc gggggccctc gactactact actacggttt ggacgtc 57

<210> SEQ ID NO 193
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 18E7_f3 CDR3H

<400> SEQUENCE: 193

gcgagattcg gctatggttc gggggccctc gactactact actacggttt ggacgtc 57

<210> SEQ ID NO 194
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 19C4_f3 CDR3H

<400> SEQUENCE: 194

gcgagagatt tagaagtggc tggaggtttt gatatc 36

<210> SEQ ID NO 195
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 2C1_f4 CDR3H

<400> SEQUENCE: 195

actagagtgt ccgggtatag caacatctgg ttctttgcct ac 42

<210> SEQ ID NO 196
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 4E3_f4 CDR3H

<400> SEQUENCE: 196

gcgagaaaag attattcgaa gacattttat ggatactact ttgactat 48

<210> SEQ ID NO 197
<211> LENGTH: 33
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 7D2_f4 CDR3H

<400> SEQUENCE: 197

gcgagagatc tagtcatcta cggtatggac gtc 33

<210> SEQ ID NO 198
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 9C5_f4 CDR3H

<400> SEQUENCE: 198

gcgagaaaag atggttcgaa gacatattat ggatactact ttgactat 48

<210> SEQ ID NO 199
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 10A3_f4 CDR3H

<400> SEQUENCE: 199

gcgagaaaag atggttcgaa gacatattat ggatactact ttgactat 48

<210> SEQ ID NO 200
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 14G5_f4 CDR3H

<400> SEQUENCE: 200

gcgagagatg cgaatttcta tggttcgggg agttcttact ttgactac 48

<210> SEQ ID NO 201
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 13A12_f3 CDR3H

<400> SEQUENCE: 201

gcgagagatc aagattacta tggttcgggg agttccctct ttgactac 48

<210> SEQ ID NO 202
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 5B6_f3 CDR3H

<400> SEQUENCE: 202

accaccagca gtggctac 18

<210> SEQ ID NO 203
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 2G6_f4 CDR3H

<400> SEQUENCE: 203

gcgaggtatt actatgatgg taatggttat tacccc 36

<210> SEQ ID NO 204
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 1C12_f3 CDR1H

<400> SEQUENCE: 204

Gly Tyr Thr Phe Thr Ser Tyr Asp
1 5

<210> SEQ ID NO 205
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 1D5_f3 CDR1H

<400> SEQUENCE: 205

Gly Tyr Thr Phe Thr Ser Tyr Asp
1 5

<210> SEQ ID NO 206
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 1D10_f3 CDR1H

<400> SEQUENCE: 206

Gly Tyr Thr Phe Thr Ser Tyr Asp
1 5

<210> SEQ ID NO 207
<211> LENGTH: 8

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 1E2_f3 CDR1H

<400> SEQUENCE: 207

Gly Tyr Thr Phe Thr Ser Tyr Asp
1 5

<210> SEQ ID NO 208
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 1G9_f3 CDR1H

<400> SEQUENCE: 208

Gly Tyr Thr Phe Thr Ser Tyr Asp
1 5

<210> SEQ ID NO 209
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 5D7_f3 CDR1H

<400> SEQUENCE: 209

Gly Tyr Thr Phe Thr Ser Tyr Asp
1 5

<210> SEQ ID NO 210
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 5H12_f3 CDR1H

<400> SEQUENCE: 210

Gly Tyr Thr Phe Pro Ser Tyr Asp
1 5

<210> SEQ ID NO 211
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 7C10_f3 CDR1H

<400> SEQUENCE: 211

Gly Tyr Thr Phe Thr Ser Tyr Asp
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<210> SEQ ID NO 212
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 8H4_f3 CDR1H

<400> SEQUENCE: 212

Gly Tyr Thr Phe Thr Ser Tyr Asp
1 5

<210> SEQ ID NO 213
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 9C6_f3 CDR1H

<400> SEQUENCE: 213

Gly Tyr Thr Phe Thr Ser Tyr Asp
1 5

<210> SEQ ID NO 214
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 10D6_f3 CDR1H

<400> SEQUENCE: 214

Gly Ile Thr Val Ser Ser Asn Tyr
1 5

<210> SEQ ID NO 215
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 11D5_f3 CDR1H

<400> SEQUENCE: 215

Gly Ile Thr Val Ser Ser Asn Tyr
1 5

<210> SEQ ID NO 216
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 11G2_f3 CDR1H

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<400> SEQUENCE: 216

Gly Tyr Thr Phe Thr Ser Tyr Asp
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<210> SEQ ID NO 217
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 11G7_f2 CDR1H

<400> SEQUENCE: 217

Gly Gly Ser Ile Ser Ser Ser Asn Trp
1 5

<210> SEQ ID NO 218
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 16C5_f3 CDR1H

<400> SEQUENCE: 218

Gly Tyr Thr Phe Thr Ser Tyr Asp
1 5

<210> SEQ ID NO 219
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 16C12_f3 CDR1H

<400> SEQUENCE: 219

Gly Tyr Thr Phe Thr Ser Tyr Asp
1 5

<210> SEQ ID NO 220
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 17A8_f3 CDR1H

<400> SEQUENCE: 220

Gly Tyr Thr Phe Thr Ser Tyr Asp
1 5

<210> SEQ ID NO 221
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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peptide
<220> FEATURE:
<223> OTHER INFORMATION: 17F2_f3 CDR1H

<400> SEQUENCE: 221

Gly Tyr Thr Phe Thr Ser Tyr Asp
1 5

<210> SEQ ID NO 222
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
peptide
<220> FEATURE:
<223> OTHER INFORMATION: 18E7_f3 CDR1H

<400> SEQUENCE: 222

Gly Tyr Thr Phe Thr Ser Tyr Asp
1 5

<210> SEQ ID NO 223
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
peptide
<220> FEATURE:
<223> OTHER INFORMATION: 19C4_f3 CDR1H

<400> SEQUENCE: 223

Gly Ile Thr Val Ser Ser Asn Tyr
1 5

<210> SEQ ID NO 224
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
peptide
<220> FEATURE:
<223> OTHER INFORMATION: 2C1_f4 CDR1H

<400> SEQUENCE: 224

Gly Phe Thr Phe Gly Asp Tyr Thr
1 5

<210> SEQ ID NO 225
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
peptide
<220> FEATURE:
<223> OTHER INFORMATION: 4E3_f4 CDR1H

<400> SEQUENCE: 225

Gly Phe Thr Phe Ser Ser Tyr Gly
1 5

<210> SEQ ID NO 226
<211> LENGTH: 8

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 7D2_f4 CDR1H

<400> SEQUENCE: 226

Gly Phe Thr Val Ser Ser Asn Tyr
1 5

<210> SEQ ID NO 227
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 9C5_f4 CDR1H

<400> SEQUENCE: 227

Gly Phe Thr Phe Ser Ser Tyr Gly
1 5

<210> SEQ ID NO 228
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 10A3_f4 CDR1H

<400> SEQUENCE: 228

Gly Phe Thr Phe Ser Ser Tyr Gly
1 5

<210> SEQ ID NO 229
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 14G5_f4 CDR1H

<400> SEQUENCE: 229

Gly Gly Ser Ile Ser Ser Asn Asn Trp
1 5

<210> SEQ ID NO 230
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 13A12_f3 CDR1H

<400> SEQUENCE: 230

Gly Gly Ser Ile Tyr Ser Ser Asn Cys
1 5

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<210> SEQ ID NO 231
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 5B6_f3 CDR1H

<400> SEQUENCE: 231

Gly Phe Thr Phe Ser Asn Ala Trp
1 5

<210> SEQ ID NO 232
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 2G6_f4 CDR1H

<400> SEQUENCE: 232

Gly Gly Ser Phe Ser Val Tyr Tyr
1 5

<210> SEQ ID NO 233
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 1C12_f3 CDR2H

