US 20250263466A1

(19) United States
(12) Patent Application Publication
CORTI et al.
(10) Pub. No.: US 2025/0263466 A1
(43) Pub. Date: Aug. 21, 2025

(54) **ANTIBODIES AGAINST SARS-COV-2 AND METHODS OF USING THE SAME**

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(21) Appl. No.: **17/760,032**

(22) PCT Filed: **Feb. 2, 2021**

(86) PCT No.: **PCT/US2021/016172**

§ 371 (c)(1),
(2) Date: **Aug. 3, 2022**

Related U.S. Application Data

(60) Provisional application No. 62/969,592, filed on Feb. 3, 2020, provisional application No. 62/970,062, filed on Feb. 4, 2020, provisional application No. 62/971,552, filed on Feb. 7, 2020, provisional application No. 62/977,941, filed on Feb. 18, 2020, provisional application No. 63/016,228, filed on Apr. 27, 2020, provisional application No. 63/023,858, filed on May 12, 2020.

Publication Classification

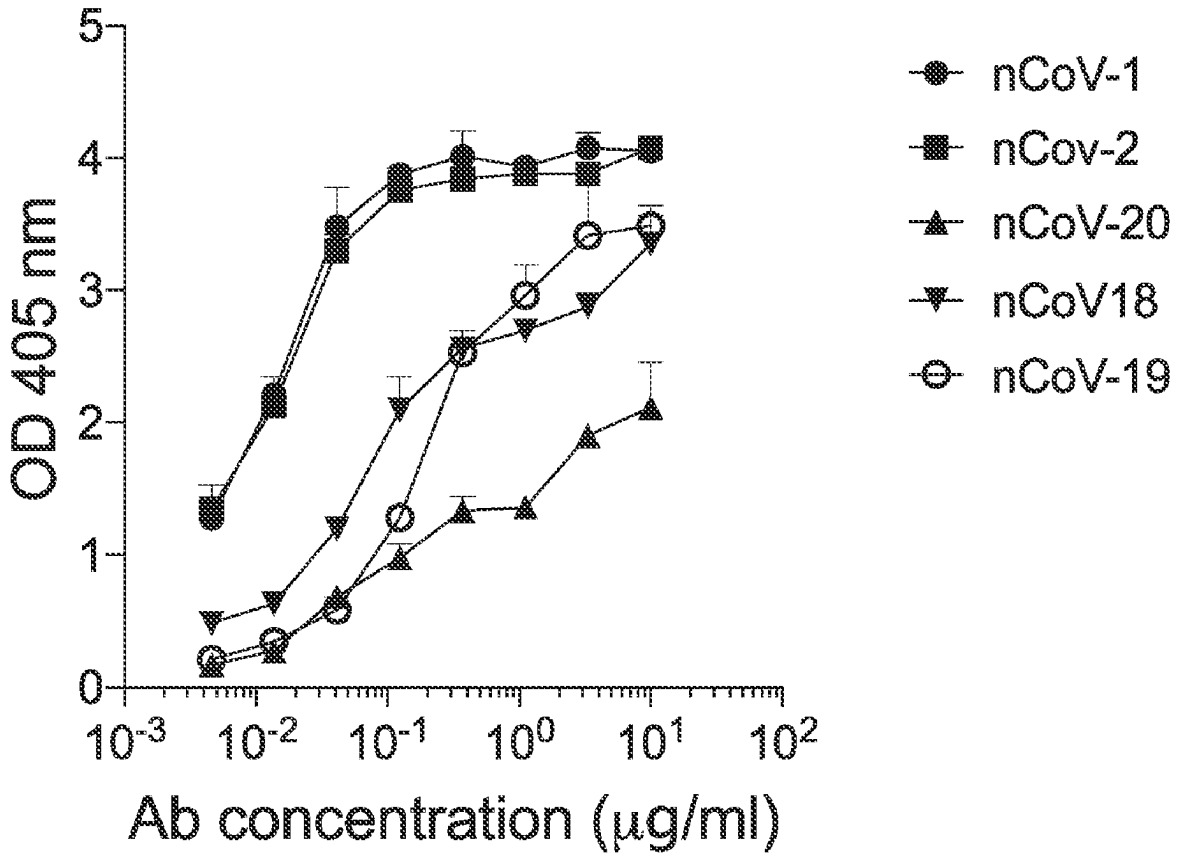
(51) **Int. Cl.**
C07K 16/10 (2006.01)
A61P 31/14 (2006.01)
G01N 33/569 (2006.01)

(52) **U.S. Cl.**
CPC ***C07K 16/1003*** (2023.08); ***A61P 31/14*** (2018.01); ***G01N 33/56983*** (2013.01); *C07K 2317/21* (2013.01); *C07K 2317/24* (2013.01); *C07K 2317/31* (2013.01); *G01N 2333/165* (2013.01); *G01N 2469/10* (2013.01)

(57) **ABSTRACT**

The instant disclosure provides antibodies and antigen-binding fragments thereof that can bind to a SARS-CoV-2 antigen and, in certain embodiments, are capable of neutralizing a SARS-CoV-2 infection in a subject. Also provided are polynucleotides that encode an antibody or antigen-binding fragment, vectors and host cells that comprise a polynucleotide, pharmaceutical compositions, and methods of using the presently disclosed antibodies, antigen-binding fragments, polynucleotides, vectors, host cells, and compositions to treat or diagnose a sarbecovirus and/or SARS-CoV-2 infection.

Specification includes a Sequence Listing.



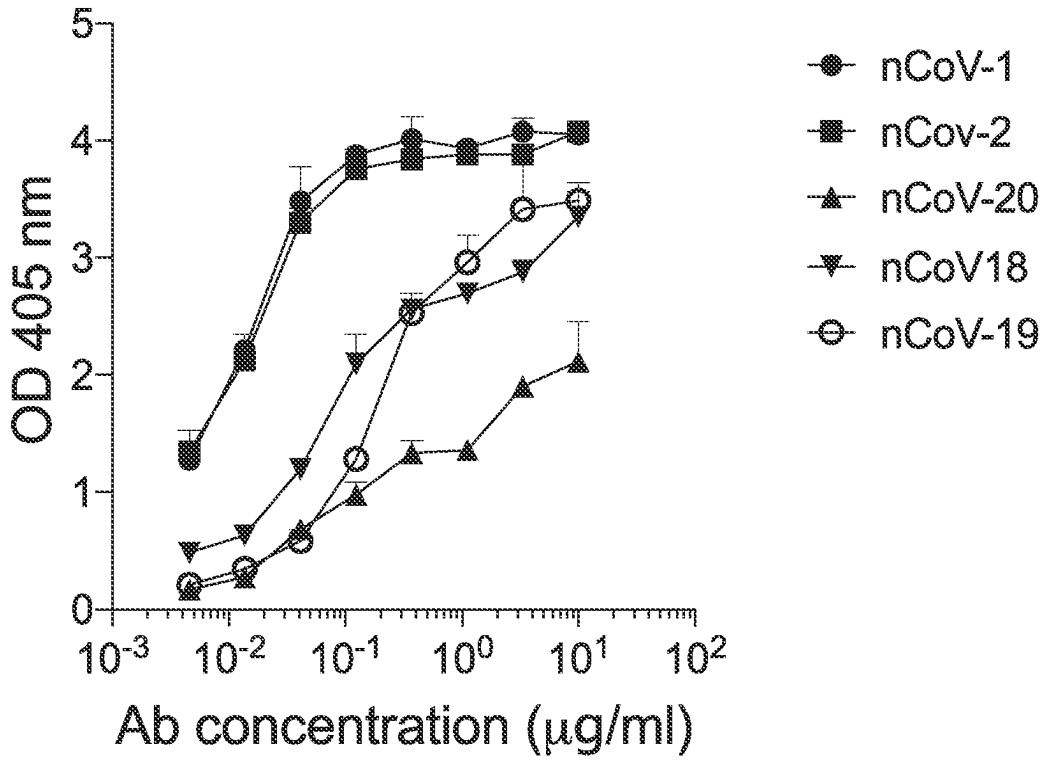

5
4
3
2
1
0
OD 405 nm
10^{-3}
10^{-2}
10^{-1}
10^{0}
10^{1}
10^{2}
Ab concentration (μg/ml)
nCoV-1
nCov-2
nCoV-20
nCoV18
nCoV-19

FIG. 1A

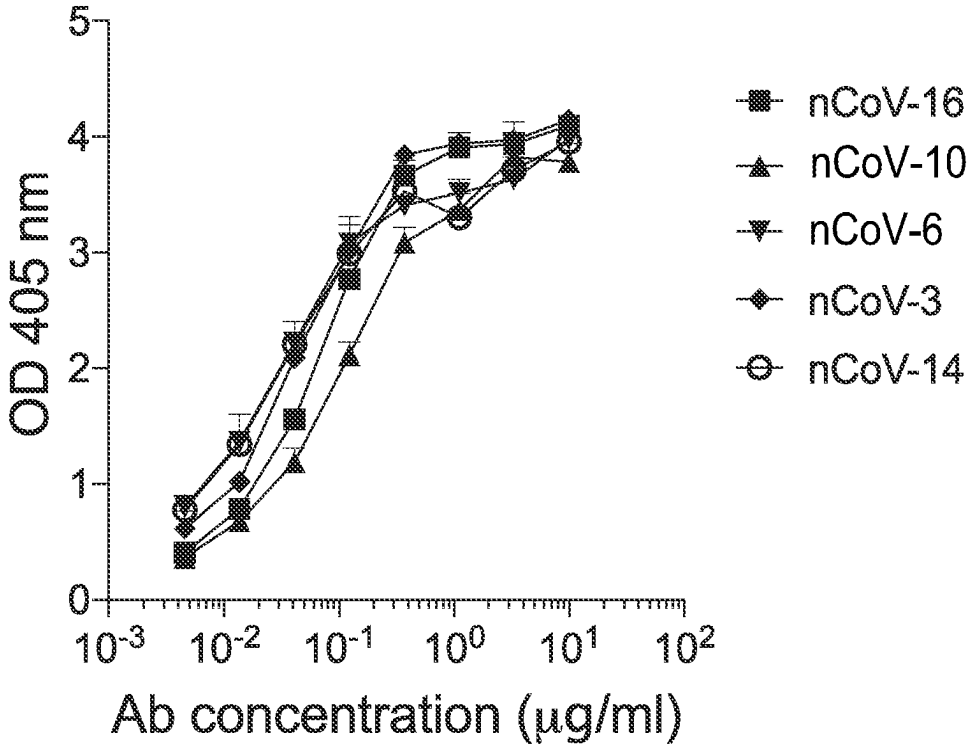

5
4
3
2
1
0
OD 405 nm
10^{-3}
10^{-2}
10^{-1}
10^{0}
10^{1}
10^{2}
Ab concentration (μg/ml)
nCoV-16
nCoV-10
nCoV-6
nCoV-3
nCoV-14

FIG. 1B

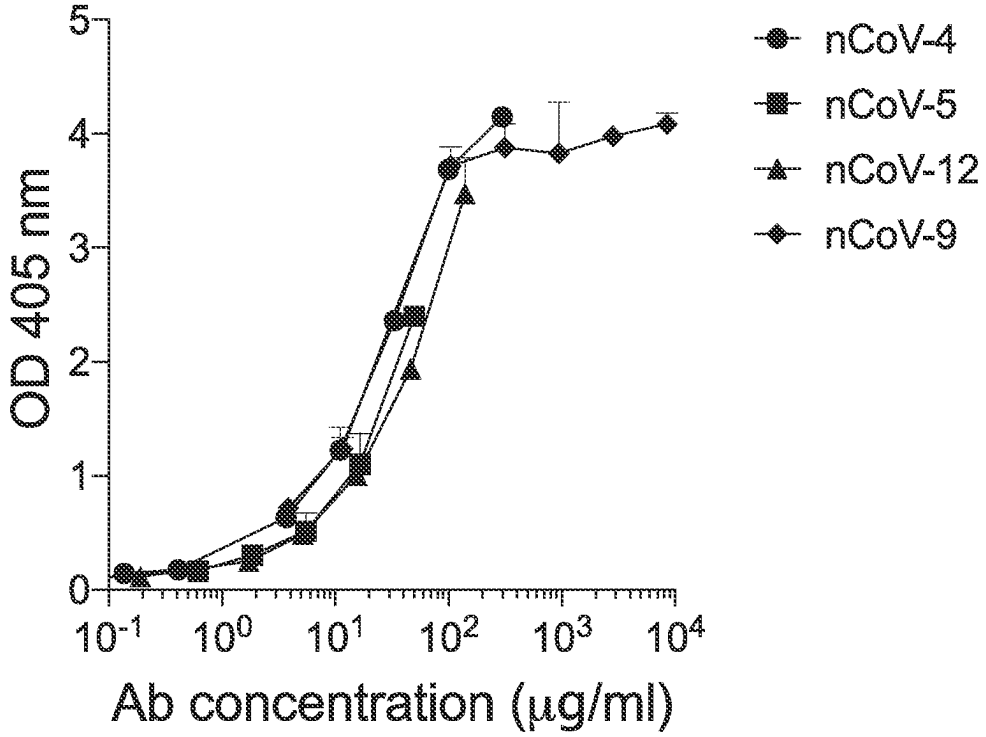

5
4
3
2
1
0
OD 405 nm
10^{-1}
10^{0}
10^{1}
10^{2}
10^{3}
10^{4}
Ab concentration (μg/ml)
nCoV-4
nCoV-5
nCoV-12
nCoV-9

FIG. 1C

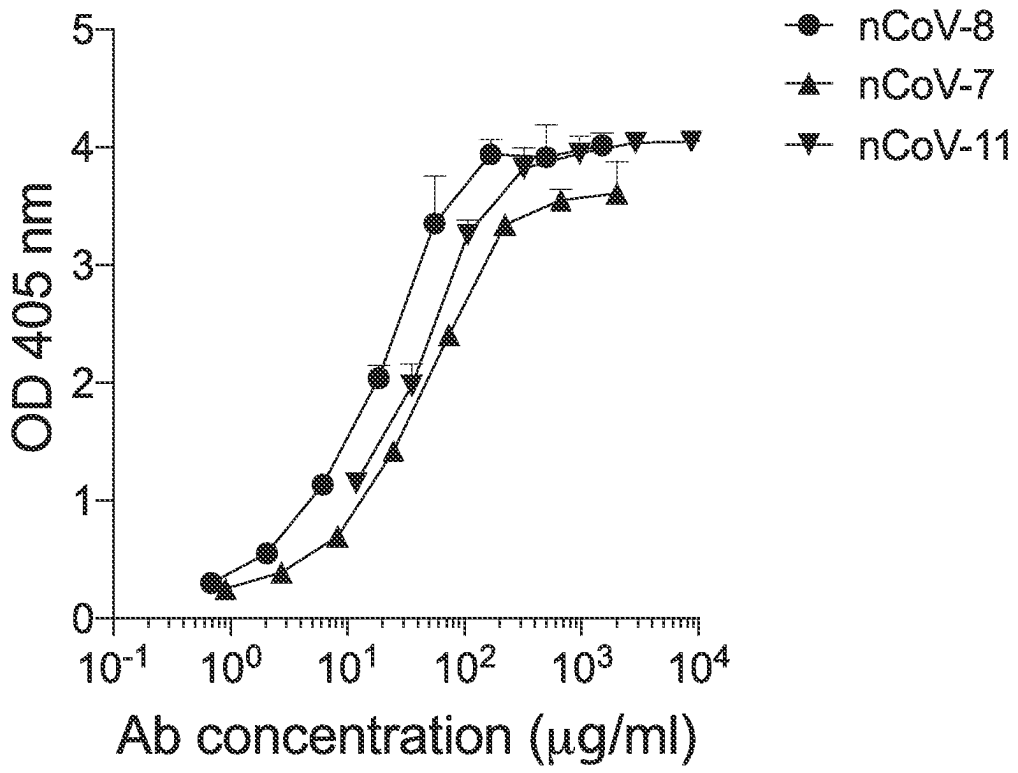

nCoV-8
nCoV-7
nCoV-11
OD 405 nm
0
1
2
3
4
5
10^{-1}
10^{0}
10^{1}
10^{2}
10^{3}
10^{4}
Ab concentration (μg/ml)