<400> SEQUENCE: 233

Met Ser Pro Asn Ser Gly Asn Thr
1 5

<210> SEQ ID NO 234
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 1D5_f3 CDR2H

<400> SEQUENCE: 234

Met Ser Pro Asn Ser Gly Asn Thr
1 5

<210> SEQ ID NO 235
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 1D10_f3 CDR2H

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<400> SEQUENCE: 235

Met Ser Pro Asn Ser Gly Asn Thr
1 5

<210> SEQ ID NO 236
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 1E2_f3 CDR2H

<400> SEQUENCE: 236

Met Ser Pro Asn Ser Gly Asn Thr
1 5

<210> SEQ ID NO 237
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 1G9_f3 CDR2H

<400> SEQUENCE: 237

Met Ser Pro Asn Ser Gly Asn Thr
1 5

<210> SEQ ID NO 238
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 5D7_f3 CDR2H

<400> SEQUENCE: 238

Met Ser Pro Lys Asn Gly Asn Thr
1 5

<210> SEQ ID NO 239
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 5H12_f3 CDR2H

<400> SEQUENCE: 239

Met Ser Pro Lys Asn Gly Asn Thr
1 5

<210> SEQ ID NO 240
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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peptide
<220> FEATURE:
<223> OTHER INFORMATION: 7C10_f3 CDR2H

<400> SEQUENCE: 240

Met Ser Pro Asn Ser Gly Asn Thr
1 5

<210> SEQ ID NO 241
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
peptide
<220> FEATURE:
<223> OTHER INFORMATION: 8H4_f3 CDR2H

<400> SEQUENCE: 241

Met Ser Pro Asn Ser Gly Asn Thr
1 5

<210> SEQ ID NO 242
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
peptide
<220> FEATURE:
<223> OTHER INFORMATION: 9C6_f3 CDR2H

<400> SEQUENCE: 242

Met Ser Pro Lys Ser Gly Asn Thr
1 5

<210> SEQ ID NO 243
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
peptide
<220> FEATURE:
<223> OTHER INFORMATION: 10D6_f3 CDR2H

<400> SEQUENCE: 243

Ile Tyr Ser Gly Gly Ser Thr
1 5

<210> SEQ ID NO 244
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
peptide
<220> FEATURE:
<223> OTHER INFORMATION: 11D5_f3 CDR2H

<400> SEQUENCE: 244

Ile Tyr Ser Gly Gly Ser Thr
1 5

<210> SEQ ID NO 245
<211> LENGTH: 8

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 11G2_f3 CDR2H

<400> SEQUENCE: 245

Met Ser Pro Asn Ser Gly Asn Thr
1 5

<210> SEQ ID NO 246
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 11G7_f2 CDR2H

<400> SEQUENCE: 246

Ile Phe His Ser Gly Ser Thr
1 5

<210> SEQ ID NO 247
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 16C5_f3 CDR2H

<400> SEQUENCE: 247

Met Ser Pro Asn Ser Gly Asn Thr
1 5

<210> SEQ ID NO 248
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 16C12_f3 CDR2H

<400> SEQUENCE: 248

Met Ser Pro Asn Ser Gly Asn Thr
1 5

<210> SEQ ID NO 249
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 17A8_f3 CDR2H

<400> SEQUENCE: 249

Met Ser Pro Asn Ser Gly Asn Thr
1 5

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<210> SEQ ID NO 250
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 17F2_f3 CDR2H

<400> SEQUENCE: 250

Met Ser Pro Asp Ser Gly Asn Thr
1 5

<210> SEQ ID NO 251
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 18E7_f3 CDR2H

<400> SEQUENCE: 251

Met Ser Pro Asn Ser Gly Asn Thr
1 5

<210> SEQ ID NO 252
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 19C4_f3 CDR2H

<400> SEQUENCE: 252

Ile Tyr Ser Gly Gly Ser Thr
1 5

<210> SEQ ID NO 253
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 2C1_f4 CDR2H

<400> SEQUENCE: 253

Ile Arg Ser Lys Pro Phe Gly Gly Thr Thr
1 5 10

<210> SEQ ID NO 254
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 4E3_f4 CDR2H

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<400> SEQUENCE: 254

Ile Trp Tyr Asp Gly Asn Asn Lys
1 5

<210> SEQ ID NO 255
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 7D2_f4 CDR2H

<400> SEQUENCE: 255

Ile Tyr Ser Gly Gly Ser Thr
1 5

<210> SEQ ID NO 256
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 9C5_f4 CDR2H

<400> SEQUENCE: 256

Ile Trp Tyr Asp Gly Asn Asn Lys
1 5

<210> SEQ ID NO 257
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 10A3_f4 CDR2H

<400> SEQUENCE: 257

Ile Trp Tyr Asp Gly Asn Asn Thr
1 5

<210> SEQ ID NO 258
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 14G5_f4 CDR2H

<400> SEQUENCE: 258

Ile Leu His Gly Glu Ile Thr
1 5

<210> SEQ ID NO 259
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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peptide
<220> FEATURE:
<223> OTHER INFORMATION: 13A12_f3 CDR2H

<400> SEQUENCE: 259

Ile Tyr His Ser Gly Gly Thr
1 5

<210> SEQ ID NO 260
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
peptide
<220> FEATURE:
<223> OTHER INFORMATION: 5B6_f3 CDR2H

<400> SEQUENCE: 260

Phe Lys Ser Lys Thr Asp Gly Gly Thr Thr
1 5 10

<210> SEQ ID NO 261
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
peptide
<220> FEATURE:
<223> OTHER INFORMATION: 2G6_f4 CDR2H

<400> SEQUENCE: 261

Ile Asn His Ser Gly Asn Thr
1 5

<210> SEQ ID NO 262
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
peptide
<220> FEATURE:
<223> OTHER INFORMATION: 1C12_f3 CDR3H

<400> SEQUENCE: 262

Ala Arg Phe Gly Tyr Gly Ser Gly Ala Leu Asp Tyr Tyr Tyr Tyr Gly
1 5 10 15

Leu Asp Val

<210> SEQ ID NO 263
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
peptide
<220> FEATURE:
<223> OTHER INFORMATION: 1D5_f3 CDR3H

<400> SEQUENCE: 263

Ala Arg Phe Gly Tyr Gly Ser Gly Ala Leu Asp Tyr Tyr Tyr Tyr Gly
1 5 10 15

Leu Asp Val

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<210> SEQ ID NO 264
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 1D10_f3 CDR3H

<400> SEQUENCE: 264

Ala Arg Phe Gly Tyr Gly Ser Gly Ala Leu Asp Tyr Tyr Tyr Tyr Gly
1 5 10 15

Leu Asp Val

<210> SEQ ID NO 265
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 1E2_f3 CDR3H

<400> SEQUENCE: 265

Ala Arg Phe Gly Tyr Gly Ser Gly Ala Leu Asp Tyr Tyr Tyr Tyr Gly
1 5 10 15

Leu Asp Val

<210> SEQ ID NO 266
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 1G9_f3 CDR3H

<400> SEQUENCE: 266

Ala Arg Phe Gly Tyr Gly Ser Gly Ala Leu Asp Tyr Tyr Tyr Tyr Gly
1 5 10 15

Leu Asp Val

<210> SEQ ID NO 267
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 5D7_f3 CDR3H

<400> SEQUENCE: 267

Ala Arg Phe Gly Tyr Gly Ser Gly Ala Leu Asp Tyr Tyr Tyr Tyr Gly
1 5 10 15

Leu Asp Val

<210> SEQ ID NO 268
<211> LENGTH: 19

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 5H12_f3 CDR3H

<400> SEQUENCE: 268

Ala Arg Phe Gly Tyr Gly Ser Gly Ala Leu Gly Tyr Tyr Tyr Tyr Gly
1 5 10 15

Leu Asp Val

<210> SEQ ID NO 269
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 7C10_f3 CDR3H

<400> SEQUENCE: 269

Ala Arg Phe Gly Tyr Gly Ser Gly Ala Leu Asp Tyr Tyr Tyr Tyr Gly
1 5 10 15

Leu Asp Val

<210> SEQ ID NO 270
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 8H4_f3 CDR3H

<400> SEQUENCE: 270

Ala Arg Phe Gly Tyr Gly Ser Gly Ala Leu Asp Tyr Tyr Tyr Tyr Gly
1 5 10 15

Leu Asp Val

<210> SEQ ID NO 271
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 9C6_f3 CDR3H

<400> SEQUENCE: 271

Ala Arg Phe Gly Tyr Gly Ser Gly Ala Leu Asp Tyr Tyr Tyr Tyr Gly
1 5 10 15

Leu Asp Val

<210> SEQ ID NO 272
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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peptide
<220> FEATURE:
<223> OTHER INFORMATION: 10D6_f3 CDR3H

<400> SEQUENCE: 272

Ala Arg Asp Leu Glu Leu Ala Gly Ala Phe Asp Ile
1 5 10

<210> SEQ ID NO 273
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
peptide
<220> FEATURE:
<223> OTHER INFORMATION: 11D5_f3 CDR3H

<400> SEQUENCE: 273

Ala Arg Asp Leu Ala Val Ala Gly Ala Phe Asp Ile
1 5 10

<210> SEQ ID NO 274
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
peptide
<220> FEATURE:
<223> OTHER INFORMATION: 11G2_f3 CDR3H

<400> SEQUENCE: 274

Ala Arg Phe Gly Tyr Gly Ser Gly Ala Leu Asp Tyr Tyr Tyr Tyr Gly
1 5 10 15

Leu Asp Val

<210> SEQ ID NO 275
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
peptide
<220> FEATURE:
<223> OTHER INFORMATION: 11G7_f2 CDR3H

<400> SEQUENCE: 275

Ala Arg Phe Arg Arg Ile Val Ala Thr Ser Tyr Tyr Phe Asp Tyr
1 5 10 15

<210> SEQ ID NO 276
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
peptide
<220> FEATURE:
<223> OTHER INFORMATION: 16C5_f3 CDR3H

<400> SEQUENCE: 276

Ala Arg Phe Gly Tyr Gly Ser Gly Ala Leu Asp Tyr Tyr Tyr Tyr Gly
1 5 10 15

Leu Asp Val

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<210> SEQ ID NO 277
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 16C12_f3 CDR3H

<400> SEQUENCE: 277

Ala Arg Phe Gly Tyr Gly Ser Gly Ala Leu Asp Tyr Tyr Tyr Tyr Gly
1 5 10 15

Leu Asp Val

<210> SEQ ID NO 278
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 17A8_f3 CDR3H

<400> SEQUENCE: 278

Ala Arg Phe Gly Tyr Gly Ser Gly Ala Leu Asp Tyr Tyr Tyr Tyr Gly
1 5 10 15

Leu Asp Val

<210> SEQ ID NO 279
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 17F2_f3 CDR3H

<400> SEQUENCE: 279

Ala Arg Phe Gly Tyr Gly Ser Gly Ala Leu Asp Tyr Tyr Tyr Tyr Gly
1 5 10 15

Leu Asp Val

<210> SEQ ID NO 280
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 18E7_f3 CDR3H

<400> SEQUENCE: 280

Ala Arg Phe Gly Tyr Gly Ser Gly Ala Leu Asp Tyr Tyr Tyr Tyr Gly
1 5 10 15

Leu Asp Val

<210> SEQ ID NO 281
<211> LENGTH: 12

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 19C4_f3 CDR3H

<400> SEQUENCE: 281

Ala Arg Asp Leu Glu Val Ala Gly Gly Phe Asp Ile
1 5 10

<210> SEQ ID NO 282
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 2C1_f4 CDR3H

<400> SEQUENCE: 282

Thr Arg Val Ser Gly Tyr Ser Asn Ile Trp Phe Phe Ala Tyr
1 5 10

<210> SEQ ID NO 283
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 4E3_f4 CDR3H

<400> SEQUENCE: 283

Ala Arg Lys Asp Tyr Ser Lys Thr Phe Tyr Gly Tyr Tyr Phe Asp Tyr
1 5 10 15

<210> SEQ ID NO 284
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 7D2_f4 CDR3H

<400> SEQUENCE: 284

Ala Arg Asp Leu Val Ile Tyr Gly Met Asp Val
1 5 10

<210> SEQ ID NO 285
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 9C5_f4 CDR3H

<400> SEQUENCE: 285

Ala Arg Lys Asp Gly Ser Lys Thr Tyr Tyr Gly Tyr Tyr Phe Asp Tyr
1 5 10 15

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<210> SEQ ID NO 286
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 10A3_f4 CDR3H

<400> SEQUENCE: 286

Ala Arg Lys Asp Gly Ser Lys Thr Tyr Tyr Gly Tyr Tyr Phe Asp Tyr
1 5 10 15

<210> SEQ ID NO 287
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 14G5_f4 CDR3H

<400> SEQUENCE: 287

Ala Arg Asp Ala Asn Phe Tyr Gly Ser Gly Ser Ser Tyr Phe Asp Tyr
1 5 10 15

<210> SEQ ID NO 288
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 13A12_f3 CDR3H

<400> SEQUENCE: 288

Ala Arg Asp Gln Asp Tyr Tyr Gly Ser Gly Ser Ser Leu Phe Asp Tyr
1 5 10 15

<210> SEQ ID NO 289
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 5B6_f3 CDR3H

<400> SEQUENCE: 289

Thr Thr Ser Ser Gly Tyr
1 5

<210> SEQ ID NO 290
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 2G6_f4 CDR3H

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<400> SEQUENCE: 290

Ala Arg Tyr Tyr Tyr Asp Gly Asn Gly Tyr Tyr Pro
1 5 10

<210> SEQ ID NO 291
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 1C12_f3 CDR1L

<400> SEQUENCE: 291

cagagtgtta ggagcagtca c 21

<210> SEQ ID NO 292
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 1D5_f3 CDR1L

<400> SEQUENCE: 292

cagagtgtta ggagcagtca c 21

<210> SEQ ID NO 293
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 1D10_f3 CDR1L

<400> SEQUENCE: 293

cagagtgtta gcagcagcca c 21

<210> SEQ ID NO 294
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 1E2_f3 CDR1L

<400> SEQUENCE: 294

cagagtgtta ggagcagtca c 21

<210> SEQ ID NO 295
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<400> SEQUENCE: 295

cagagtgtta ggagcagtca c 21

<210> SEQ ID NO 296
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<400> SEQUENCE: 296

cagagtgtta ggagcagtca c 21

<210> SEQ ID NO 297
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<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<400> SEQUENCE: 297

cagagtgtta ggagcagtca c 21

<210> SEQ ID NO 298
<211> LENGTH: 21
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<220> FEATURE:
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<400> SEQUENCE: 298

cagagtgtta ggagcagtca c 21

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<400> SEQUENCE: 299

cagagtgtta ggagcagtca c 21

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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<400> SEQUENCE: 300

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cagagtgtta ggagcagtca c 21

<210> SEQ ID NO 301
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<400> SEQUENCE: 301

cagggcatta gcagttat 18

<210> SEQ ID NO 302
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 11D5_f3 CDR1L

<400> SEQUENCE: 302

cagggcatta gcagttat 18

<210> SEQ ID NO 303
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 11G2_f3 CDR1L

<400> SEQUENCE: 303

cagagtgtta ggaacagtca c 21

<210> SEQ ID NO 304
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<400> SEQUENCE: 304

cagagcctcc tgcatagtaa tggatacaac tat 33

<210> SEQ ID NO 305
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<220> FEATURE:
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<400> SEQUENCE: 305