FIG. 1D

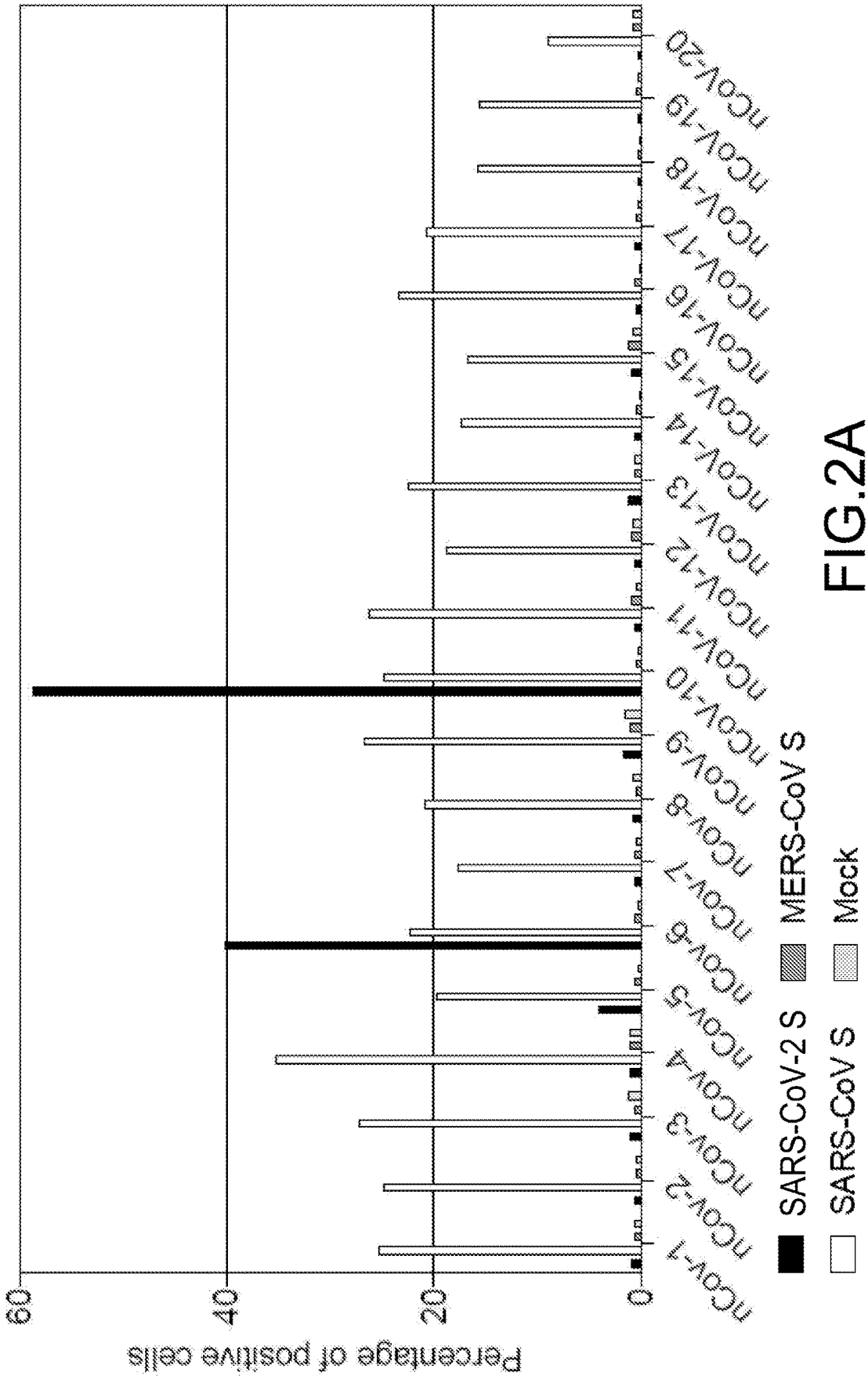

Percentage of positive cells
60
40
20
0
nCoV-1
nCoV-2
nCoV-3
nCoV-4
nCoV-5
nCoV-6
nCoV-7
nCoV-8
nCoV-9
nCoV-10
nCoV-11
nCoV-12
nCoV-13
nCoV-14
nCoV-15
nCoV-16
nCoV-17
nCoV-18
nCoV-19
nCoV-20
SARS-CoV-2 S
MERS-CoV S
SARS-CoV S
Mock

FIG.2A

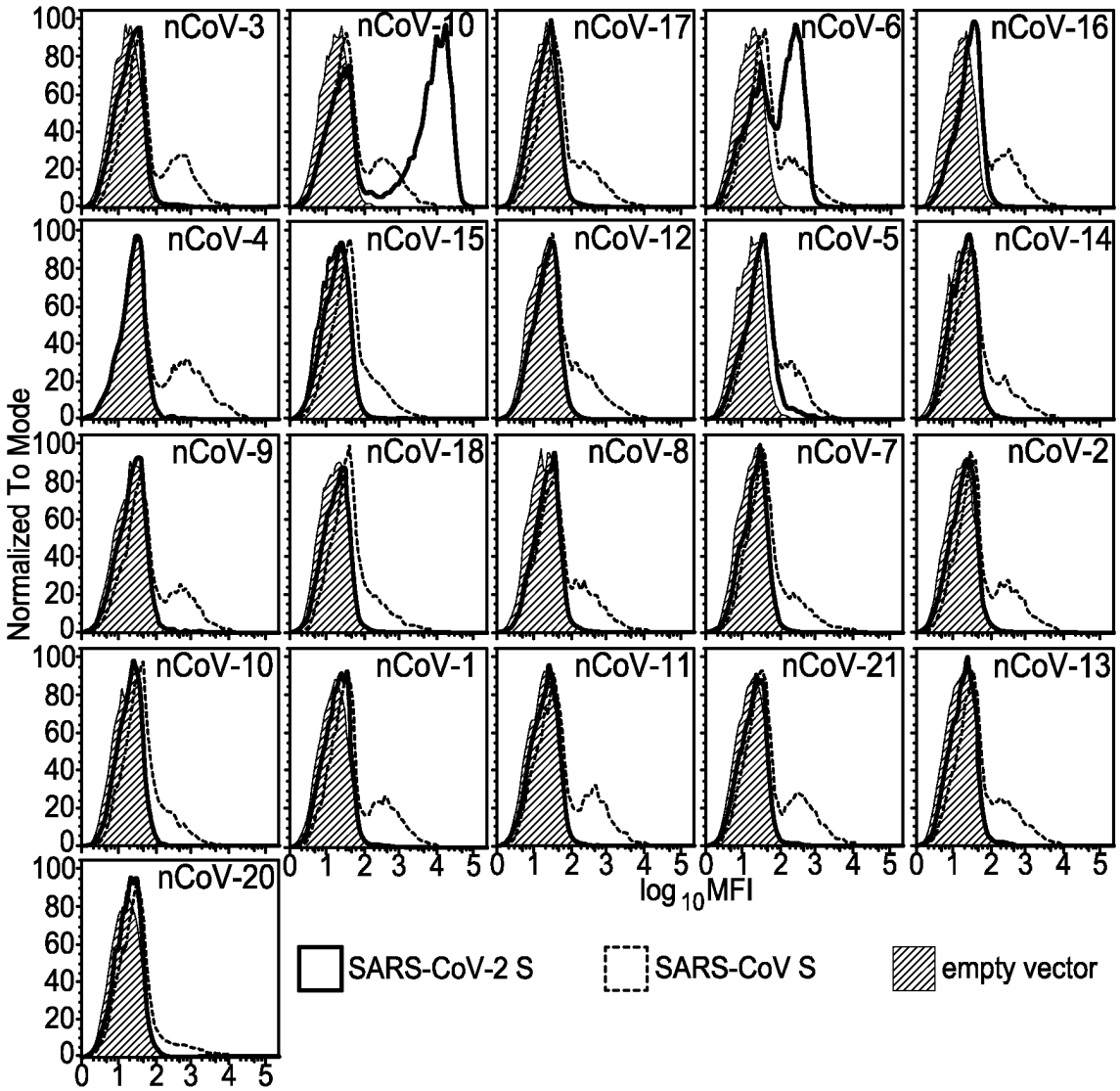

nCoV-3
nCoV-10
nCoV-17
nCoV-6
nCoV-16
nCoV-4
nCoV-15
nCoV-12
nCoV-5
nCoV-14
nCoV-9
nCoV-18
nCoV-8
nCoV-7
nCoV-2
nCoV-10
nCoV-1
nCoV-11
nCoV-21
nCoV-13
nCoV-20
Normalized To Mode
log10MFI
SARS-CoV-2 S
SARS-CoV S
empty vector

FIG. 2B

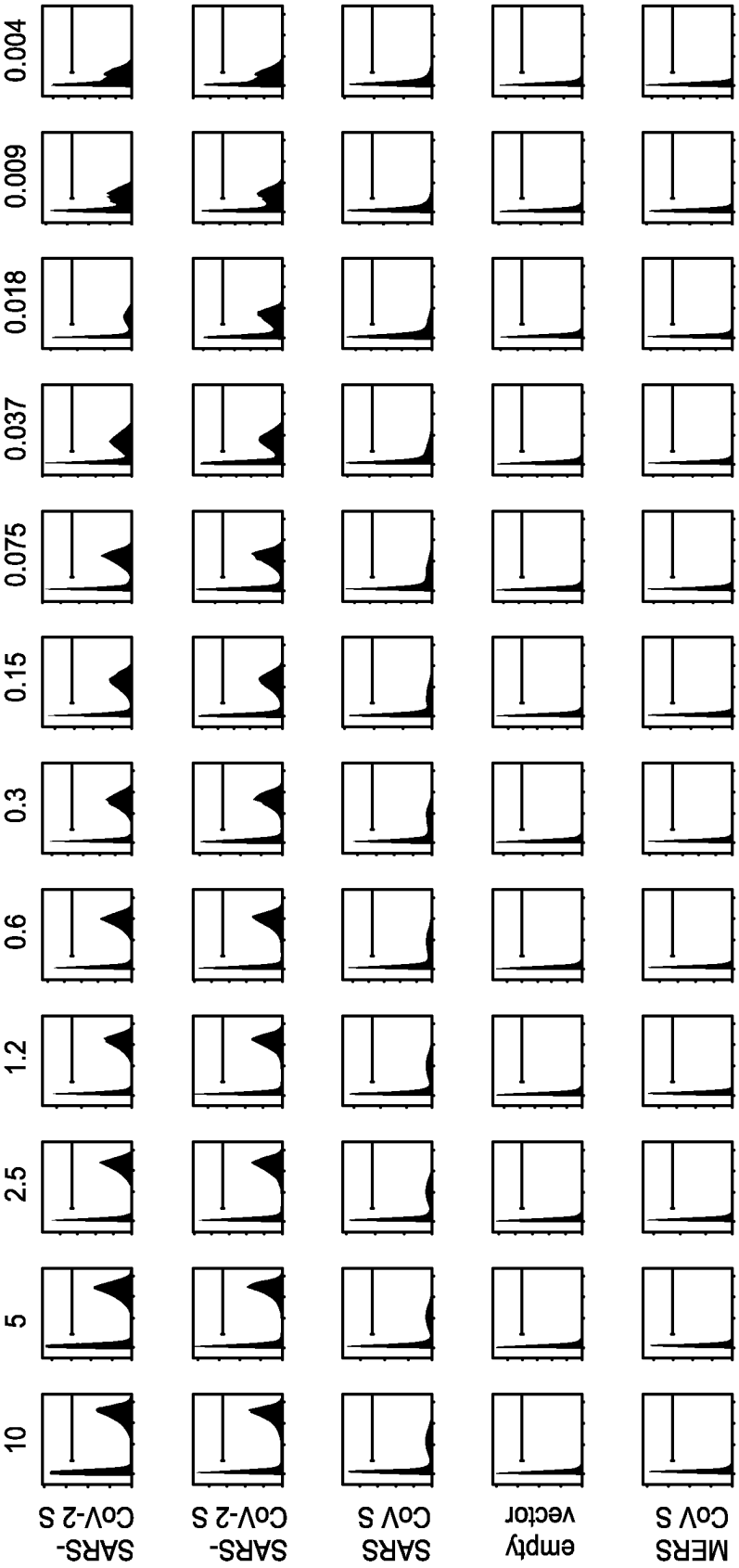

10
5
2.5
1.2
0.6
0.3
0.15
0.075
0.037
0.018
0.009
0.004
SARS-CoV-2 S
SARS-CoV-2 S
SARS CoV S
empty vector
MERS CoV S

FIG. 3A

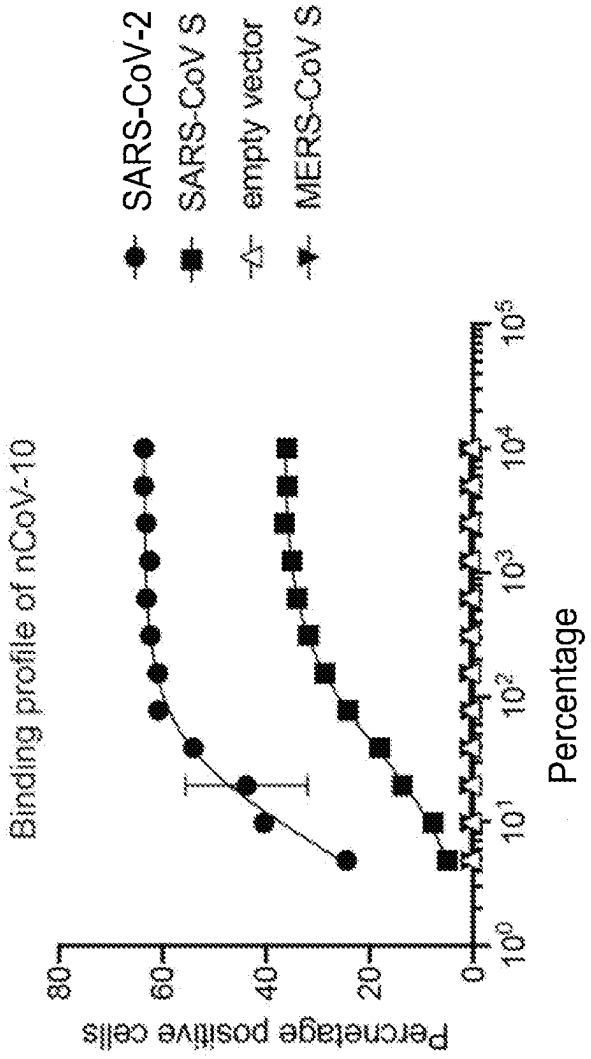

Binding profile of nCoV-10
SARS-CoV-2
SARS-CoV S
empty vector
MERS-CoV S
Percentage positive cells
80
60
40
20
0
10^0
10^1
10^2
10^3
10^4
10^5
Percentage

FIG. 3B

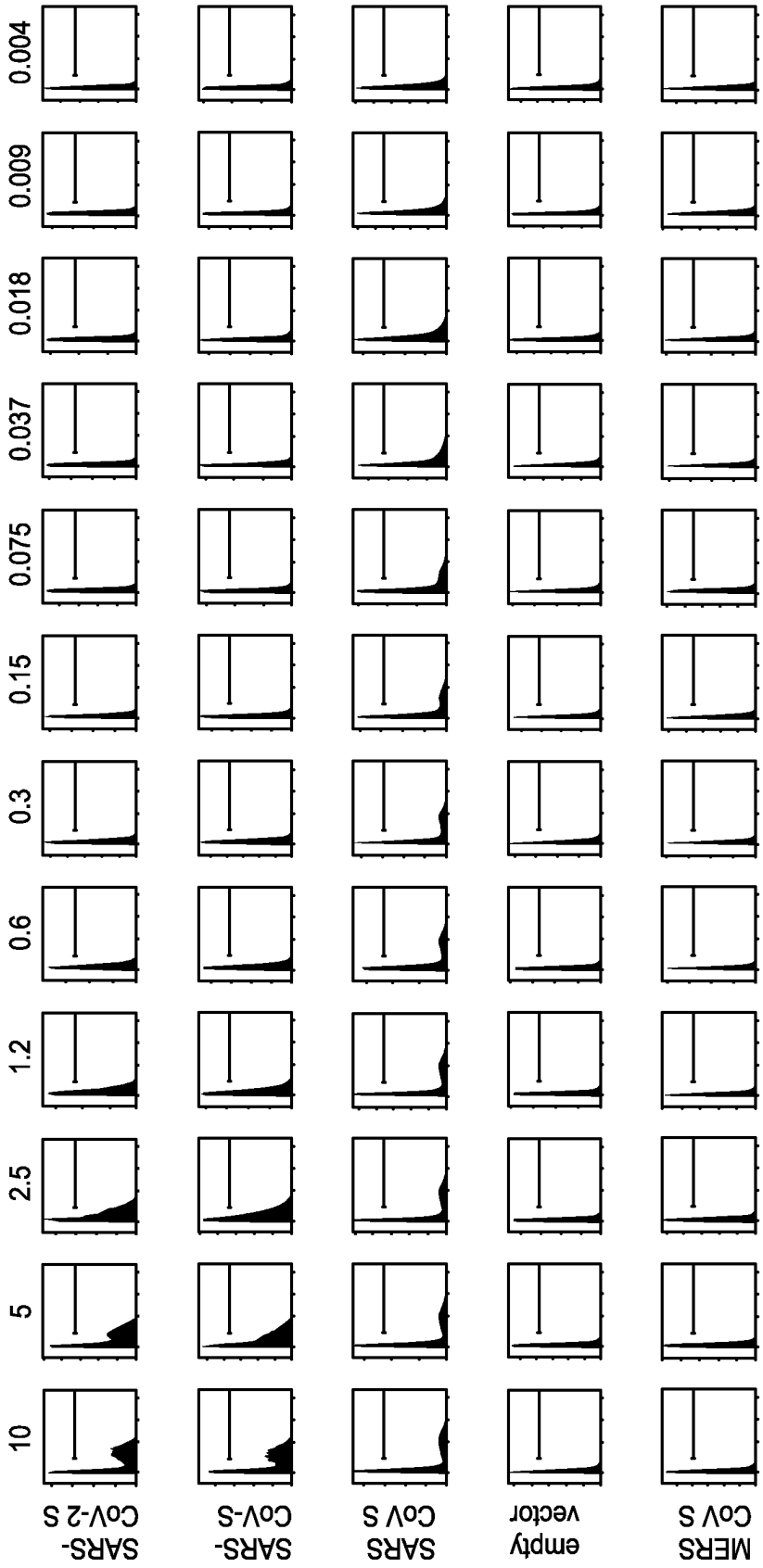

10
5
2.5
1.2
0.6
0.3
0.15
0.075
0.037
0.018
0.009
0.004
SARS-CoV-2 S
SARS-CoV-S
SARS CoV S
empty vector
MERS CoV S

FIG. 4A

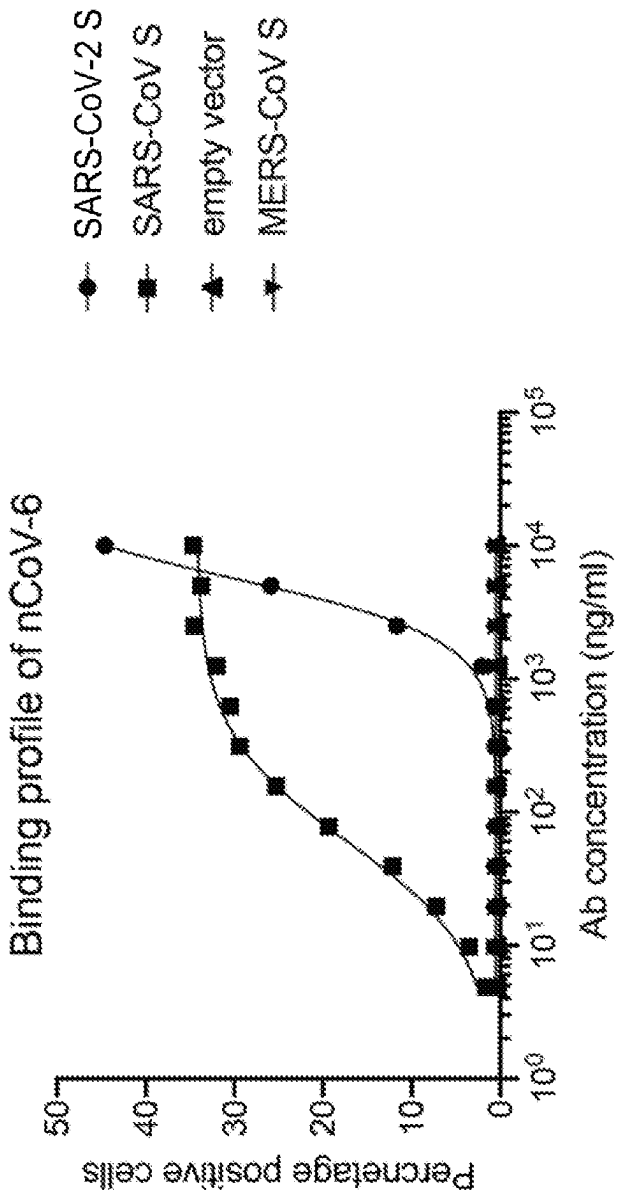

Binding profile of nCoV-6
Percentage positive cells
50
40
30
20
10
0
10^0
10^1
10^2
10^3
10^4
10^5
Ab concentration (ng/ml)
SARS-CoV-2 S
SARS-CoV S
empty vector
MERS-CoV S

FIG. 4B

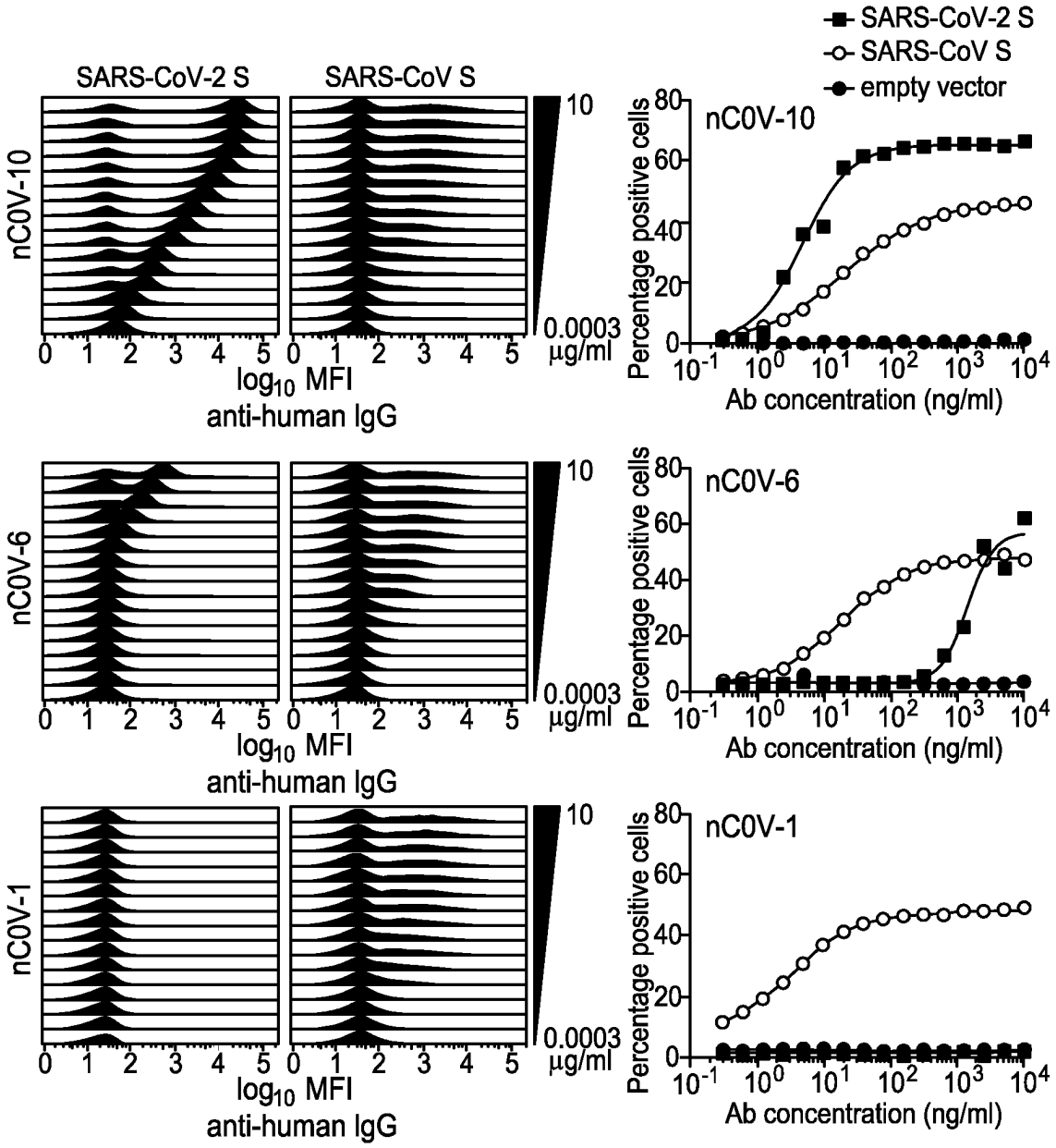

SARS-CoV-2 S
SARS-CoV S
empty vector
SARS-CoV-2 S
SARS-CoV S
nC0V-10
nC0V-6
nC0V-1
10
0.0003
µg/ml
0 1 2 3 4 5
log10 MFI
anti-human IgG
Percentage positive cells
0 20 40 60 80
10-1 100 101 102 103 104
Ab concentration (ng/ml)

FIG. 4C

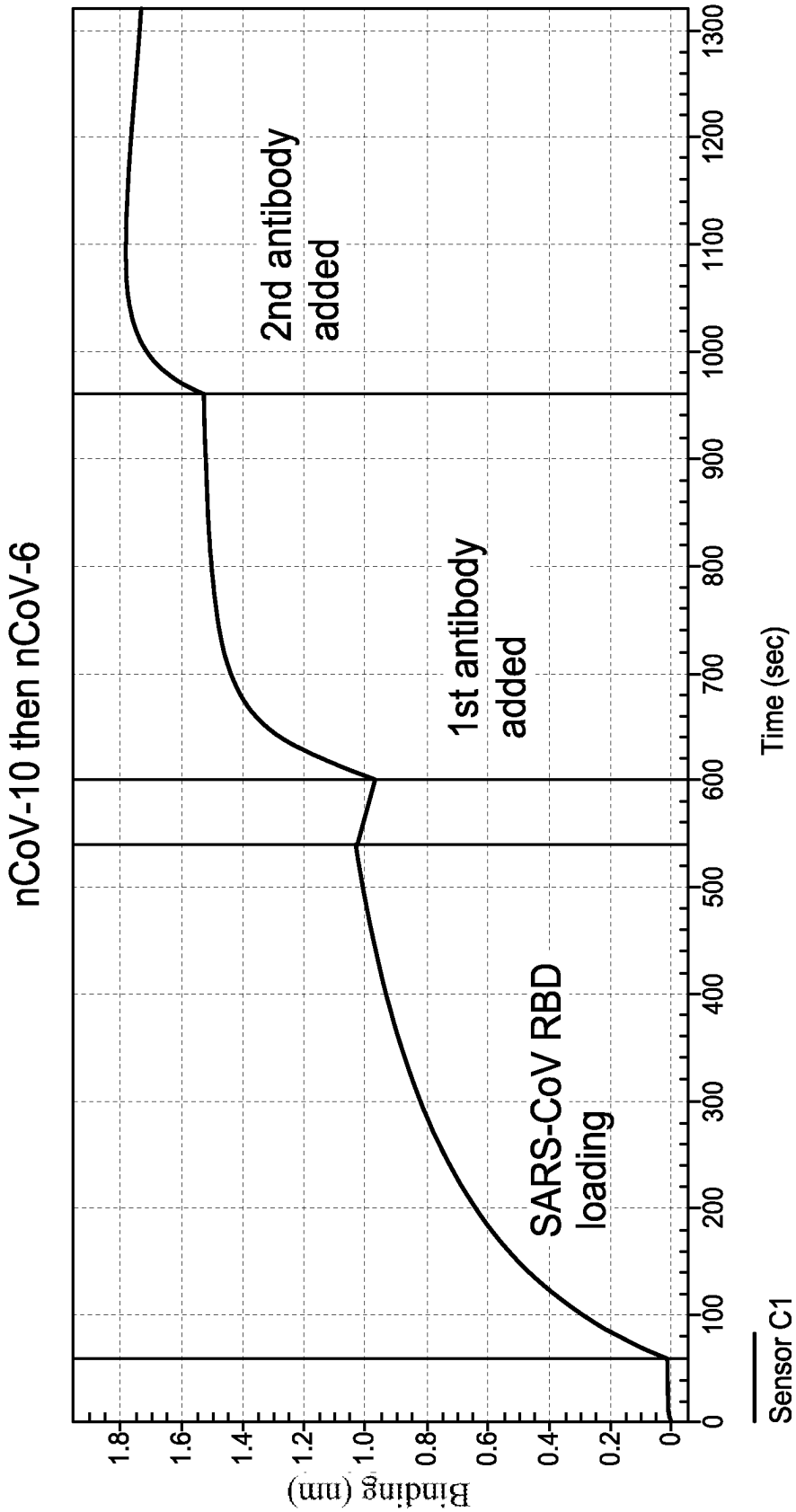

nCoV-10 then nCoV-6
Binding (nm)
1.8
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0
0
100
200
300
400
500
600
700
800
900
1000
1100
1200
1300
Time (sec)
SARS-CoV RBD loading
1st antibody added
2nd antibody added
Sensor C1

FIG. 5A

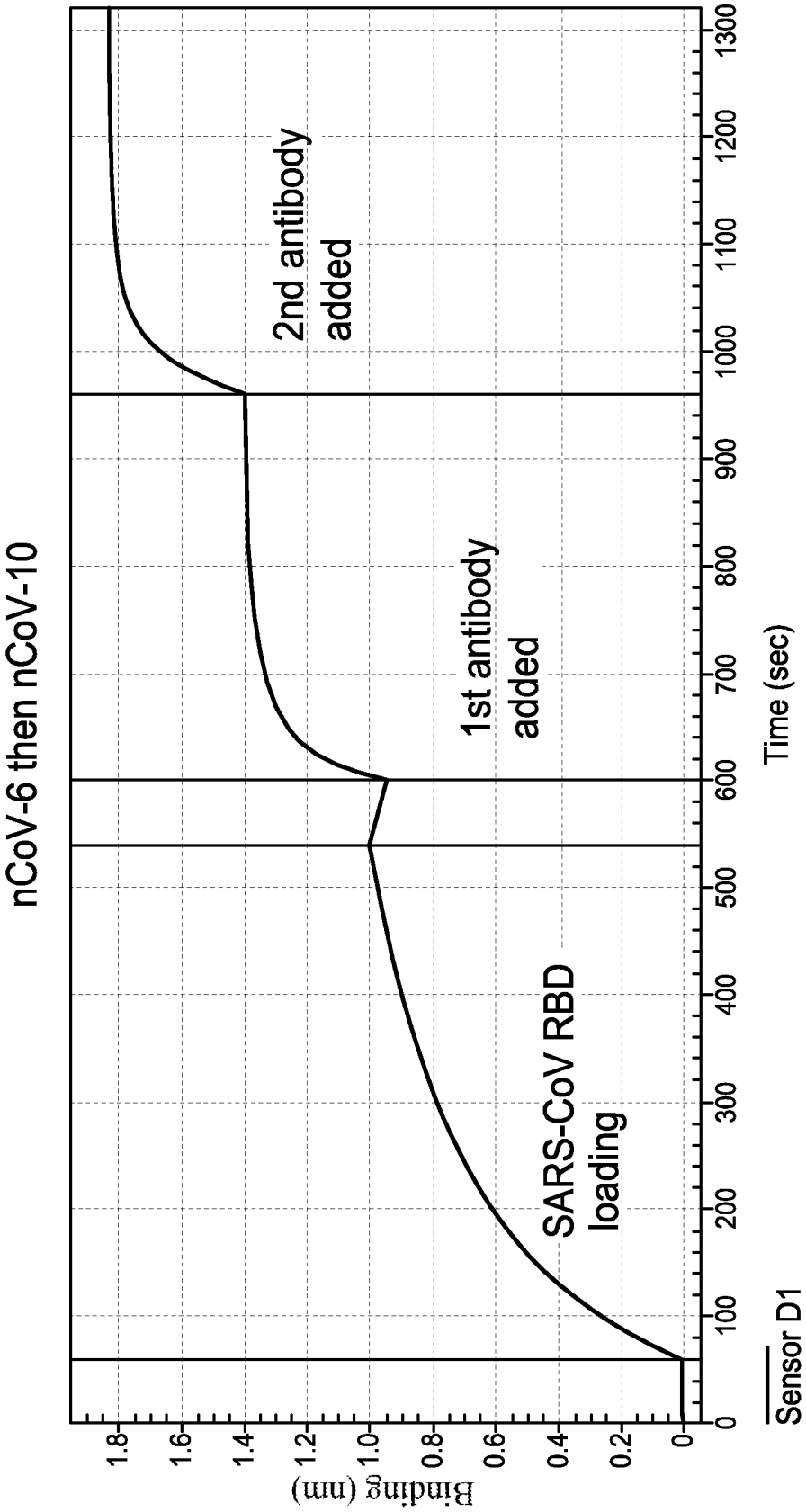

nCoV-6 then nCoV-10
Binding (nm)
1.8
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0
0
100
200
300
400
500
600
700
800
900
1000
1100
1200
1300
Time (sec)
Sensor D1
SARS-CoV RBD loading
1st antibody added
2nd antibody added