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cagagtgtta ggagcagtca c 21

<210> SEQ ID NO 306
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<400> SEQUENCE: 306

cagagtgtta ggagcagtca c 21

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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 17A8_f3 CDR1L

<400> SEQUENCE: 307

cagagtgtta ggagcagtca c 21

<210> SEQ ID NO 308
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<400> SEQUENCE: 308

cagagtgtta ggagcagtca c 21

<210> SEQ ID NO 309
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<400> SEQUENCE: 309

cagagtgtta ggagcagtca c 21

<210> SEQ ID NO 310
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<220> FEATURE:
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<400> SEQUENCE: 310

cagggcatta gcagttat 18

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<400> SEQUENCE: 311

cagagtgtta gcatcaac 18

<210> SEQ ID NO 312
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 4E3_f4 CDR1L

<400> SEQUENCE: 312

cagagcattc acagcttt 18

<210> SEQ ID NO 313
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<400> SEQUENCE: 313

cagagtgtta gcagcaac 18

<210> SEQ ID NO 314
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<400> SEQUENCE: 314

cagagcattc acagcttt 18

<210> SEQ ID NO 315
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<400> SEQUENCE: 315

cagagcattc acagcttt 18

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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<400> SEQUENCE: 316

cagagtgtta gcagcaac 18

<210> SEQ ID NO 317
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<212> TYPE: DNA
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<400> SEQUENCE: 317

cagagtgtta gcagcaac 18

<210> SEQ ID NO 318
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<223> OTHER INFORMATION: 5B6_f3 CDR1L

<400> SEQUENCE: 318

cagggcatta gcaattat 18

<210> SEQ ID NO 319
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 2G6_f4 CDR1L

<400> SEQUENCE: 319

cagggcatta gcagttat 18

<210> SEQ ID NO 320
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 1C12_f3 CDR2L

<400> SEQUENCE: 320

ggtgcatcc 9

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<210> SEQ ID NO 321
<211> LENGTH: 9
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 1D5_f3 CDR2L

<400> SEQUENCE: 321

ggtgcatcc 9

<210> SEQ ID NO 322
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 1D10_f3 CDR2L

<400> SEQUENCE: 322

ggtgcatcc 9

<210> SEQ ID NO 323
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 1E2_f3 CDR2L

<400> SEQUENCE: 323

ggtgcatcc 9

<210> SEQ ID NO 324
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 1G9_f3 CDR2L

<400> SEQUENCE: 324

ggtgcatcc 9

<210> SEQ ID NO 325
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 5D7_f3 CDR2L

<400> SEQUENCE: 325

ggtgcctcc 9

<210> SEQ ID NO 326

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<211> LENGTH: 9
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 5H12_f3 CDR2L

<400> SEQUENCE: 326

ggtgcctcc 9

<210> SEQ ID NO 327
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<212> TYPE: DNA
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 7C10_f3 CDR2L

<400> SEQUENCE: 327

ggtgcatcc 9

<210> SEQ ID NO 328
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 8H4_f3 CDR2L

<400> SEQUENCE: 328

ggtgcatcc 9

<210> SEQ ID NO 329
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 9C6_f3 CDR2L

<400> SEQUENCE: 329

ggtgcctcc 9

<210> SEQ ID NO 330
<211> LENGTH: 9
<212> TYPE: DNA
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 10D6_f3 CDR2L

<400> SEQUENCE: 330

gctgcatcc 9

<210> SEQ ID NO 331
<211> LENGTH: 9

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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<400> SEQUENCE: 331

gctgcatcc 9

<210> SEQ ID NO 332
<211> LENGTH: 9
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 11G2_f3 CDR2L

<400> SEQUENCE: 332

ggtgcatcc 9

<210> SEQ ID NO 333
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 11G7_f2 CDR2L

<400> SEQUENCE: 333

ttgggttct 9

<210> SEQ ID NO 334
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 16C5_f3 CDR2L

<400> SEQUENCE: 334

ggtgcatcc 9

<210> SEQ ID NO 335
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 16C12_f3 CDR2L

<400> SEQUENCE: 335

ggtgcatcc 9

<210> SEQ ID NO 336
<211> LENGTH: 9
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 17A8_f3 CDR2L

<400> SEQUENCE: 336

ggtgcatcc 9

<210> SEQ ID NO 337
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 17F2_f3 CDR2L

<400> SEQUENCE: 337

ggtgcatcc 9

<210> SEQ ID NO 338
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<400> SEQUENCE: 338

ggtgcatcc 9

<210> SEQ ID NO 339
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 19C4_f3 CDR2L

<400> SEQUENCE: 339

gctgcatcc 9

<210> SEQ ID NO 340
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 2C1_f4 CDR2L

<400> SEQUENCE: 340

ggtgcatcc 9

<210> SEQ ID NO 341
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 4E3_f4 CDR2L

<400> SEQUENCE: 341

gctgcatcc 9

<210> SEQ ID NO 342
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 7D2_f4 CDR2L

<400> SEQUENCE: 342

ggtgcatcc 9

<210> SEQ ID NO 343
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 9C5_f4 CDR2L

<400> SEQUENCE: 343

actacatcc 9

<210> SEQ ID NO 344
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 10A3_f4 CDR2L

<400> SEQUENCE: 344

gctgcatcc 9

<210> SEQ ID NO 345
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 14G5_f4 CDR2L

<400> SEQUENCE: 345

ggtgcatcc 9

<210> SEQ ID NO 346
<211> LENGTH: 9
<212> TYPE: DNA
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 13A12_f3 CDR2L

<400> SEQUENCE: 346

ggtgcatcc 9

<210> SEQ ID NO 347
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 5B6_f3 CDR2L

<400> SEQUENCE: 347

gctgcatcc 9

<210> SEQ ID NO 348
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 2G6_f4 CDR2L

<400> SEQUENCE: 348

gctgcatcc 9

<210> SEQ ID NO 349
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 1C12_f3 CDR3L

<400> SEQUENCE: 349

cagcagtata ataactcacc gatcacc 27

<210> SEQ ID NO 350
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 1D5_f3 CDR3L

<400> SEQUENCE: 350

cagcagtttg gtagctcacc gatcacc 27

<210> SEQ ID NO 351
<211> LENGTH: 27
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 1D10_f3 CDR3L

<400> SEQUENCE: 351

cagcagtata atagctcacc gatcacc 27

<210> SEQ ID NO 352
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 1E2_f3 CDR3L

<400> SEQUENCE: 352

cagcagtatg gtagctcacc gatcacc 27

<210> SEQ ID NO 353
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 1G9_f3 CDR3L

<400> SEQUENCE: 353

cagcagtatg gtagctcacc gatcacc 27

<210> SEQ ID NO 354
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 5D7_f3 CDR3L

<400> SEQUENCE: 354

cagcagtata atatctcacc gatcacc 27

<210> SEQ ID NO 355
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 5H12_f3 CDR3L

<400> SEQUENCE: 355

cagcagtata atttctcacc gatcacc 27

<210> SEQ ID NO 356
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

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<220> FEATURE:
<223> OTHER INFORMATION: 7C10_f3 CDR3L

<400> SEQUENCE: 356

cagcagtttg gtagctcacc gatcacc 27

<210> SEQ ID NO 357
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<400> SEQUENCE: 357

cagcagtttg gtagctcacc gatcacc 27

<210> SEQ ID NO 358
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 9C6_f3 CDR3L

<400> SEQUENCE: 358

cagcagtata atagctcacc gatcacc 27

<210> SEQ ID NO 359
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<400> SEQUENCE: 359

caacagctta atagttaccc tccgtccact 30

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 11D5_f3 CDR3L

<400> SEQUENCE: 360

caacagctta atagttaccc tccgtccact 30

<210> SEQ ID NO 361
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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<223> OTHER INFORMATION: 11G2_f3 CDR3L