FIG. 5B

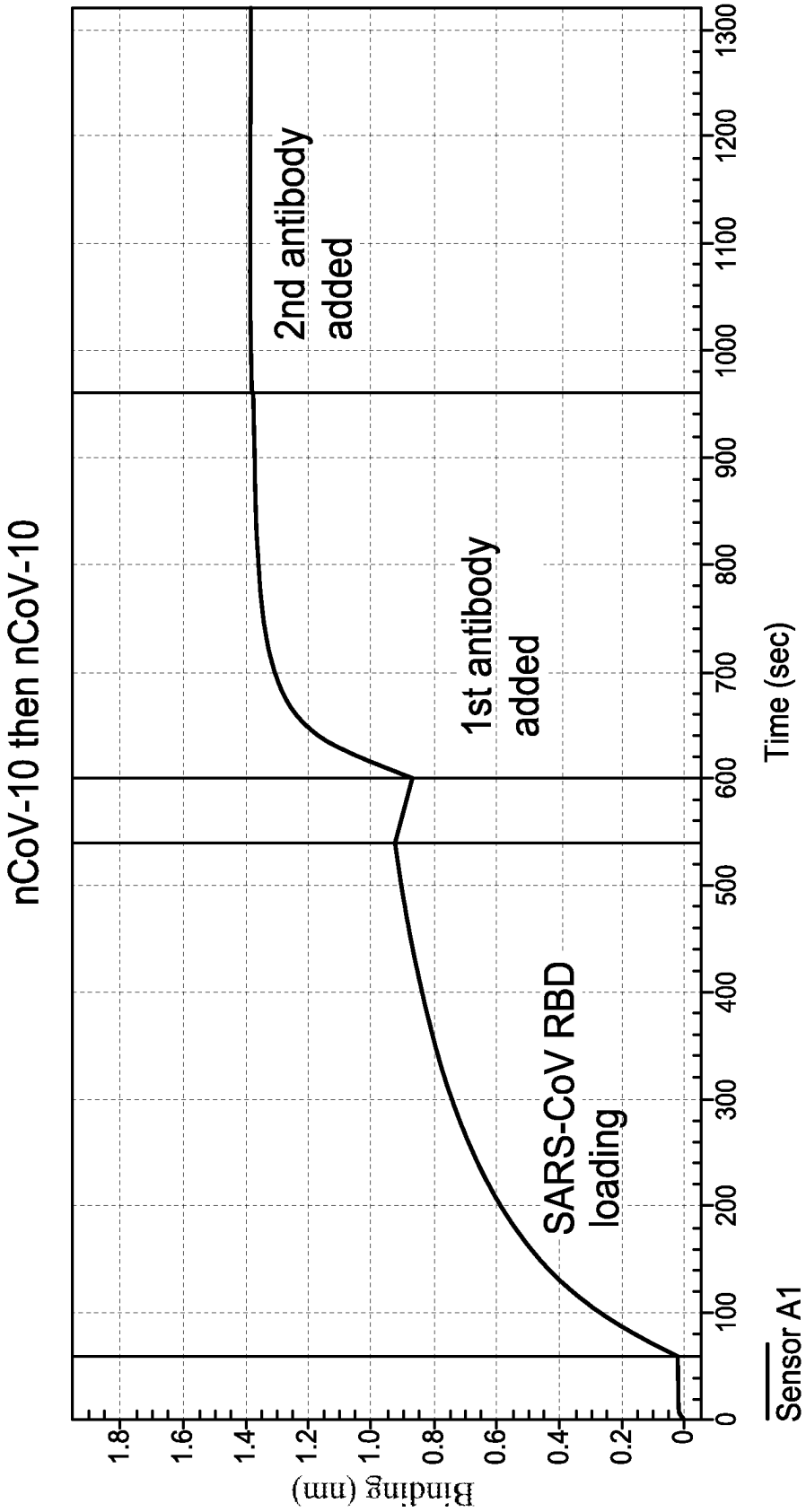

nCoV-10 then nCoV-10
Binding (nm)
1.8
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0
0
100
200
300
400
500
600
700
800
900
1000
1100
1200
1300
Time (sec)
Sensor A1
SARS-CoV RBD loading
1st antibody added
2nd antibody added

FIG. 5C

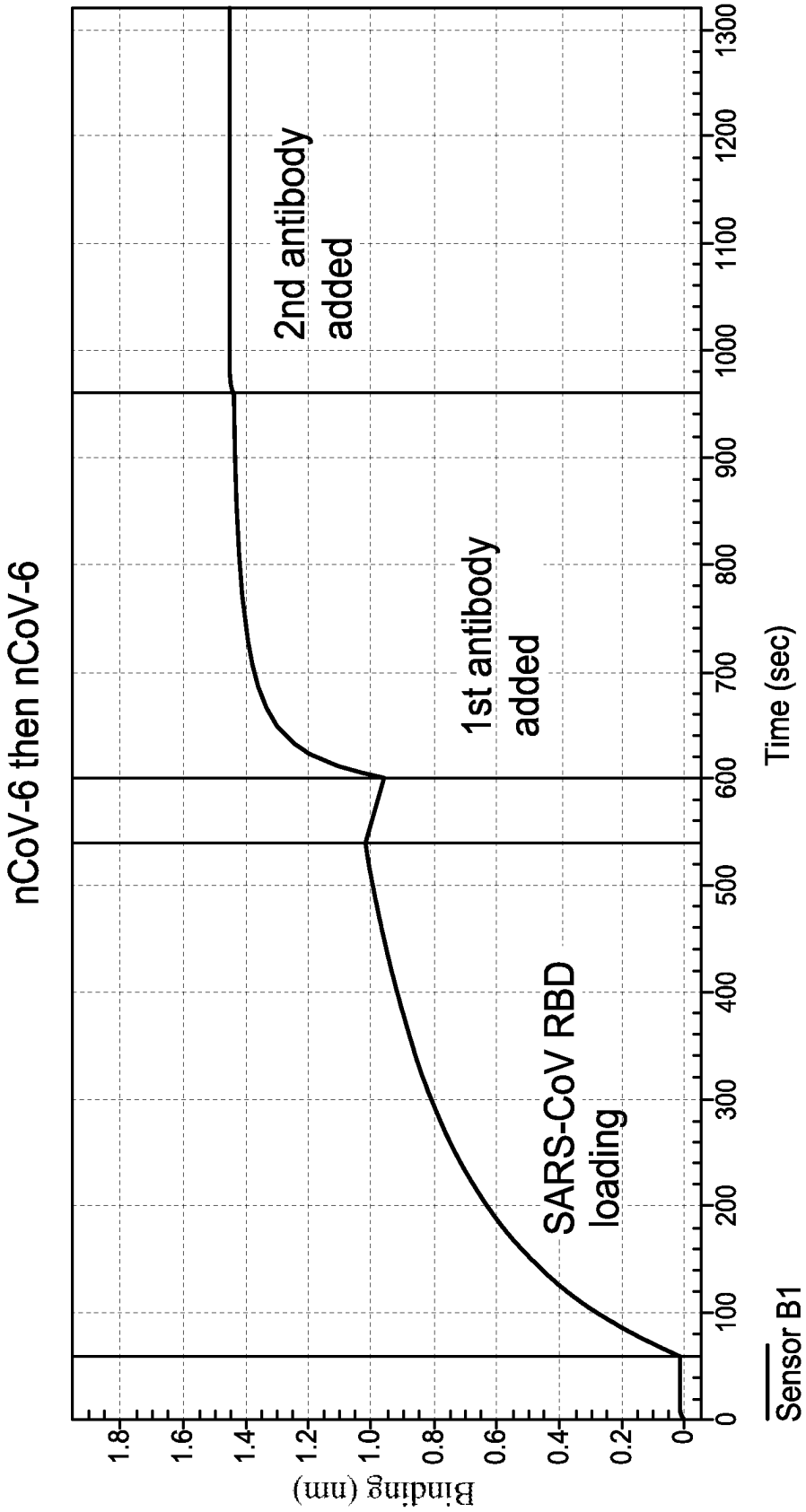

nCoV-6 then nCoV-6
Binding (nm)
1.8
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0
0
100
200
300
400
500
600
700
800
900
1000
1100
1200
1300
Time (sec)
Sensor B1
SARS-CoV RBD loading
1st antibody added
2nd antibody added

FIG. 5D

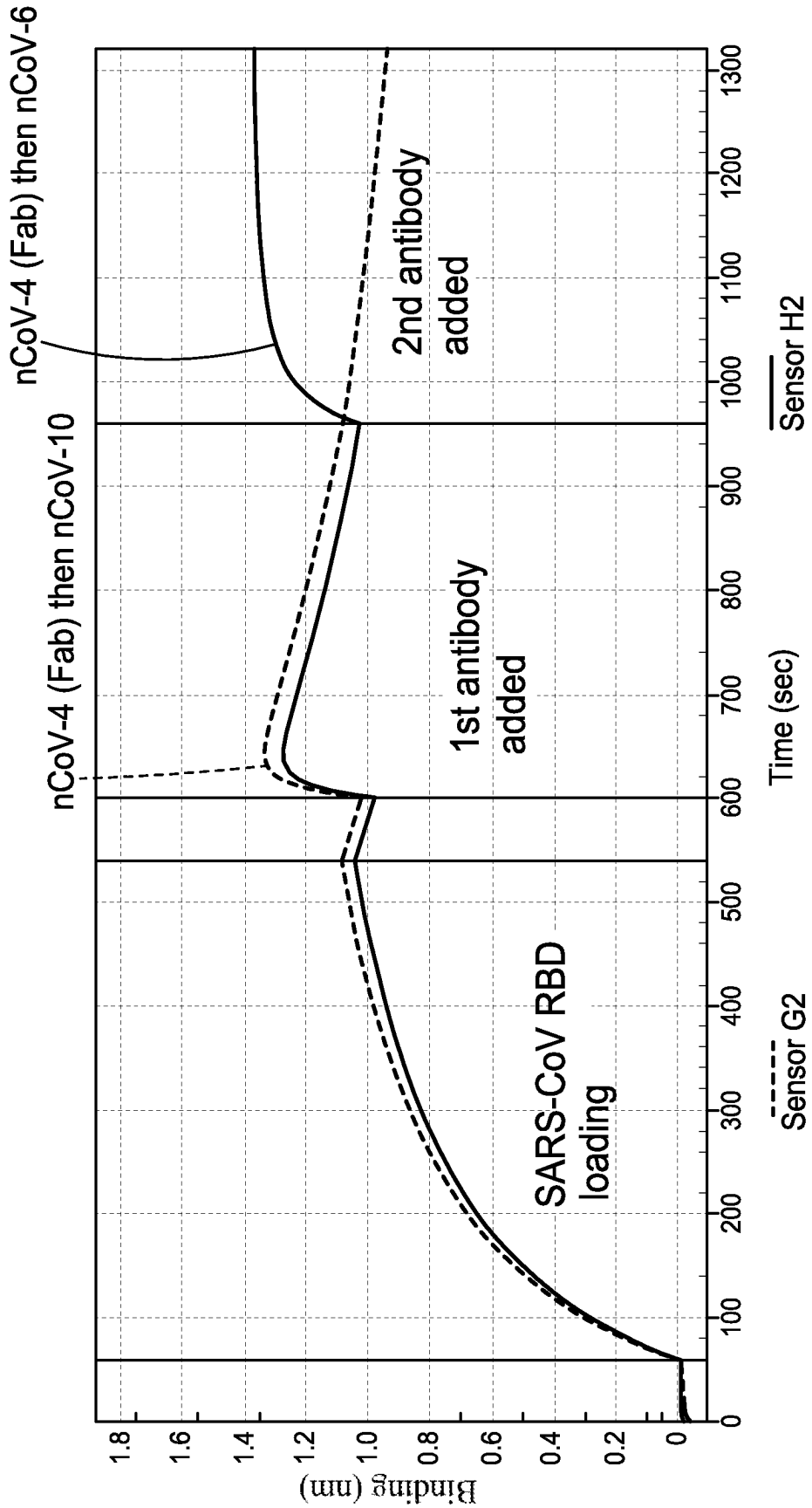

nCoV-4 (Fab) then nCoV-6
nCoV-4 (Fab) then nCoV-10
2nd antibody added
1st antibody added
SARS-CoV RBD loading
Binding (nm)
1.8
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0
0
100
200
300
400
500
600
700
800
900
1000
1100
1200
1300
Time (sec)
Sensor H2
Sensor G2

FIG. 5E

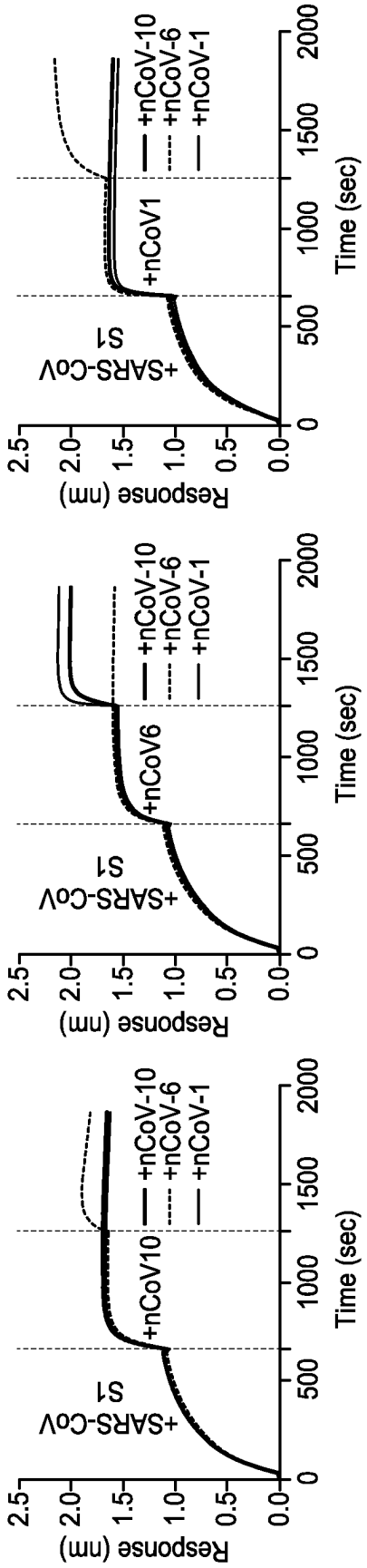

+SARS-CoV S1
+nCoV10
+nCoV-10
+nCoV-6
+nCoV-1
Response (nm)
Time (sec)
+SARS-CoV S1
+nCoV6
+nCoV-10
+nCoV-6
+nCoV-1
Response (nm)
Time (sec)
+SARS-CoV S1
+nCoV1
+nCoV-10
+nCoV-6
+nCoV-1
Response (nm)
Time (sec)

FIG. 5F

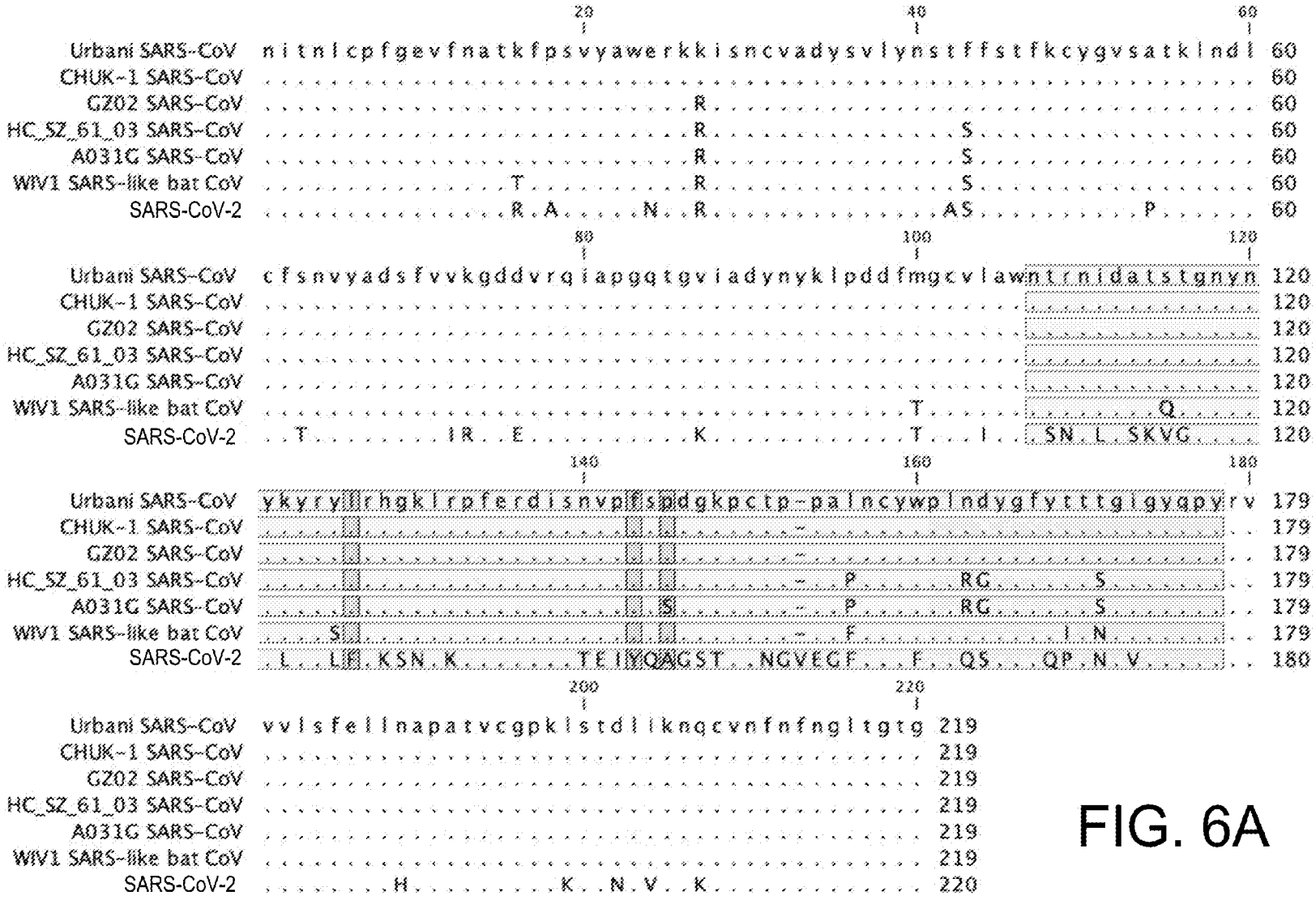

20 40 60
Urbani SARS-CoV nitnlcpfgevfnatkfpsvyawerkkisncvadysvlynstffstfkcygvsatklndl 60
CHUK-1 SARS-CoV 60
GZ02 SARS-CoV 60
HC_SZ_61_03 SARS-CoV 60
A031G SARS-CoV 60
WIV1 SARS-like bat CoV 60
SARS-CoV-2 60
80 100 120
Urbani SARS-CoV cfsnvyadsfvvkgddvrqiapgqtgviadynyklpddfmgcvlawntrnidatstgnyn 120
CHUK-1 SARS-CoV 120
GZ02 SARS-CoV 120
HC_SZ_61_03 SARS-CoV 120
A031G SARS-CoV 120
WIV1 SARS-like bat CoV 120
SARS-CoV-2 120
140 160 180
Urbani SARS-CoV ykyryrhgklrpferdisnvpfspdgkpctp-palncywplndygfytttglgvqpyrv 179
CHUK-1 SARS-CoV 179
GZ02 SARS-CoV 179
HC_SZ_61_03 SARS-CoV 179
A031G SARS-CoV 179
WIV1 SARS-like bat CoV 179
SARS-CoV-2 180
200 220
Urbani SARS-CoV vvlsfellnapatvcgpklstdlikngcvnfnfngltgtg 219
CHUK-1 SARS-CoV 219
GZ02 SARS-CoV 219
HC_SZ_61_03 SARS-CoV 219
A031G SARS-CoV 219
WIV1 SARS-like bat CoV 219
SARS-CoV-2 220