<400> SEQUENCE: 361

cagcagtttg gtagctcacc gatcacc 27

<210> SEQ ID NO 362
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 11G7_f2 CDR3L

<400> SEQUENCE: 362

atgcaagctc tacaaactcc tctcact 27

<210> SEQ ID NO 363
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 16C5_f3 CDR3L

<400> SEQUENCE: 363

cagcagtata ataactcacc gatcacc 27

<210> SEQ ID NO 364
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 16C12_f3 CDR3L

<400> SEQUENCE: 364

cagcagtatg gtagctcacc gatcacc 27

<210> SEQ ID NO 365
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 17A8_f3 CDR3L

<400> SEQUENCE: 365

cagcagtatg gtagctcacc gatcacc 27

<210> SEQ ID NO 366
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 17F2_f3 CDR3L

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<400> SEQUENCE: 366

cagcagtata atagctcacc gatcacc 27

<210> SEQ ID NO 367
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 18E7_f3 CDR3L

<400> SEQUENCE: 367

cagcagtatg gtagctcacc gatcacc 27

<210> SEQ ID NO 368
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 19C4_f3 CDR3L

<400> SEQUENCE: 368

caacagctta atagtttccc tccgtccact 30

<210> SEQ ID NO 369
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 2C1_f4 CDR3L

<400> SEQUENCE: 369

cagcagtata ataactggtg gacg 24

<210> SEQ ID NO 370
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 4E3_f4 CDR3L

<400> SEQUENCE: 370

caacagagtt acattacccc tccgacg 27

<210> SEQ ID NO 371
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
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<400> SEQUENCE: 371

cagcagtata ataactggcc ccct 24

<210> SEQ ID NO 372
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 9C5_f4 CDR3L

<400> SEQUENCE: 372

caacagagtt acattacccc tccgacg 27

<210> SEQ ID NO 373
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 10A3_f4 CDR3L

<400> SEQUENCE: 373

caacagagtt acattacccc tccgacg 27

<210> SEQ ID NO 374
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 14G5_f4 CDR3L

<400> SEQUENCE: 374

cagcagtata ataactggcc tccgact 27

<210> SEQ ID NO 375
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 13A12_f3 CDR3L

<400> SEQUENCE: 375

cagcagtatg ataactggcc tctcact 27

<210> SEQ ID NO 376
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 5B6_f3 CDR3L

<400> SEQUENCE: 376

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caaaagtata acagtgcccc tcacact 27

<210> SEQ ID NO 377
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
<220> FEATURE:
<223> OTHER INFORMATION: 2G6_f4 CDR3L

<400> SEQUENCE: 377

caacagctta atagttaccc gctcact 27

<210> SEQ ID NO 378
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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
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<400> SEQUENCE: 378

Gln Ser Val Arg Ser Ser His
1 5

<210> SEQ ID NO 379
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 1D5_f3 CDR1L

<400> SEQUENCE: 379

Gln Ser Val Arg Ser Ser His
1 5

<210> SEQ ID NO 380
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 1D10_f3 CDR1L

<400> SEQUENCE: 380

Gln Ser Val Ser Ser Ser His
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<210> SEQ ID NO 381
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 1E2_f3 CDR1L

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<400> SEQUENCE: 381

Gln Ser Val Arg Ser Ser His
1 5

<210> SEQ ID NO 382
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 1G9_f3 CDR1L

<400> SEQUENCE: 382

Gln Ser Val Arg Ser Ser His
1 5

<210> SEQ ID NO 383
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 5D7_f3 CDR1L

<400> SEQUENCE: 383

Gln Ser Val Arg Ser Ser His
1 5

<210> SEQ ID NO 384
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 5H12_f3 CDR1L

<400> SEQUENCE: 384

Gln Ser Val Arg Ser Ser His
1 5

<210> SEQ ID NO 385
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 7C10_f3 CDR1L

<400> SEQUENCE: 385

Gln Ser Val Arg Ser Ser His
1 5

<210> SEQ ID NO 386
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 8H4_f3 CDR1L

<400> SEQUENCE: 386

Gln Ser Val Arg Ser Ser His
1 5

<210> SEQ ID NO 387
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 9C6_f3 CDR1L

<400> SEQUENCE: 387

Gln Ser Val Arg Ser Ser His
1 5

<210> SEQ ID NO 388
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 10D6_f3 CDR1L

<400> SEQUENCE: 388

Gln Gly Ile Ser Ser Tyr
1 5

<210> SEQ ID NO 389
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 11D5_f3 CDR1L

<400> SEQUENCE: 389

Gln Gly Ile Ser Ser Tyr
1 5

<210> SEQ ID NO 390
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 11G2_f3 CDR1L

<400> SEQUENCE: 390

Gln Ser Val Arg Asn Ser His
1 5

<210> SEQ ID NO 391

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<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 11G7_f2 CDR1L

<400> SEQUENCE: 391

Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr
1 5 10

<210> SEQ ID NO 392
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 16C5_f3 CDR1L

<400> SEQUENCE: 392

Gln Ser Val Arg Ser Ser His
1 5

<210> SEQ ID NO 393
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 16C12_f3 CDR1L

<400> SEQUENCE: 393

Gln Ser Val Arg Ser Ser His
1 5

<210> SEQ ID NO 394
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 17A8_f3 CDR1L

<400> SEQUENCE: 394

Gln Ser Val Arg Ser Ser His
1 5

<210> SEQ ID NO 395
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 17F2_f3 CDR1L

<400> SEQUENCE: 395

Gln Ser Val Arg Ser Ser His

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1 5

<210> SEQ ID NO 396
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 18E7_f3 CDR1L

<400> SEQUENCE: 396

Gln Ser Val Arg Ser Ser His
1 5

<210> SEQ ID NO 397
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 19C4_f3 CDR1L

<400> SEQUENCE: 397

Gln Gly Ile Ser Ser Tyr
1 5

<210> SEQ ID NO 398
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 2C1_f4 CDR1L

<400> SEQUENCE: 398

Gln Ser Val Ser Ile Asn
1 5

<210> SEQ ID NO 399
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 4E3_f4 CDR1L

<400> SEQUENCE: 399

Gln Ser Ile His Ser Phe
1 5

<210> SEQ ID NO 400
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 7D2_f4 CDR1L

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<400> SEQUENCE: 400

Gln Ser Val Ser Ser Asn
1 5

<210> SEQ ID NO 401
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 9C5_f4 CDR1L

<400> SEQUENCE: 401

Gln Ser Ile His Ser Phe
1 5

<210> SEQ ID NO 402
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 10A3_f4 CDR1L

<400> SEQUENCE: 402

Gln Ser Ile His Ser Phe
1 5

<210> SEQ ID NO 403
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 14G5_f4 CDR1L

<400> SEQUENCE: 403

Gln Ser Val Ser Ser Asn
1 5

<210> SEQ ID NO 404
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 13A12_f3 CDR1L

<400> SEQUENCE: 404

Gln Ser Val Ser Ser Asn
1 5

<210> SEQ ID NO 405
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 5B6_f3 CDR1L

<400> SEQUENCE: 405

Gln Gly Ile Ser Asn Tyr
1 5

<210> SEQ ID NO 406
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 2G6_f4 CDR1L

<400> SEQUENCE: 406

Gln Gly Ile Ser Ser Tyr
1 5

<210> SEQ ID NO 407
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 1C12_f3 CDR3L

<400> SEQUENCE: 407

Gln Gln Tyr Asn Asn Ser Pro Ile Thr
1 5

<210> SEQ ID NO 408
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 1D5_f3 CDR3L

<400> SEQUENCE: 408

Gln Gln Phe Gly Ser Ser Pro Ile Thr
1 5

<210> SEQ ID NO 409
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 1D10_f3 CDR3L

<400> SEQUENCE: 409

Gln Gln Tyr Asn Ser Ser Pro Ile Thr
1 5

<210> SEQ ID NO 410

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<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 1E2_f3 CDR3L

<400> SEQUENCE: 410

Gln Gln Tyr Gly Ser Ser Pro Ile Thr
1 5

<210> SEQ ID NO 411
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 1G9_f3 CDR3L

<400> SEQUENCE: 411

Gln Gln Tyr Gly Ser Ser Pro Ile Thr
1 5

<210> SEQ ID NO 412
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 5D7_f3 CDR3L

<400> SEQUENCE: 412

Gln Gln Tyr Asn Ile Ser Pro Ile Thr
1 5

<210> SEQ ID NO 413
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 5H12_f3 CDR3L

<400> SEQUENCE: 413

Gln Gln Tyr Asn Phe Ser Pro Ile Thr
1 5

<210> SEQ ID NO 414
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 7C10_f3 CDR3L

<400> SEQUENCE: 414

Gln Gln Phe Gly Ser Ser Pro Ile Thr

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1 5

<210> SEQ ID NO 415
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 8H4_f3 CDR3L

<400> SEQUENCE: 415

Gln Gln Phe Gly Ser Ser Pro Ile Thr
1 5

<210> SEQ ID NO 416
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 9C6_f3 CDR3L

<400> SEQUENCE: 416

Gln Gln Tyr Asn Ser Ser Pro Ile Thr
1 5

<210> SEQ ID NO 417
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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 10D6_f3 CDR3L

<400> SEQUENCE: 417

Gln Gln Leu Asn Ser Tyr Pro Pro Ser Thr
1 5 10

<210> SEQ ID NO 418
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 11D5_f3 CDR3L

<400> SEQUENCE: 418

Gln Gln Leu Asn Ser Tyr Pro Pro Ser Thr
1 5 10

<210> SEQ ID NO 419
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 11G2_f3 CDR3L

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<400> SEQUENCE: 419

Gln Gln Phe Gly Ser Ser Pro Ile Thr
1 5

<210> SEQ ID NO 420
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 11G7_f2 CDR3L

<400> SEQUENCE: 420

Met Gln Ala Leu Gln Thr Pro Leu Thr
1 5

<210> SEQ ID NO 421
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 16C5_f3 CDR3L

<400> SEQUENCE: 421

Gln Gln Tyr Asn Asn Ser Pro Ile Thr
1 5

<210> SEQ ID NO 422
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 16C12_f3 CDR3L

<400> SEQUENCE: 422

Gln Gln Tyr Gly Ser Ser Pro Ile Thr
1 5

<210> SEQ ID NO 423
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 17A8_f3 CDR3L

<400> SEQUENCE: 423

Gln Gln Tyr Gly Ser Ser Pro Ile Thr
1 5

<210> SEQ ID NO 424
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 17F2_f3 CDR3L

<400> SEQUENCE: 424

Gln Gln Tyr Asn Ser Ser Pro Ile Thr
1 5

<210> SEQ ID NO 425
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 18E7_f3 CDR3L

<400> SEQUENCE: 425

Gln Gln Tyr Gly Ser Ser Pro Ile Thr
1 5

<210> SEQ ID NO 426
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 19C4_f3 CDR3L

<400> SEQUENCE: 426

Gln Gln Leu Asn Ser Phe Pro Pro Ser Thr
1 5 10

<210> SEQ ID NO 427
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 2C1_f4 CDR3L

<400> SEQUENCE: 427

Gln Gln Tyr Asn Asn Trp Trp Thr
1 5

<210> SEQ ID NO 428
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 4E3_f4 CDR3L

<400> SEQUENCE: 428

Gln Gln Ser Tyr Ile Thr Pro Pro Thr
1 5

<210> SEQ ID NO 429

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<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 7D2_f4 CDR3L

<400> SEQUENCE: 429

Gln Gln Tyr Asn Asn Trp Pro Pro
1 5

<210> SEQ ID NO 430
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 9C5_f4 CDR3L

<400> SEQUENCE: 430

Gln Gln Ser Tyr Ile Thr Pro Pro Thr
1 5

<210> SEQ ID NO 431
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 10A3_f4 CDR3L

<400> SEQUENCE: 431

Gln Gln Ser Tyr Ile Thr Pro Pro Thr
1 5

<210> SEQ ID NO 432
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
<220> FEATURE:
<223> OTHER INFORMATION: 14G5_f4 CDR3L

<400> SEQUENCE: 432

Gln Gln Tyr Asn Asn Trp Pro Pro Thr
1 5

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Gln Gln Tyr Asp Asn Trp Pro Leu Thr

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Gln Lys Tyr Asn Ser Ala Pro His Thr
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<210> SEQ ID NO 435
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Gln Gln Leu Asn Ser Tyr Pro Leu Thr
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1. An isolated antibody or antigen-binding fragment thereof that binds to SARS-CoV-2 spike protein, wherein the antibody or antigen-binding fragment thereof comprises a variable heavy chain region comprising a CDR1H, a CDR2H, and a CDR3H, and a variable light chain region comprising a CDR1L, a CDR2L, and a CDR3L, wherein:

a) CDR1H comprises SEQ ID NO:204, CDR2H comprises SEQ ID NO:233, CDR3H comprises SEQ ID NO:262, CDR1L comprises SEQ ID NO:378, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:407;

b) CDR1H comprises SEQ ID NO:205, CDR2H comprises SEQ ID NO:234, CDR3H comprises SEQ ID NO:263, CDR1L comprises SEQ ID NO:379, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:408;

c) CDR1H comprises SEQ ID NO:206, CDR2H comprises SEQ ID NO:235, CDR3H comprises SEQ ID NO:264, CDR1L comprises SEQ ID NO:380, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:409;

d) CDR1H comprises SEQ ID NO:207, CDR2H comprises SEQ ID NO:236, CDR3H comprises SEQ ID NO:265, CDR1L comprises SEQ ID NO:381, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:410;

e) CDR1H comprises SEQ ID NO:208, CDR2H comprises SEQ ID NO:237, CDR3H comprises SEQ ID NO:266, CDR1L comprises SEQ ID NO:382, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:411;

f) CDR1H comprises SEQ ID NO:209, CDR2H comprises SEQ ID NO:238, CDR3H comprises SEQ ID NO:267, CDR1L comprises SEQ ID NO:383, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:412;

g) CDR1H comprises SEQ ID NO:210, CDR2H comprises SEQ ID NO:239, CDR3H comprises SEQ ID NO:268, CDR1L comprises SEQ ID NO:384, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:413;

h) CDR1H comprises SEQ ID NO:211, CDR2H comprises SEQ ID NO:240, CDR3H comprises SEQ ID NO:269, CDR1L comprises SEQ ID NO:385, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:414;

i) CDR1H comprises SEQ ID NO:212, CDR2H comprises SEQ ID NO:241, CDR3H comprises SEQ ID NO:270, CDR1L comprises SEQ ID NO:386, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:415;

j) CDR1H comprises SEQ ID NO:213, CDR2H comprises SEQ ID NO:242, CDR3H comprises SEQ ID NO:271, CDR1L comprises SEQ ID NO:387, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:416;

k) CDR1H comprises SEQ ID NO:214, CDR2H comprises SEQ ID NO:243, CDR3H comprises SEQ ID NO:272, CDR1L comprises SEQ ID NO:388, CDR2L comprises sequence AAS, and CDR3L comprises SEQ ID NO:417;

l) CDR1H comprises SEQ ID NO:215, CDR2H comprises SEQ ID NO:244, CDR3H comprises SEQ ID NO:273, CDR1L comprises SEQ ID NO:389, CDR2L comprises sequence AAS, and CDR3L comprises SEQ ID NO:418;

m) CDR1H comprises SEQ ID NO:216, CDR2H comprises SEQ ID NO:245, CDR3H comprises SEQ ID NO:274, CDR1L comprises SEQ ID NO:390, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:419;