FIG. 6A

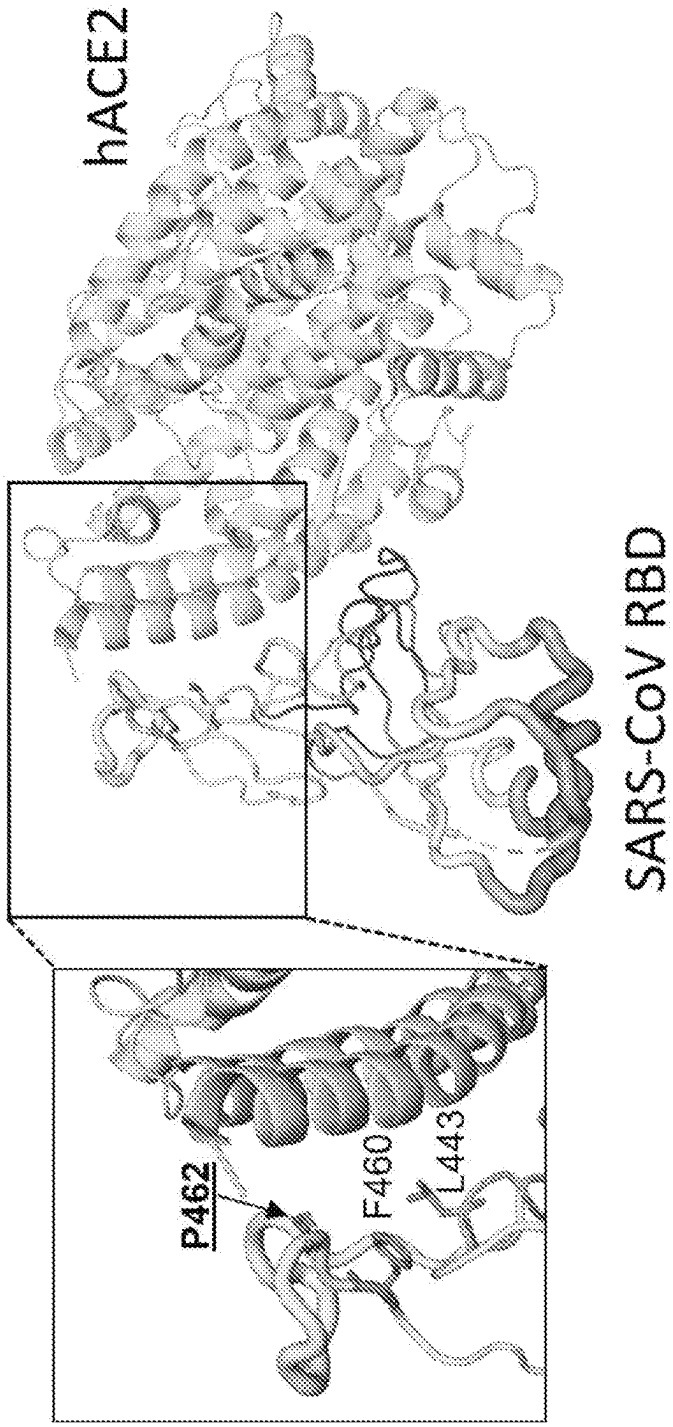


FIG. 6B

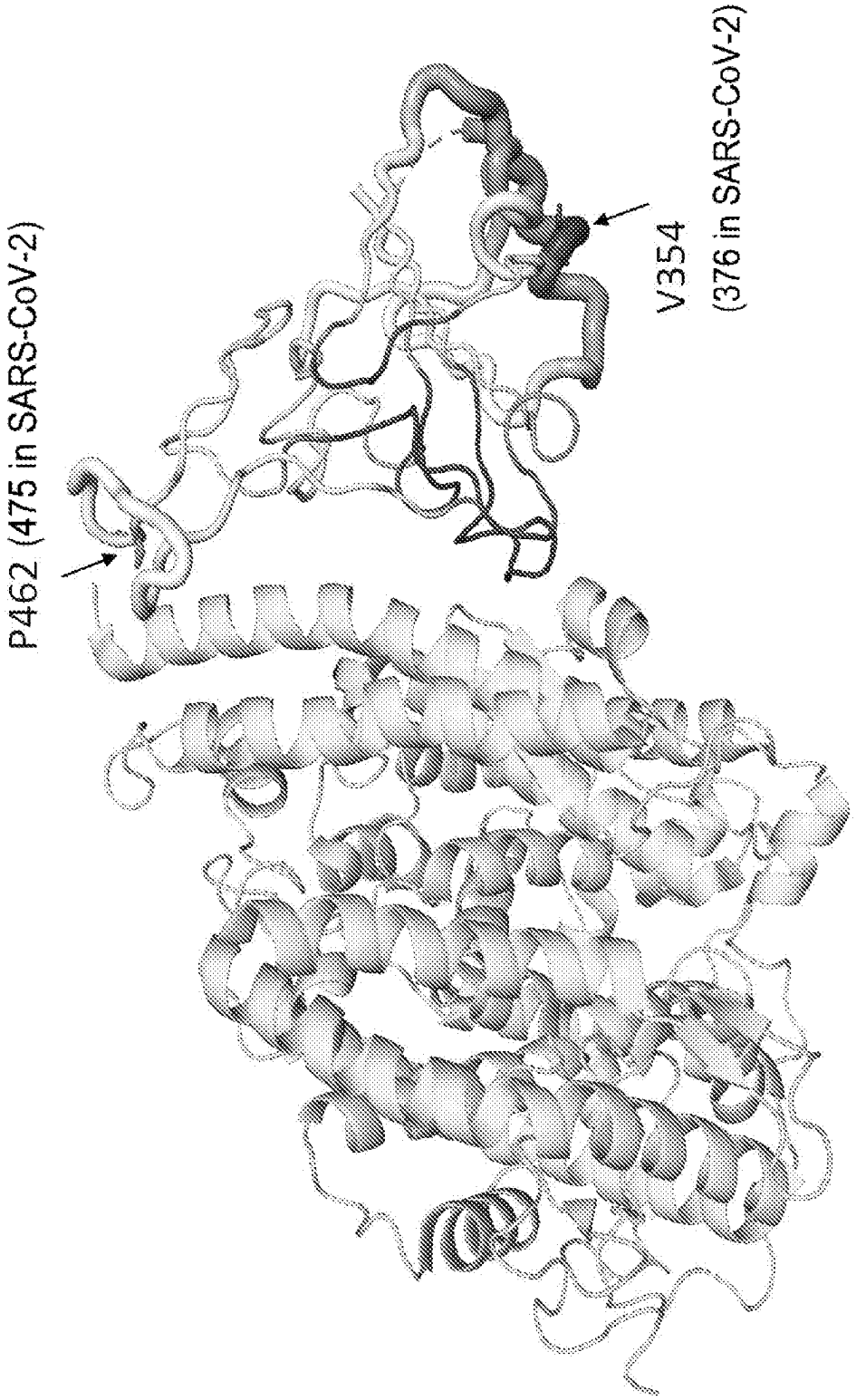


FIG. 7

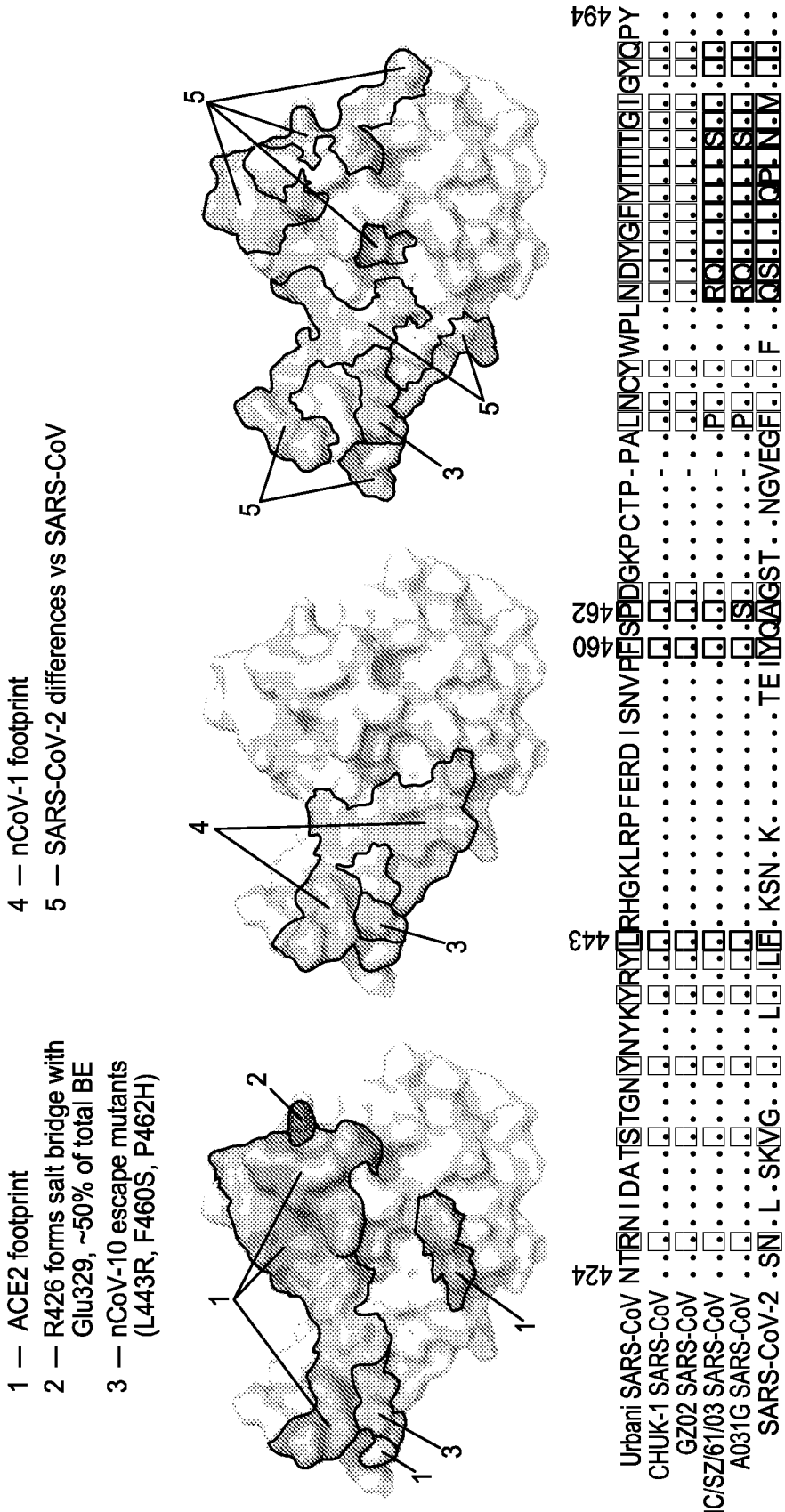

1 — ACE2 footprint
2 — R426 forms salt bridge with Glu329, ~50% of total BE
3 — nCoV-10 escape mutants (L443R, F460S, P462H)
4 — nCoV-1 footprint
5 — SARS-CoV-2 differences vs SARS-CoV
424
443
460
462
494
Urbani SARS-CoV NTRNIDATSTGNYNYKYRYLRHGKLRPFERDISNVPFSPDGKPCTP-PALNCYWPLNDYGFYTTTGIGYQPY
CHUK-1 SARS-CoV
GZ02 SARS-CoV
HC/SZ/61/03 SARS-CoV
A031G SARS-CoV
SARS-CoV-2

FIG. 8

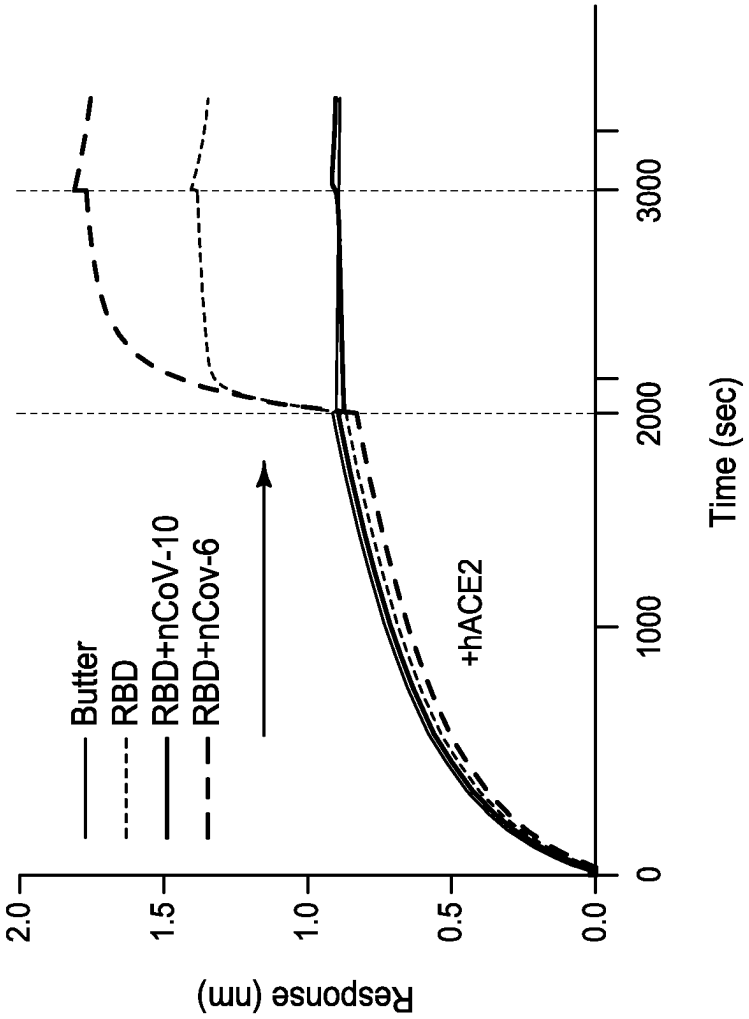

Butter
RBD
RBD+nCoV-10
RBD+nCov-6
+hACE2
Response (nm)
2.0
1.5
1.0
0.5
0.0
0
1000
2000
3000
Time (sec)