n) CDR1H comprises SEQ ID NO:217, CDR2H comprises SEQ ID NO:246, CDR3H comprises SEQ ID NO:275, CDR1L comprises SEQ ID NO:391, CDR2L comprises sequence LGS, and CDR3L comprises SEQ ID NO:420;

o) CDR1H comprises SEQ ID NO:218, CDR2H comprises SEQ ID NO:247, CDR3H comprises SEQ ID NO:276, CDR1L comprises SEQ ID NO:392, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:421;

p) CDR1H comprises SEQ ID NO:219, CDR2H comprises SEQ ID NO:248, CDR3H comprises SEQ ID NO:277, CDR1L comprises SEQ ID NO:393, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:422;

q) CDR1H comprises SEQ ID NO:220, CDR2H comprises SEQ ID NO:249, CDR3H comprises SEQ ID NO:278, CDR1L comprises SEQ ID NO:394, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:423;

r) CDR1H comprises SEQ ID NO:221, CDR2H comprises SEQ ID NO:250, CDR3H comprises SEQ ID NO:279, CDR1L comprises SEQ ID NO:395, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:424;

s) CDR1H comprises SEQ ID NO:222, CDR2H comprises SEQ ID NO:251, CDR3H comprises SEQ ID NO:280, CDR1L comprises SEQ ID NO:396, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:425;

t) CDR1H comprises SEQ ID NO:223, CDR2H comprises SEQ ID NO:252, CDR3H comprises SEQ ID NO:281, CDR1L comprises SEQ ID NO:397, CDR2L comprises sequence AAS, and CDR3L comprises SEQ ID NO:426;

u) CDR1H comprises SEQ ID NO:224, CDR2H comprises SEQ ID NO:253, CDR3H comprises SEQ ID NO:282, CDR1L comprises SEQ ID NO:398, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:427;

v) CDR1H comprises SEQ ID NO:225, CDR2H comprises SEQ ID NO:254, CDR3H comprises SEQ ID NO:283, CDR1L comprises SEQ ID NO:399, CDR2L comprises sequence AAS, and CDR3L comprises SEQ ID NO:428;

w) CDR1H comprises SEQ ID NO:226, CDR2H comprises SEQ ID NO:255, CDR3H comprises SEQ ID NO:284, CDR1L comprises SEQ ID NO:400, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:429;

x) CDR1H comprises SEQ ID NO:227, CDR2H comprises SEQ ID NO:256, CDR3H comprises SEQ ID NO:285, CDR1L comprises SEQ ID NO:401, CDR2L comprises sequence TTS, and CDR3L comprises SEQ ID NO:430;

y) CDR1H comprises SEQ ID NO:228, CDR2H comprises SEQ ID NO:257, CDR3H comprises SEQ ID NO:286, CDR1L comprises SEQ ID NO:402, CDR2L comprises sequence AAS, and CDR3L comprises SEQ ID NO:431;

z) CDR1H comprises SEQ ID NO:229, CDR2H comprises SEQ ID NO:258, CDR3H comprises SEQ ID NO:287, CDR1L comprises SEQ ID NO:403, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:432;

aa) CDR1H comprises SEQ ID NO:230, CDR2H comprises SEQ ID NO:259, CDR3H comprises SEQ ID NO:288, CDR1L comprises SEQ ID NO:404, CDR2L comprises sequence GAS, and CDR3L comprises SEQ ID NO:433;

bb) CDR1H comprises SEQ ID NO:231, CDR2H comprises SEQ ID NO:260, CDR3H comprises SEQ ID NO:289, CDR1L comprises SEQ ID NO:405, CDR2L comprises sequence AAS, and CDR3L comprises SEQ ID NO:434; or

cc) CDR1H comprises SEQ ID NO:232, CDR2H comprises SEQ ID NO:261, CDR3H comprises SEQ ID NO:290, CDR1L comprises SEQ ID NO:406, CDR2L comprises sequence AAS, and CDR3L comprises SEQ ID NO:435.

2. The antibody or antigen-binding fragment thereof of claim **1**, wherein:

a) the variable heavy chain region comprises a sequence that is at least 90% identical to SEQ ID NO:59 and the variable light chain region comprises a sequence that is at least 90% identical to SEQ ID NO:88;

b) the variable heavy chain region comprises a sequence that is at least 90% identical to SEQ ID NO:60 and the variable light chain region comprises a sequence that is at least 90% identical to SEQ ID NO:89;

c) the variable heavy chain region comprises a sequence that is at least 90% identical to SEQ ID NO:61 and the variable light chain region comprises a sequence that is at least 90% identical to SEQ ID NO:90;

d) the variable heavy chain region comprises a sequence that is at least 90% identical to SEQ ID NO:62 and the variable light chain region comprises a sequence that is at least 90% identical to SEQ ID NO:91;

e) the variable heavy chain region comprises a sequence that is at least 90% identical to SEQ ID NO:63 and the variable light chain region comprises a sequence that is at least 90% identical to SEQ ID NO:92;

f) the variable heavy chain region comprises a sequence that is at least 90% identical to SEQ ID NO:64 and the variable light chain region comprises a sequence that is at least 90% identical to SEQ ID NO:93;

g) the variable heavy chain region comprises a sequence that is at least 90% identical to SEQ ID NO:65 and the variable light chain region comprises a sequence that is at least 90% identical to SEQ ID NO:94;

h) the variable heavy chain region comprises a sequence that is at least 90% identical to SEQ ID NO:66 and the variable light chain region comprises a sequence that is at least 90% identical to SEQ ID NO:95;

i) the variable heavy chain region comprises a sequence that is at least 90% identical to SEQ ID NO:67 and the variable light chain region comprises a sequence that is at least 90% identical to SEQ ID NO:96;

j) the variable heavy chain region comprises a sequence that is at least 90% identical to SEQ ID NO:68 and the

variable light chain region comprises a sequence that is at least 90% identical to SEQ ID NO:97;

k) the variable heavy chain region comprises a sequence that is at least 90% identical to SEQ ID NO:69 and the variable light chain region comprises a sequence that is at least 90% identical to SEQ ID NO:98;

l) the variable heavy chain region comprises a sequence that is at least 90% identical to SEQ ID NO:70 and the variable light chain region comprises a sequence that is at least 90% identical to SEQ ID NO:99;

m) the variable heavy chain region comprises a sequence that is at least 90% identical to SEQ ID NO:71 and the variable light chain region comprises a sequence that is at least 90% identical to SEQ ID NO:100;

n) the variable heavy chain region comprises a sequence that is at least 90% identical to SEQ ID NO:72 and the variable light chain region comprises a sequence that is at least 90% identical to SEQ ID NO:101;

o) the variable heavy chain region comprises a sequence that is at least 90% identical to SEQ ID NO:73 and the variable light chain region comprises a sequence that is at least 90% identical to SEQ ID NO:102;

p) the variable heavy chain region comprises a sequence that is at least 90% identical to SEQ ID NO:74 and the variable light chain region comprises a sequence that is at least 90% identical to SEQ ID NO:103;

q) the variable heavy chain region comprises a sequence that is at least 90% identical to SEQ ID NO:75 and the variable light chain region comprises a sequence that is at least 90% identical to SEQ ID NO:104;

r) the variable heavy chain region comprises a sequence that is at least 90% identical to SEQ ID NO:76 and the variable light chain region comprises a sequence that is at least 90% identical to SEQ ID NO:105;

s) the variable heavy chain region comprises a sequence that is at least 90% identical to SEQ ID NO:77 and the variable light chain region comprises a sequence that is at least 90% identical to SEQ ID NO:106;

t) the variable heavy chain region comprises a sequence that is at least 90% identical to SEQ ID NO:78 and the variable light chain region comprises a sequence that is at least 90% identical to SEQ ID NO:107;

u) the variable heavy chain region comprises a sequence that is at least 90% identical to SEQ ID NO:79 and the variable light chain region comprises a sequence that is at least 90% identical to SEQ ID NO:108;