FIG. 9

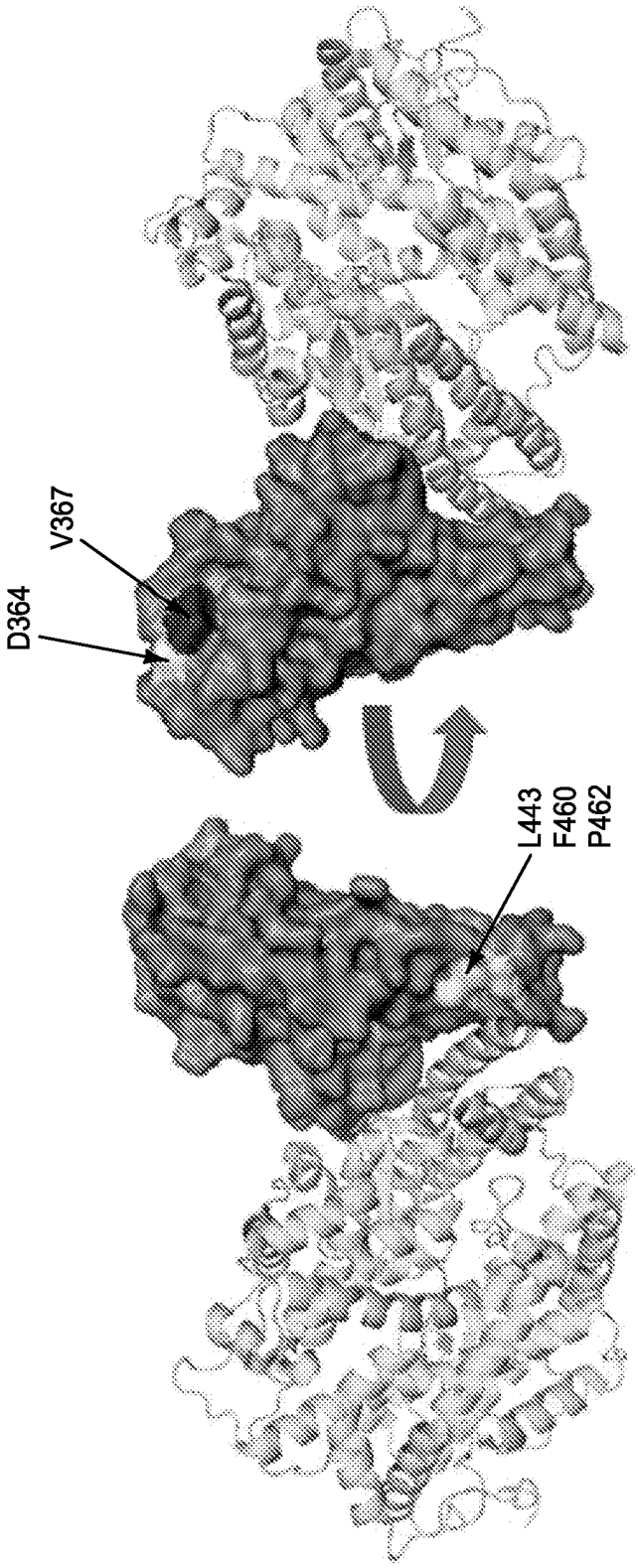


FIG. 10

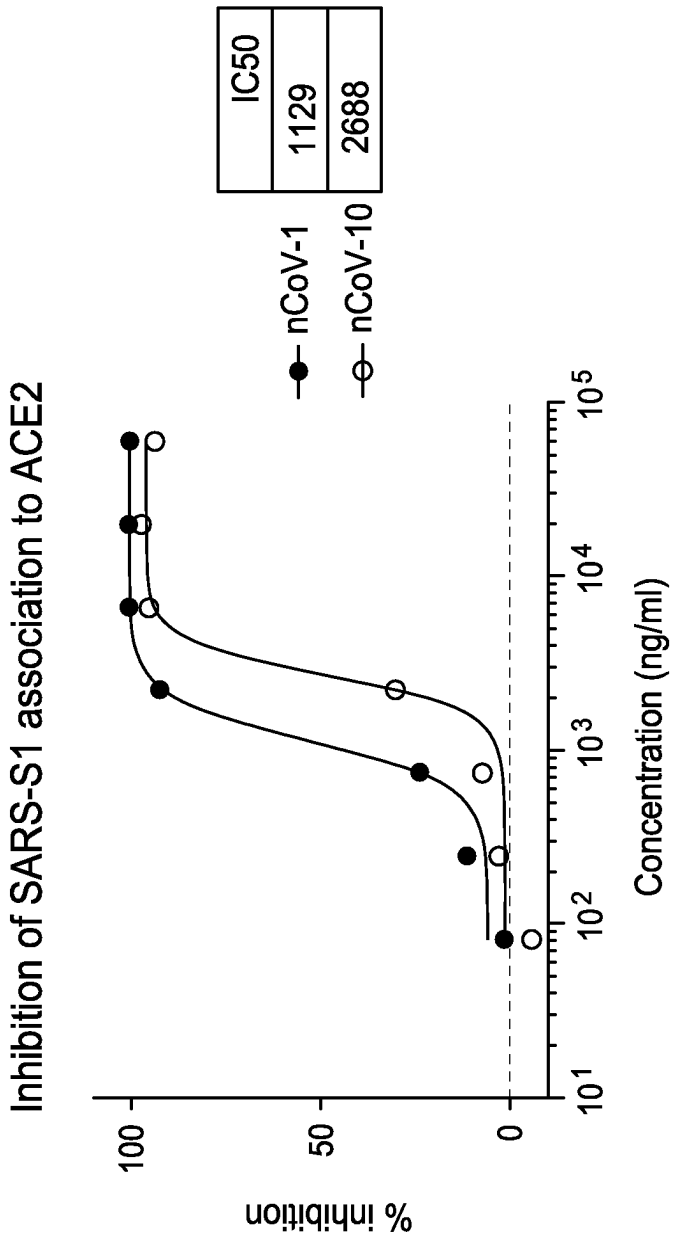

Inhibition of SARS-S1 association to ACE2
% inhibition
100
50
0
10^1
10^2
10^3
10^4
10^5
Concentration (ng/ml)
nCoV-1
nCoV-10
IC50
1129
2688

FIG. 11A

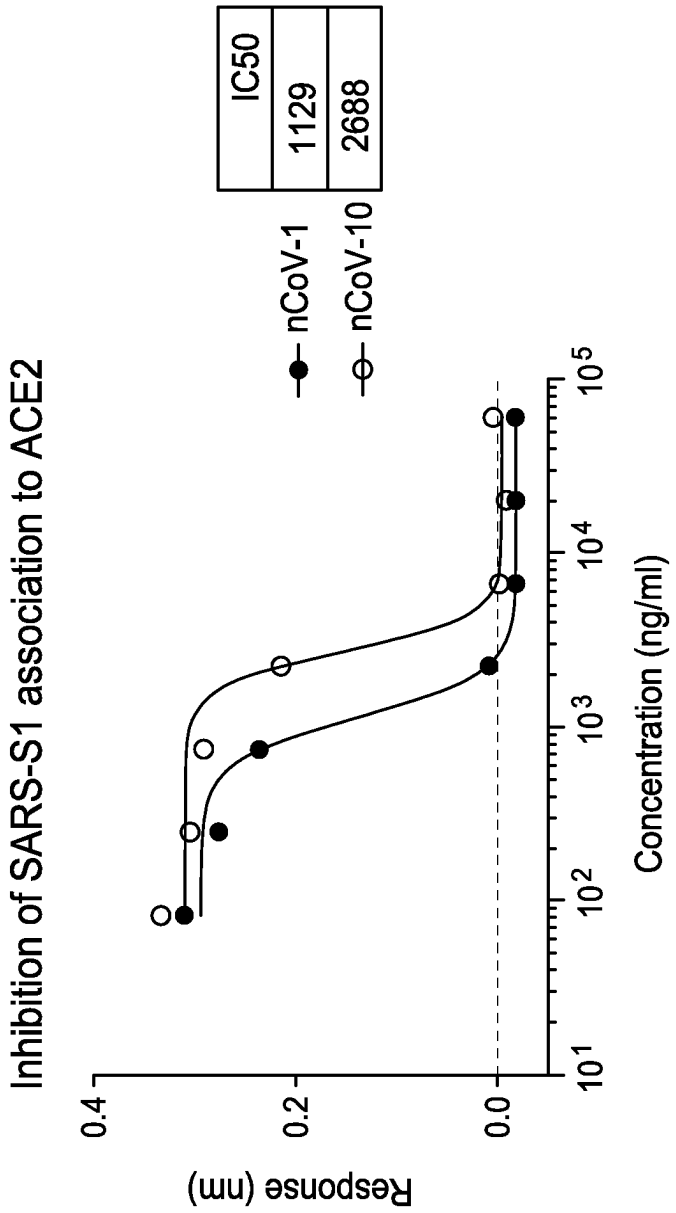

Inhibition of SARS-S1 association to ACE2
Response (nm)
0.4
0.2
0.0
10^1
10^2
10^3
10^4
10^5
Concentration (ng/ml)
nCoV-1
nCoV-10
IC50
1129
2688

FIG. 11B

ANTIBODIES AGAINST SARS-COV-2 AND METHODS OF USING THE SAME

STATEMENT REGARDING SEQUENCE LISTING

[0001] The Sequence Listing associated with this application is provided in text format in lieu of a paper copy, and is hereby incorporated by reference into the specification. The name of the text file containing the Sequence Listing is 930585_401WO_SEQUENCE_LISTING.txt. The text file is 269 KB, was created on Jan. 31, 2021, and is being submitted electronically via EFS-Web.

BACKGROUND

[0002] A novel betacoronavirus emerged in Wuhan, China, in late 2019. As of Jan. 23, 2021, approximately 98,573,000 cases of infection by this virus (termed, among other names, SARS-CoV-2), were confirmed worldwide, and had resulted in approximately 2,116,000 deaths. Therapies for preventing or treating SARS-CoV-2 infection, and diagnostic tools for detecting and diagnosis a SARS-CoV-2 infection, are needed.

BRIEF DESCRIPTION OF THE DRAWINGS

[0003] FIGS. **1**A-ID show binding of exemplary antibodies of the present disclosure to recombinant SARS-CoV S1 protein, as measured by ELISA. Antibody nCoV-1 comprises the VH sequence of SEQ ID NO: 325 and the VL sequence of SEQ ID NO:333. Antibody nCoV-2 comprises the VH sequence of SEQ ID NO:293 and the VL sequence of SEQ ID NO:301. Antibody nCoV-20 comprises the VH sequence of SEQ ID NO:101 and the VL sequence of SEQ ID NO:109. Antibody nCoV-18 comprises the VH sequence of SEQ ID NO:245 and the VL sequence of SEQ ID NO:253. Antibody nCoV-19 comprises the VH sequence of SEQ ID NO:309 and the VL sequence of SEQ ID NO:317. (FIG. **1**A.) Antibody nCoV-16 comprises the VH sequence of SEQ ID NO:85 and the VL sequence of SEQ ID NO:93. Antibody nCoV-10 comprises the VH sequence of SEQ ID NO:21 and the VL sequence of SEQ ID NO:29. Antibody nCoV-6 comprises the VH sequence of SEQ ID NO:69 and the VL sequence of SEQ ID NO:77. Antibody nCoV-3 comprises the VH sequence of SEQ ID NO:5 and the VL sequence of SEQ ID NO:13. Antibody nCoV-14 comprises the VH sequence of SEQ ID NO:213 and the VL sequence of SEQ ID NO:221. (FIG. **1**B.) Antibody nCoV-4 comprises the VH sequence of SEQ ID NO:117 and the VL sequence of SEQ ID NO:125. Antibody nCoV-5 comprises the VH sequence of SEQ ID NO:197 and the VL sequence of SEQ ID NO:205. Antibody nCoV-12 comprises the VH sequence of SEQ ID NO:181 and the VL sequence of SEQ ID NO:189. Antibody nCoV-9 comprises the VH sequence of SEQ ID NO:229 and the VL sequence of SEQ ID NO:237. (FIG. **1**C.) Antibody nCoV-8 comprises the VH sequence of SEQ ID NO:261 and the VL sequence of SEQ ID NO:269. Antibody nCoV-7 comprises the VH sequence of SEQ ID NO:277 and the VL sequence of SEQ ID NO:285. Antibody nCoV-11 comprises the VH sequence of SEQ ID NO:341 and the VL sequence of SEQ IDNO:349. (FIG. **1**D.)

[0004] FIGS. **2**A and **2**B show staining of SARS-CoV-2-S, SARS-CoV-S, MERS-CoV-S and Mock transfected cells using a panel of exemplary human monoclonal antibodies (mAbs), expressed as recombinant IgG1. All mAbs were tested at 10 μg/ml with the following exceptions: nCoV-5 (1 μg/ml); nCoV-7 (2 μg/ml); nCoV-8 (1.5 μg/ml); nCoV-9 (8.5 μg/ml); nCoV-12 (0.8 μg/ml); nCoV-13 (7 μg/ml); and nCoV-15 (0.8 μg/ml). Antibody nCoV-13 comprises the VH sequence of SEQ ID NO:357 and the VL sequence of SEQ ID NO:365. Antibody nCoV-15 comprises the VH sequence of SEQ ID NO:165 and the VL sequence of SEQ ID NO:173. (A) Percentage of staining-positive cells. (B) Percentage of staining-positive cells normalized to mode.

[0005] FIGS. **3**A and **3**B show binding by exemplary antibody nCoV-10 at different concentrations to surface-expressed S protein from viruses SARS-CoV-2, SARS-CoV, and MERS-CoV. (A) Histograms depict the number of cells vs. the fluorescence intensity of antibody binding to S-transfected cells. (B) Percentage of positive binding at 12 concentrations of nCov-10 antibody (10 μg/ml down to 0.004 μg/ml), as defined by differential staining of CoV-S-transfectants versus mock-transfectants.

[0006] FIGS. **4**A and **4**B show binding by exemplary antibody nCoV-6 at different concentrations to surface-expressed S protein from viruses SARS-CoV-2, SARS-CoV, and MERS-CoV. (A) Histograms depict the number of cells vs. the fluorescence intensity of antibody binding to S-transfected cells. (B) Graphs depict the percentage of positive binding at 12 concentrations of nCoV-6 antibody (10 μg/ml down to 0.004 μg/ml), as defined by differential staining of CoV-S-transfectants versus mock-transfectants.

[0007] FIG. **4**C shows binding by nCoV-10, nCoV-6, and nCoV-1 to SARS-CoV S protein or SARS-CoV-2 S protein expressed on cells 24 hours after transfection.

[0008] FIGS. **5**A-**5**F show results of cross-competition assays using Octet (BLI) to investigate the epitopes recognized by SARS-CoV-2 cross-reactive antibodies nCoV-6 and nCoV-10 and the SARS-CoV-specific antibodies nCoV-4 and nCoV-1. SARS-CoV Receptor Binding Domain (RBD) was first immobilized on anti-His sensors (step 1), then sensors were moved into wells containing antibody 1 (step 2) and finally into wells containing antibody 2 (step 3). If a binding event is detected at step 3, antibody 2 has a non-overlapping epitope than the epitope recognized by antibody 1; if no binding is detected at step 3, antibody 1 and 2 share overlapping epitopes. The order of the antibodies used in steps 2 and 3 was as shown above the graph in each of (A)-(F). FIGS. **5**A-**5**D show cross-competition assays using nCoV-6 and nCoV-10. In FIG. **5**E, nCoV-4 Fab was used as antibody 1, and nCoV-6 or nCoV-10 was used as antibody 2. FIG. **5**F shows data from cross-competition assays among nCoV-10, nCoV-6, and nCoV-1. The antibody used as antibody 1 is indicated in each panel of FIG. **5**F.

[0009] FIG. **6**A shows an alignment of the S protein RBD from multiple SARS-CoV isolates (Urbani, CHUK-1, GZ02, HC_SZ_61_03, A031G), the SARS-like bat CoV WIV1, and SARS-CoV-2. Indicated in dark grey are residues L443 (F455 in SARS-CoV-2), F460 (Y473 in SARS-CoV-2) and P462 (A475 in SARS-CoV-2). Indicated in in light grey is the Receptor Binding Motif (RBM). Residue numbering shown for each row of the figure is with respect to the RBD, not the full S protein.

[0010] FIG. **6**B shows the positioning of SARS-CoV (RBD) residues P462, F460, and L443 when RBD is in complex with human ACE2 (pdb, 2AJF).

[0011] FIG. **7** provides an illustration of SARS-CoV RBD bound to human ACE2 (pdb, 2AJF), with residues P462

(corresponding to residue 475 in SARS-CoV-2) and V354 (corresponding to residue 376 in SARS-CoV-2) indicated.

[0012] FIG. **8** shows SARS-CoV RBD with: (top, left) the ACE2 footprint on RBD indicated, with nCoV-10 SARS CoV escape mutant residues identified; (top, center) the nCoV-1 footprint on RBD indicated; and (top, right) amino acid residue differences between SARS-CoV-2 RBD and SARS-CoV RBD. At bottom is an alignment showing SARS CoV and SARS-CoV-2 RBM amino acid sequences.

[0013] FIG. **9** shows that exemplary antibody nCoV-10 of the present disclosure can inhibit binding of a coronavirus RBD to human ACE2.

[0014] FIG. **10** shows illustrations of the structures of SARS CoV RBD (3-d space-filling models in center) and human ACE2 (ribbon diagrams, outside relative to center).

[0015] FIGS. **11**A and **11**B show the ability of monoclonal antibodies nCoV-1 and nCoV-10 to inhibit association of SARS-S1 protein with human ACE2, as assayed by Octet (BLI). FIG. **11**A shows % inhibition on the y-axis. FIG. **11**B shows response on the y-axis.

DETAILED DESCRIPTION

[0016] Provided herein are antibodies and antigen-binding fragments that bind to SARS-CoV-2 (e.g., a SARS-CoV-2 surface glycoprotein and/or RBD, as described herein, in a SARS-CoV-2 virion and/or expressed on the surface of a cell infected by SARS-CoV-2). In certain embodiments, presently disclosed antibodies and antigen-binding fragments can neutralize a SARS-CoV-2 infection in an in vitro model of infection and/or in a human subject. Also provided are polynucleotides that encode the antibodies and antigen-binding fragments, vectors, host cells, and related compositions, as well as methods of using the antibodies, nucleic acids, vectors, host cells, and related compositions to treat (e.g., reduce, delay, eliminate, or prevent) a SARS-CoV-2 infection in a subject and/or in the manufacture of a medicament for treating or preventing a SARS-CoV-2 infection in a subject.

[0017] Prior to setting forth this disclosure in more detail, it may be helpful to an understanding thereof to provide definitions of certain terms to be used herein. Additional definitions are set forth throughout this disclosure.

[0018] As used herein, "SARS-CoV-2", also referred to herein as "Wuhan seafood market pneumonia virus", or "Wuhan coronavirus" or "Wuhan CoV", or "novel CoV", or "nCoV", or "2019 nCoV", or "Wuhan nCoV" is a betacoronavirus believed to be of lineage B (sarbecovirus). SARS-CoV-2 was first identified in Wuhan, Hubei province, China, in late 2019 and spread within China and to other parts of the world by early 2020. Symptoms of SARS-CoV-2 infection include fever, dry cough, dyspnea, fatigue, body aches, headache, new loss of taste or smell, sore throat, congestions or runny nose, nausea or vomiting, diarrhea, persistent pressure or pain in the chest, new confusion, inability to wake or stay awake, and bluish lips or face.

[0019] The genomic sequence of SARS-CoV-2 isolate Wuhan-Hu-1 is provided in SEQ ID NO.:369 (see also GenBank MN908947.3, Jan. 23, 2020), and the amino acid translation of the genome is provided in SEQ ID NO.:370 (see also GenBank QHD43416.1, Jan. 23, 2020). Like other coronaviruses (e.g., SARS CoV), SARS-CoV-2 comprises a "spike" or surface ("S") type I transmembrane glycoprotein containing a receptor binding domain (RBD). RBD is believed to mediate entry of the lineage B SARS coronavirus to respiratory epithelial cells by binding to the cell surface receptor angiotensin-converting enzyme 2 (ACE2). In particular, a receptor binding motif (RBM) in the virus RBD is believed to interact with ACE2.

[0020] The amino acid sequence of the SARS-CoV-2 Wuhan-Hu-1 surface glycoprotein is provided in SEQ ID NO.:371. The amino acid sequence of SARS-CoV-2 RBD is provided in SEQ ID NO.:382. SARS-CoV-2 S protein has approximately 73% amino acid sequence identity with SARS-CoV. The amino acid sequence of SARS-CoV-2 RBM is provided in SEQ ID NO.:390. SARS-CoV-2 RBD has approximately 75% to 77% amino acid sequence similarity to SARS coronavirus RBD, and SARS-CoV-2 RBM has approximately 50% amino acid sequence similarity to SARS coronavirus RBM.

[0021] Unless otherwise indicated herein, SARS-CoV-2 refers to a virus comprising the amino acid sequence set forth in any one or more of SEQ ID NOs.:370, 371, and 382, optionally with the genomic sequence set forth in SEQ ID NO.:369.

[0022] There have been a number of emerging SARS-CoV-2 variants. Some SARS-CoV-2 variants contain an N439K mutation, which has enhanced binding affinity to the human ACE2 receptor (Thomson, E. C., et al., *The circulating SARS-CoV-2 spike variant N439K maintains fitness while evading antibody-mediated immunity*. bioRxiv, 2020). Some SARS-CoV-2 variants contain an N501Y mutation, which is associated with increased transmissibility, including the lineages B.1.1.7 (also known as 20I/501Y.V1 and VOC 202012/01) and B.1.351 (also known as 20H/501Y.V2), which were discovered in the United Kingdom and South Africa, respectively (Tegally, H., et al., *Emergence and rapid spread of a new severe acute respiratory syndrome-related coronavirus* 2 (*SARS-CoV*-2) *lineage with multiple spike mutations in South Africa*. medRxiv, 2020: p. 2020.12.21.20248640; Leung, K., et al., *Early empirical assessment of the N501Y mutant* strains *of SARS-CoV-2 in the United Kingdom, October to November* 2020. medRxiv, 2020: p. 2020.12.20.20248581). B.1.351 also includes two other mutations in the RBD domain of SARS-CoV2 spike protein, K417N and E484K (Tegally, H., et al., *Emergence and rapid spread of a new severe acute respiratory syndrome-related coronavirus* 2 (*SARS-CoV*-2) *lineage with multiple spike mutations in South Africa*. medRxiv, 2020: p. 2020.12.21.20248640). Other SARS-CoV-2 variants include the Lineage B.1.1.28, which was first reported in Brazil; the Variant P.1, lineage B.1.1.28 (also known as 20J/501Y.V3), which was first reported in Japan; Variant L452R, which was first reported in California in the United States (Pan American Health Organization, *Epidemiological update: Occurrence ofvariants of SARS-CoV-2 in the Americas*, Jan. 20, 2021, available at https://reliefweb.int/sites/reliefweb.int/files/resources/2021-jan-20-phe-epi-update-SARS-CoV-2.pdf). Other SARS-CoV-2 variants include a SARS CoV-2 of clade 19A; SARS CoV-2 of clade 19B; a SARS CoV-2 of clade 20A; a SARS CoV-2 of clade 20B; a SARS CoV-2 of clade 20C; a SARS CoV-2 of clade 20D; a SARS CoV-2 of clade 20E (EU1); a SARS CoV-2 of clade 20F; a SARS CoV-2 of clade 20G; and SARS CoV-2 B1.1.207; and other SARS CoV-2 lineages described in Rambaut, A., et al., *A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology*. Nat Microbiol 5, 1403-1407 (2020).

[0023] Other coronaviruses are believed to enter cells by binding to other receptors (e.g., 9-O-Ac-Sia receptor analog; DPP4; APN).

[0024] In the present description, any concentration range, percentage range, ratio range, or integer range is to be understood to include the value of any integer within the recited range and, when appropriate, fractions thereof (such as one tenth and one hundredth of an integer), unless otherwise indicated. Also, any number range recited herein relating to any physical feature, such as polymer subunits, size or thickness, are to be understood to include any integer within the recited range, unless otherwise indicated. As used herein, the term "about" means±20% of the indicated range, value, or structure, unless otherwise indicated. It should be understood that the terms "a" and "an" as used herein refer to "one or more" of the enumerated components. The use of the alternative (e.g., "or") should be understood to mean either one, both, or any combination thereof of the alternatives. As used herein, the terms "include," "have," and "comprise" are used synonymously, which terms and variants thereof are intended to be construed as non-limiting.

[0025] "Optional" or "optionally" means that the subsequently described element, component, event, or circumstance may or may not occur, and that the description includes instances in which the element, component, event, or circumstance occurs and instances in which they do not.

[0026] In addition, it should be understood that the individual constructs, or groups of constructs, derived from the various combinations of the structures and subunits described herein, are disclosed by the present application to the same extent as if each construct or group of constructs was set forth individually. Thus, selection of particular structures or particular subunits is within the scope of the present disclosure.

[0027] The term "consisting essentially of" is not equivalent to "comprising" and refers to the specified materials or steps of a claim, or to those that do not materially affect the basic characteristics of a claimed subject matter. For example, a protein domain, region, or module (e.g., a binding domain) or a protein "consists essentially of" a particular amino acid sequence when the amino acid sequence of a domain, region, module, or protein includes extensions, deletions, mutations, or a combination thereof (e.g., amino acids at the amino- or carboxy-terminus or between domains) that, in combination, contribute to at most 20% (e.g., at most 15%, 10%, 8%, 6%, 5%, 4%, 3%, 2% or 1%) of the length of a domain, region, module, or protein and do not substantially affect (i.e., do not reduce the activity by more than 50%, such as no more than 40%, 30%, 25%, 20%, 15%, 10%, 5%, or 1%) the activity of the domain(s), region(s), module(s), or protein (e.g., the target binding affinity of a binding protein).

[0028] As used herein, "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function in a manner similar to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ-carboxyglutamate, and O-phosphoserine. Amino acid analogs refer to compounds that have the same basic chemical structure as a naturally occurring amino acid, i.e., an α-carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs have modified R groups (e.g., norleucine) or modified peptide backbones, but retain the same basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refer to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that functions in a manner similar to a naturally occurring amino acid.

[0029] As used herein, "mutation" refers to a change in the sequence of a nucleic acid molecule or polypeptide molecule as compared to a reference or wild-type nucleic acid molecule or polypeptide molecule, respectively. A mutation can result in several different types of change in sequence, including substitution, insertion or deletion of nucleotide(s) or amino acid(s).

[0030] A "conservative substitution" refers to amino acid substitutions that do not significantly affect or alter binding characteristics of a particular protein. Generally, conservative substitutions are ones in which a substituted amino acid residue is replaced with an amino acid residue having a similar side chain. Conservative substitutions include a substitution found in one of the following groups: Group 1: Alanine (Ala or A), Glycine (Gly or G), Serine (Ser or S), Threonine (Thr or T); Group 2: Aspartic acid (Asp or D), Glutamic acid (Glu or Z); Group 3: Asparagine (Asn or N), Glutamine (Gln or Q); Group 4: Arginine (Arg or R), Lysine (Lys or K), Histidine (His or H); Group 5: Isoleucine (Ile or I), Leucine (Leu or L), Methionine (Met or M), Valine (Val or V); and Group 6: Phenylalanine (Phe or F), Tyrosine (Tyr or Y), Tryptophan (Trp or W). Additionally or alternatively, amino acids can be grouped into conservative substitution groups by similar function, chemical structure, or composition (e.g., acidic, basic, aliphatic, aromatic, or sulfur-containing). For example, an aliphatic grouping may include, for purposes of substitution, Gly, Ala, Val, Leu, and Ile. Other conservative substitutions groups include: sulfur-containing: Met and Cysteine (Cys or C); acidic: Asp, Glu, Asn, and Gln; small aliphatic, nonpolar or slightly polar residues: Ala, Ser, Thr, Pro, and Gly; polar, negatively charged residues and their amides: Asp, Asn, Glu, and Gln; polar, positively charged residues: His, Arg, and Lys; large aliphatic, nonpolar residues: Met, Leu, Ile, Val, and Cys; and large aromatic residues: Phe, Tyr, and Trp. Additional information can be found in Creighton (1984) Proteins, W.H. Freeman and Company.

[0031] As used herein, "protein" or "polypeptide" refers to a polymer of amino acid residues. Proteins apply to naturally occurring amino acid polymers, as well as to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, and non-naturally occurring amino acid polymers. Variants of proteins, peptides, and polypeptides of this disclosure are also contemplated. In certain embodiments, variant proteins, peptides, and polypeptides comprise or consist of an amino acid sequence that is at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 99.9% identical to an amino acid sequence of a defined or reference amino acid sequence as described herein.

[0032] "Nucleic acid molecule" or "polynucleotide" or "polynucleic acid" refers to a polymeric compound including covalently linked nucleotides, which can be made up of natural subunits (e.g., purine or pyrimidine bases) or non-natural subunits (e.g., morpholine ring). Purine bases include adenine, guanine, hypoxanthine, and xanthine, and

pyrimidine bases include uracil, thymine, and cytosine. Nucleic acid molecules include polyribonucleic acid (RNA), which includes mRNA, microRNA, siRNA, viral genomic RNA, and synthetic RNA, and polydeoxyribonucleic acid (DNA), which includes cDNA, genomic DNA, and synthetic DNA, either of which may be single or double stranded. If single-stranded, the nucleic acid molecule may be the coding strand or non-coding (anti-sense) strand. A nucleic acid molecule encoding an amino acid sequence includes all nucleotide sequences that encode the same amino acid sequence. Some versions of the nucleotide sequences may also include intron(s) to the extent that the intron(s) would be removed through co- or post-transcriptional mechanisms. In other words, different nucleotide sequences may encode the same amino acid sequence as the result of the redundancy or degeneracy of the genetic code, or by splicing.

[0033] Variants of nucleic acid molecules of this disclosure are also contemplated. Variant nucleic acid molecules are at least 70%, 75%, 80%, 85%, 90%, and are preferably 95%, 96%, 97%, 98%, 99%, or 99.9% identical a nucleic acid molecule of a defined or reference polynucleotide as described herein, or that hybridize to a polynucleotide under stringent hybridization conditions of 0.015M sodium chloride, 0.0015M sodium citrate at about 65-68° C. or 0.015M sodium chloride, 0.0015M sodium citrate, and 50% formamide at about 42° C. Nucleic acid molecule variants retain the capacity to encode a binding domain thereof having a functionality described herein, such as binding a target molecule.

[0034] "Percent sequence identity" refers to a relationship between two or more sequences, as determined by comparing the sequences. Preferred methods to determine sequence identity are designed to give the best match between the sequences being compared. For example, the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in one or both of a first and a second amino acid or nucleic acid sequence for optimal alignment). Further, non-homologous sequences may be disregarded for comparison purposes. The percent sequence identity referenced herein is calculated over the length of the reference sequence, unless indicated otherwise. Methods to determine sequence identity and similarity can be found in publicly available computer programs. Sequence alignments and percent identity calculations may be performed using a BLAST program (e.g., BLAST 2.0, BLASTP, BLASTN, or BLASTX). The mathematical algorithm used in the BLAST programs can be found in Altschul et al., Nucleic Acids Res. 25:3389-3402, 1997. Within the context of this disclosure, it will be understood that where sequence analysis software is used for analysis, the results of the analysis are based on the "default values" of the program referenced. "Default values" mean any set of values or parameters which originally load with the software when first initialized.

[0035] The term "isolated" means that the material is removed from its original environment (e.g., the natural environment if it is naturally occurring). For example, a naturally occurring nucleic acid or polypeptide present in a living animal is not isolated, but the same nucleic acid or polypeptide, separated from some or all of the co-existing materials in the natural system, is isolated. Such nucleic acid could be part of a vector and/or such nucleic acid or polypeptide could be part of a composition (e.g., a cell lysate), and still be isolated in that such vector or composition is not part of the natural environment for the nucleic acid or polypeptide. Any of the presently disclosed compositions (e.g., antibody, antigen-binding fragment, pharmaceutical composition, polynucleotide, vector, host cell) can be provided in isolated form.

[0036] The term "gene" means the segment of DNA or RNA involved in producing a polypeptide chain; in certain contexts, it includes regions preceding and following the coding region (e.g., 5' untranslated region (UTR) and 3' UTR) as well as intervening sequences (introns) between individual coding segments (exons).

[0037] A "functional variant" refers to a polypeptide or polynucleotide that is structurally similar or substantially structurally similar to a parent or reference compound of this disclosure, but differs slightly in composition (e.g., one base, atom or functional group is different, added, or removed), such that the polypeptide or encoded polypeptide is capable of performing at least one function of the parent polypeptide with at least 50% efficiency, preferably at least 55%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.9%, or 100% level of activity of the parent polypeptide. In other words, a functional variant of a polypeptide or encoded polypeptide of this disclosure has "similar binding," "similar affinity" or "similar activity" when the functional variant displays no more than a 50% reduction in performance in a selected assay as compared to the parent or reference polypeptide, such as an assay for measuring binding affinity (e.g., Biacore® or tetramer staining measuring an association (Ka) or a dissociation (K_D) constant).

[0038] As used herein, a "functional portion" or "functional fragment" refers to a polypeptide or polynucleotide that comprises only a domain, portion or fragment of a parent or reference compound, and the polypeptide or encoded polypeptide retains at least 50% activity associated with the domain, portion or fragment of the parent or reference compound, preferably at least 55%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.9%, or 100% level of activity of the parent polypeptide, or provides a biological benefit (e.g., effector function). A "functional portion" or "functional fragment" of a polypeptide or encoded polypeptide of this disclosure has "similar binding" or "similar activity" when the functional portion or fragment displays no more than a 50% reduction in performance in a selected assay as compared to the parent or reference polypeptide (preferably no more than 20% or 10%, or no more than a log difference as compared to the parent or reference with regard to affinity).

[0039] As used herein, the term "engineered," "recombinant," or "non-natural" refers to an organism, microorganism, cell, nucleic acid molecule, or vector that includes at least one genetic alteration or has been modified by introduction of an exogenous or heterologous nucleic acid molecule, wherein such alterations or modifications are introduced by genetic engineering (i.e., human intervention). Genetic alterations include, for example, modifications introducing expressible nucleic acid molecules encoding functional RNA, proteins, fusion proteins or enzymes, or other nucleic acid molecule additions, deletions, substitutions, or other functional disruption of a cell's genetic material. Additional modifications include, for example, non-coding regulatory regions in which the modifications alter expression of a polynucleotide, gene, or operon.