v) the variable heavy chain region comprises a sequence that is at least 90% identical to SEQ ID NO:80 and the variable light chain region comprises a sequence that is at least 90% identical to SEQ ID NO:109;

w) the variable heavy chain region comprises a sequence that is at least 90% identical to SEQ ID NO:81 and the variable light chain region comprises a sequence that is at least 90% identical to SEQ ID NO:110;

x) the variable heavy chain region comprises a sequence that is at least 90% identical to SEQ ID NO:82 and the variable light chain region comprises a sequence that is at least 90% identical to SEQ ID NO:111;

y) the variable heavy chain region comprises a sequence that is at least 90% identical to SEQ ID NO:83 and the variable light chain region comprises a sequence that is at least 90% identical to SEQ ID NO:112;

z) the variable heavy chain region comprises a sequence that is at least 90% identical to SEQ ID NO:84 and the variable light chain region comprises a sequence that is at least 90% identical to SEQ ID NO:113;

aa) the variable heavy chain region comprises a sequence that is at least 90% identical to SEQ ID NO:85 and the variable light chain region comprises a sequence that is at least 90% identical to SEQ ID NO:114;

bb) the variable heavy chain region comprises a sequence that is at least 90% identical to SEQ ID NO:86 and the variable light chain region comprises a sequence that is at least 90% identical to SEQ ID NO:115; or

cc) the variable heavy chain region comprises a sequence that is at least 90% identical to SEQ ID NO:87 and the variable light chain region comprises a sequence that is at least 90% identical to SEQ ID NO:116.

3. The antibody or antigen-binding fragment thereof of claim **2**, wherein:

a) the variable heavy chain region comprises SEQ ID NO:59 and the variable light chain region comprises SEQ ID NO:88;

b) the variable heavy chain region comprises SEQ ID NO:60 and the variable light chain region comprises SEQ ID NO:89;

c) the variable heavy chain region comprises SEQ ID NO:61 and the variable light chain region comprises SEQ ID NO:90;

d) the variable heavy chain region comprises SEQ ID NO:62 and the variable light chain region comprises SEQ ID NO:91;

e) the variable heavy chain region comprises SEQ ID NO:63 and the variable light chain region comprises SEQ ID NO:92;

f) the variable heavy chain region comprises SEQ ID NO:64 and the variable light chain region comprises SEQ ID NO:93;

g) the variable heavy chain region comprises SEQ ID NO:65 and the variable light chain region comprises SEQ ID NO:94;

h) the variable heavy chain region comprises SEQ ID NO:66 and the variable light chain region comprises SEQ ID NO:95;

i) the variable heavy chain region comprises SEQ ID NO:67 and the variable light chain region comprises SEQ ID NO:96;

j) the variable heavy chain region comprises SEQ ID NO:68 and the variable light chain region comprises SEQ ID NO:97;

k) the variable heavy chain region comprises SEQ ID NO:69 and the variable light chain region comprises SEQ ID NO:98;

l) the variable heavy chain region comprises SEQ ID NO:70 and the variable light chain region comprises SEQ ID NO:99;

m) the variable heavy chain region comprises SEQ ID NO:71 and the variable light chain region comprises SEQ ID NO:100;

n) the variable heavy chain region comprises SEQ ID NO:72 and the variable light chain region comprises SEQ ID NO:101;

o) the variable heavy chain region comprises SEQ ID NO:73 and the variable light chain region comprises SEQ ID NO:102;

p) the variable heavy chain region comprises SEQ ID NO:74 and the variable light chain region comprises SEQ ID NO:103;

q) the variable heavy chain region comprises SEQ ID NO:75 and the variable light chain region comprises SEQ ID NO:104;
r) the variable heavy chain region comprises SEQ ID NO:76 and the variable light chain region comprises SEQ ID NO:105;
s) the variable heavy chain region comprises SEQ ID NO:77 and the variable light chain region comprises SEQ ID NO:106;
t) the variable heavy chain region comprises SEQ ID NO:78 and the variable light chain region comprises SEQ ID NO:107;
u) the variable heavy chain region comprises SEQ ID NO:79 and the variable light chain region comprises SEQ ID NO:108;
v) the variable heavy chain region comprises SEQ ID NO:80 and the variable light chain region comprises SEQ ID NO:109;
w) the variable heavy chain region comprises SEQ ID NO:81 and the variable light chain region comprises SEQ ID NO:110;
x) the variable heavy chain region comprises SEQ ID NO:82 and the variable light chain region comprises SEQ ID NO:111;
y) the variable heavy chain region comprises SEQ ID NO:83 and the variable light chain region comprises SEQ ID NO:112;
z) the variable heavy chain region comprises SEQ ID NO:84 and the variable light chain region comprises SEQ ID NO:113;
aa) the variable heavy chain region comprises SEQ ID NO:85 and the variable light chain region comprises SEQ ID NO:114;
bb) the variable heavy chain region comprises SEQ ID NO:86 and the variable light chain region comprises SEQ ID NO:115; or
cc) the variable heavy chain region comprises SEQ ID NO:87 and the variable light chain region comprises SEQ ID NO:116.

4. The antibody or antigen-binding fragment thereof of claim **1**, wherein the antibody comprises human-derived heavy and light chain constant regions.

5. The antibody or antigen-binding fragment thereof of claim **1**, wherein the antibody is an immunoglobulin comprising two identical heavy chains and two identical light chains.

6. The antibody or antigen-binding fragment thereof of claim **1**, wherein the antibody is a monoclonal antibody.

7. The antibody or antigen-binding fragment thereof of claim **1**, wherein the antigen-binding fragment is a scFv.

8. The antibody or antigen-binding fragment thereof of claim **1**, wherein the antibody is conjugated to a detectable agent or a therapeutic agent.

9. An isolated nucleic acid sequence comprising a nucleotide sequence encoding the antibody or antigen-binding fragment thereof of claim **1**.

10. An expression vector comprising the nucleic acid sequence of claim **9**.

11. The expression vector of claim **10**, wherein the nucleotide sequence is operably linked to one or more regulatory regions.

12. A host cell comprising the nucleic acid sequence of claim **9**.

13. A method for expressing the antibody or antigen-binding fragment thereof of claim **1**, comprising:
a. culturing a host cell comprising a nucleotide sequence encoding the antibody or antigen-binding fragment thereof, and
b. isolating the antibody or antigen-binding fragment thereof from the host cell or cell culture.

14. A method for detecting SARS-CoV-2, comprising:
a. contacting cells or a biological sample with the antibody or antigen-binding fragment thereof of claim **1**; and
b. detecting the binding of the antibody to SARS-CoV-2 spike protein, wherein SARS-CoV-2 is detected if the level of binding of the antibody or antigen-binding fragment thereof to SARS-CoV-2 protein is greater than the level of binding of the antibody or antigen-binding fragment thereof to non-SARS-CoV-2 infected cells or a biological sample not infected with SARS-CoV-2.

15. A pharmaceutical composition comprising the antibody or antigen-binding fragment thereof of claim **1**, and pharmaceutically acceptable carrier.

16. A method for treating SARS-CoV-2 infection or COVID-19 in a subject, comprising administering to the subject an effective amount of the antibody or antigen-binding fragment thereof of any one of claim **1**.

17. The method of claim **16**, wherein the subject is diagnosed with SARS-CoV-2 infection or COVID-19.

18. A method for preventing COVID-19 in a subject, comprising administering to the subject to the subject an effective amount of the antibody or antigen-binding fragment thereof of claim **1**.

19. A method for treating SARS-CoV-2 infection or COVID-19 in a subject, comprising administering to the subject an effective amount of the antibody or antigen-binding fragment thereof of claim **1**.

20. The method of claim **16**, wherein the subject is a human.

21. (canceled)

22. (canceled)

23. (canceled)

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