[0040] As used herein, "heterologous" or "non-endogenous" or "exogenous" refers to any gene, protein, com-

pound, nucleic acid molecule, or activity that is not native to a host cell or a subject, or any gene, protein, compound, nucleic acid molecule, or activity native to a host cell or a subject that has been altered. Heterologous, non-endogenous, or exogenous includes genes, proteins, compounds, or nucleic acid molecules that have been mutated or otherwise altered such that the structure, activity, or both is different as between the native and altered genes, proteins, compounds, or nucleic acid molecules. In certain embodiments, heterologous, non-endogenous, or exogenous genes, proteins, or nucleic acid molecules (e.g., receptors, ligands, etc.) may not be endogenous to a host cell or a subject, but instead nucleic acids encoding such genes, proteins, or nucleic acid molecules may have been added to a host cell by conjugation, transformation, transfection, electroporation, or the like, wherein the added nucleic acid molecule may integrate into a host cell genome or can exist as extra-chromosomal genetic material (e.g., as a plasmid or other self-replicating vector). The term "homologous" or "homolog" refers to a gene, protein, compound, nucleic acid molecule, or activity found in or derived from a host cell, species, or strain. For example, a heterologous or exogenous polynucleotide or gene encoding a polypeptide may be homologous to a native polynucleotide or gene and encode a homologous polypeptide or activity, but the polynucleotide or polypeptide may have an altered structure, sequence, expression level, or any combination thereof. A non-endogenous polynucleotide or gene, as well as the encoded polypeptide or activity, may be from the same species, a different species, or a combination thereof.

[0041] In certain embodiments, a nucleic acid molecule or portion thereof native to a host cell will be considered heterologous to the host cell if it has been altered or mutated, or a nucleic acid molecule native to a host cell may be considered heterologous if it has been altered with a heterologous expression control sequence or has been altered with an endogenous expression control sequence not normally associated with the nucleic acid molecule native to a host cell. In addition, the term "heterologous" can refer to a biological activity that is different, altered, or not endogenous to a host cell. As described herein, more than one heterologous nucleic acid molecule can be introduced into a host cell as separate nucleic acid molecules, as a plurality of individually controlled genes, as a polycistronic nucleic acid molecule, as a single nucleic acid molecule encoding an antibody or antigen-binding fragment or other polypeptide, or any combination thereof.

[0042] As used herein, the term "endogenous" or "native" refers to a polynucleotide, gene, protein, compound, molecule, or activity that is normally present in a host cell or a subject.

[0043] The term "expression", as used herein, refers to the process by which a polypeptide is produced based on the encoding sequence of a nucleic acid molecule, such as a gene. The process may include transcription, post-transcriptional control, post-transcriptional modification, translation, post-translational control, post-translational modification, or any combination thereof. An expressed nucleic acid molecule is typically operably linked to an expression control sequence (e.g., a promoter).

[0044] The term "operably linked" refers to the association of two or more nucleic acid molecules on a single nucleic acid fragment so that the function of one is affected by the other. For example, a promoter is operably linked with a coding sequence when it is capable of affecting the expression of that coding sequence (i.e., the coding sequence is under the transcriptional control of the promoter). "Unlinked" means that the associated genetic elements are not closely associated with one another and the function of one does not affect the other.

[0045] As described herein, more than one heterologous nucleic acid molecule can be introduced into a host cell as separate nucleic acid molecules, as a plurality of individually controlled genes, as a polycistronic nucleic acid molecule, as a single nucleic acid molecule encoding a protein (e.g., a heavy chain of an antibody), or any combination thereof. When two or more heterologous nucleic acid molecules are introduced into a host cell, it is understood that the two or more heterologous nucleic acid molecules can be introduced as a single nucleic acid molecule (e.g., on a single vector), on separate vectors, integrated into the host chromosome at a single site or multiple sites, or any combination thereof. The number of referenced heterologous nucleic acid molecules or protein activities refers to the number of encoding nucleic acid molecules or the number of protein activities, not the number of separate nucleic acid molecules introduced into a host cell.

[0046] The term "construct" refers to any polynucleotide that contains a recombinant nucleic acid molecule (or, when the context clearly indicates, a fusion protein of the present disclosure). A (polynucleotide) construct may be present in a vector (e.g., a bacterial vector, a viral vector) or may be integrated into a genome. A "vector" is a nucleic acid molecule that is capable of transporting another nucleic acid molecule. Vectors may be, for example, plasmids, cosmids, viruses, a RNA vector or a linear or circular DNA or RNA molecule that may include chromosomal, non-chromosomal, semi-synthetic or synthetic nucleic acid molecules. Vectors of the present disclosure also include transposon systems (e.g., Sleeping Beauty, see, e.g., *Geurts et al., Mol. Ther.* 8:108, 2003: Mátés et al., Nat. Genet. 41:753, 2009). Exemplary vectors are those capable of autonomous replication (episomal vector), capable of delivering a polynucleotide to a cell genome (e.g., viral vector), or capable of expressing nucleic acid molecules to which they are linked (expression vectors).

[0047] As used herein, "expression vector" or "vector" refers to a DNA construct containing a nucleic acid molecule that is operably linked to a suitable control sequence capable of effecting the expression of the nucleic acid molecule in a suitable host. Such control sequences include a promoter to effect transcription, an optional operator sequence to control such transcription, a sequence encoding suitable mRNA ribosome binding sites, and sequences which control termination of transcription and translation. The vector may be a plasmid, a phage particle, a virus, or simply a potential genomic insert. Once transformed into a suitable host, the vector may replicate and function independently of the host genome, or may, in some instances, integrate into the genome itself or deliver the polynucleotide contained in the vector into the genome without the vector sequence. In the present specification, "plasmid," "expression plasmid," "virus," and "vector" are often used interchangeably.

[0048] The term "introduced" in the context of inserting a nucleic acid molecule into a cell, means "transfection", "transformation," or "transduction" and includes reference to the incorporation of a nucleic acid molecule into a eukaryotic or prokaryotic cell wherein the nucleic acid

molecule may be incorporated into the genome of a cell (e.g., chromosome, plasmid, plastid, or mitochondrial DNA), converted into an autonomous replicon, or transiently expressed (e.g., transfected mRNA).

[0049] In certain embodiments, polynucleotides of the present disclosure may be operatively linked to certain elements of a vector. For example, polynucleotide sequences that are needed to effect the expression and processing of coding sequences to which they are ligated may be operatively linked. Expression control sequences may include appropriate transcription initiation, termination, promoter, and enhancer sequences; efficient RNA processing signals such as splicing and polyadenylation signals; sequences that stabilize cytoplasmic mRNA; sequences that enhance translation efficiency (i.e., Kozak consensus sequences); sequences that enhance protein stability; and possibly sequences that enhance protein secretion. Expression control sequences may be operatively linked to a gene of interest if they are contiguous with the gene of interest or if they act in trans or at a distance to control the gene of interest.

[0050] In certain embodiments, the vector comprises a plasmid vector or a viral vector (e.g., a lentiviral vector or a γ-retroviral vector). Viral vectors include retrovirus, adenovirus, parvovirus (e.g., adeno-associated viruses), coronavirus, negative strand RNA viruses such as orthomyxovirus (e.g., influenza virus), rhabdovirus (e.g., rabies and vesicular stomatitis virus), paramyxovirus (e.g., measles and Sendai), positive strand RNA viruses such as picornavirus and alphavirus, and double-stranded DNA viruses including adenovirus, herpesvirus (e.g., Herpes Simplex virus types 1 and 2, Epstein-Barr virus, cytomegalovirus), and poxvirus (e.g., vaccinia, fowlpox, and canarypox). Other viruses include, for example, Norwalk virus, togavirus, flavivirus, reoviruses, papovavirus, hepadnavirus, and hepatitis virus. Examples of retroviruses include avian leukosis-sarcoma, mammalian C-type, B-type viruses, D type viruses, HTLV-BLV group, lentivirus, spumavirus (Coffin, J. M., Retroviridae: The viruses and their replication, In Fundamental Virology, Third Edition, B. N. Fields et al., Eds., Lippincott-Raven Publishers, Philadelphia, 1996).

[0051] "Retroviruses" are viruses having an RNA genome, which is reverse-transcribed into DNA using a reverse transcriptase enzyme, the reverse-transcribed DNA is then incorporated into the host cell genome. "Gammaretrovirus" refers to a genus of the retroviridae family. Examples of gammaretroviruses include mouse stem cell virus, murine leukemia virus, feline leukemia virus, feline sarcoma virus, and avian reticuloendotheliosis viruses.

[0052] "Lentiviral vectors" include HIV-based lentiviral vectors for gene delivery, which can be integrative or non-integrative, have relatively large packaging capacity, and can transduce a range of different cell types. Lentiviral vectors are usually generated following transient transfection of three (packaging, envelope, and transfer) or more plasmids into producer cells. Like HIV, lentiviral vectors enter the target cell through the interaction of viral surface glycoproteins with receptors on the cell surface. On entry, the viral RNA undergoes reverse transcription, which is mediated by the viral reverse transcriptase complex. The product of reverse transcription is a double-stranded linear viral DNA, which is the substrate for viral integration into the DNA of infected cells.

[0053] In certain embodiments, the viral vector can be a gammaretrovirus, e.g., Moloney murine leukemia virus (MLV)-derived vectors. In other embodiments, the viral vector can be a more complex retrovirus-derived vector, e.g., a lentivirus-derived vector. HIV-1-derived vectors belong to this category. Other examples include lentivirus vectors derived from HIV-2, FIV, equine infectious anemia virus, SIV, and Maedi-Visna virus (ovine lentivirus). Methods of using retroviral and lentiviral viral vectors and packaging cells for transducing mammalian host cells with viral particles containing transgenes are known in the art and have been previous described, for example, in: U.S. Pat. No. 8,119,772; Walchli et al., *PLoS One* 6:327930, 2011; Zhao et al., *J. Immunol.* 174:4415, 2005; Engels et al., *Hum. Gene Ther.* 14:1155, 2003; Frecha et al., *Mol. Ther.* 18:1748, 2010; and Verhoeyen et al., *Methods Mol. Biol.* 506:97, 2009. Retroviral and lentiviral vector constructs and expression systems are also commercially available. Other viral vectors also can be used for polynucleotide delivery including DNA viral vectors, including, for example adenovirus-based vectors and adeno-associated virus (AAV)-based vectors; vectors derived from herpes simplex viruses (HSVs), including amplicon vectors, replication-defective HSV and attenuated HSV (Krisky et al., *Gene Ther.* 5:1517, 1998).

[0054] Other vectors that can be used with the compositions and methods of this disclosure include those derived from baculoviruses and α-viruses. (Jolly, D J. 1999. Emerging Viral Vectors. pp 209-40 in Friedmann T. ed. The Development of Human Gene Therapy. New York: Cold Spring Harbor Lab), or plasmid vectors (such as sleeping beauty or other transposon vectors).

[0055] When a viral vector genome comprises a plurality of polynucleotides to be expressed in a host cell as separate transcripts, the viral vector may also comprise additional sequences between the two (or more) transcripts allowing for bicistronic or multicistronic expression. Examples of such sequences used in viral vectors include internal ribosome entry sites (IRES), furin cleavage sites, viral 2A peptide, or any combination thereof.

[0056] Plasmid vectors, including DNA-based antibody or antigen-binding fragment-encoding plasmid vectors for direct administration to a subject, are described further herein.

[0057] As used herein, the term "host" refers to a cell or microorganism targeted for genetic modification with a heterologous nucleic acid molecule to produce a polypeptide of interest (e.g., an antibody of the present disclosure).

[0058] A host cell may include any individual cell or cell culture which may receive a vector or the incorporation of nucleic acids or express proteins. The term also encompasses progeny of the host cell, whether genetically or phenotypically the same or different. Suitable host cells may depend on the vector and may include mammalian cells, animal cells, human cells, simian cells, insect cells, yeast cells, and bacterial cells. These cells may be induced to incorporate the vector or other material by use of a viral vector, transformation via calcium phosphate precipitation, DEAE-dextran, electroporation, microinjection, or other methods. See, for example, Sambrook et al., *Molecular Cloning: A Laboratory Manual* 2d ed. (Cold Spring Harbor Laboratory, 1989).

[0059] In the context of a SARS-CoV-2 infection, a "host" refers to a cell or a subject infected with SARS-CoV-2.

[0060] "Antigen" or "Ag", as used herein, refers to an immunogenic molecule that provokes an immune response. This immune response may involve antibody production,

activation of specific immunologically-competent cells, activation of complement, antibody dependent cytotoxicity, or any combination thereof. An antigen (immunogenic molecule) may be, for example, a peptide, glycopeptide, polypeptide, glycopolypeptide, polynucleotide, polysaccharide, lipid, or the like. It is readily apparent that an antigen can be synthesized, produced recombinantly, or derived from a biological sample. Exemplary biological samples that can contain one or more antigens include tissue samples, stool samples, cells, biological fluids, or combinations thereof. Antigens can be produced by cells that have been modified or genetically engineered to express an antigen. Antigens can also be present in SARS-CoV-2 (e.g., a surface glycoprotein or portion thereof), such as present in a virion, or expressed or presented on the surface of a cell infected by SARS-CoV-2.

[0061] The term "epitope" or "antigenic epitope" includes any molecule, structure, amino acid sequence, or protein determinant that is recognized and specifically bound by a cognate binding molecule, such as an immunoglobulin, or other binding molecule, domain, or protein. Epitopic determinants generally contain chemically active surface groupings of molecules, such as amino acids or sugar side chains, and can have specific three-dimensional structural characteristics, as well as specific charge characteristics. Where an antigen is or comprises a peptide or protein, the epitope can be comprised of consecutive amino acids (e.g., a linear epitope), or can be comprised of amino acids from different parts or regions of the protein that are brought into proximity by protein folding (e.g., a discontinuous or conformational epitope), or non-contiguous amino acids that are in close proximity irrespective of protein folding.

Antibodies and Antigen-Binding Fragments

[0062] In one aspect, the present disclosure provides an isolated antibody, or an antigen-binding fragment thereof, that comprises a heavy chain variable domain (VH) comprising a CDRH1, a CDRH2, and a CDRH3, and a light chain variable domain (VL) comprising a CDRL1, a CDRL2, and a CDRL3, and is capable of binding to a surface glycoprotein of SARS-CoV-2. In certain embodiments, the antibody or antigen-binding fragment is capable of binding to a surface glycoprotein of SARS-CoV-2 expressed on a cell surface of a host cell and/or on a SARS-CoV-2 virion.

[0063] In certain embodiments, an antibody or antigen-binding fragment of the present disclosure associates with or unites with a SARS-CoV-2 surface glycoprotein epitope or antigen comprising the epitope, while not significantly associating or uniting with any other molecules or components in a sample.

[0064] In certain embodiments, an antibody or antigen-binding fragment of the present disclosure associates with or unites (e.g., binds) to a SARS-CoV-2 surface glycoprotein epitope, and can also associate with or unite with an epitope from another coronavirus (e.g., SARS CoV) present in the sample, but does not significantly associate or unite with any other molecules or components in the sample. In other words, in certain embodiments, an antibody or antigen binding fragment of the present disclosure is cross-reactive for SARS-CoV-2 and one or more additional coronavirus, and is specific for the SARS-CoV-2 and one or more additional coronavirus.

[0065] In certain embodiments, an antibody or antigen-binding fragment of the present disclosure specifically binds to a SARS-CoV-2 surface glycoprotein. As used herein, "specifically binds" refers to an association or union of an antibody or antigen-binding fragment to an antigen with an affinity or K_a (i.e., an equilibrium association constant of a particular binding interaction with units of 1/M) equal to or greater than 10^{-5} M^{-1} (which equals the ratio of the on-rate [K_{on}] to the off rate [K_{off}] for this association reaction), while not significantly associating or uniting with any other molecules or components in a sample. Alternatively, affinity may be defined as an equilibrium dissociation constant (K_a) of a particular binding interaction with units of M (e.g., 10^{-5} M to 10^{-13} M). Antibodies may be classified as "high-affinity" antibodies or as "low-affinity" antibodies. "High-affinity" antibodies refer to those antibodies having a K_a of at least 10^7 M^{-1}, at least 10^8 M^{-1}, at least 10^9 M^{-1}, at least 10^{10} M^{-1}, at least 10^{11} M^{-1}, at least 10^{12} M^{-1}, or at least 10^{-13} M^{-1}. "Low-affinity" antibodies refer to those antibodies having a K_a of up to 10^7 M^{-1}, up to 10^6 M^{-1}, up to 10^5 M^{-1}. Alternatively, affinity may be defined as an equilibrium dissociation constant (K_a) of a particular binding interaction with units of M (e.g., 10^{-5} M to 10^{-13} M).

[0066] A variety of assays are known for identifying antibodies of the present disclosure that bind a particular target, as well as determining binding domain or binding protein affinities, such as Western blot, ELISA, analytical ultracentrifugation, spectroscopy, and surface plasmon resonance (Biacore®) analysis (see, e.g., Scatchard et al., *Ann. N.Y. Acad. Sci.* 51:660, 1949; *Wilson, Science* 295:2103, 2002; Wolff et al., *Cancer Res.* 53:2560, 1993; and U.S. Pat. Nos. 5,283,173, 5,468,614, or the equivalent). Assays for assessing affinity or apparent affinity or relative affinity are also known.

[0067] In certain examples, binding can be determined by recombinantly expressing a SARS-CoV-2 antigen in a host cell (e.g., by transfection) and immunostaining the (e.g., fixed, or fixed and permeabilized) host cell with antibody and analyzing binding by flow cytometry (e.g., using a ZE5 Cell Analyzer (BioRad®) and FlowJo software (TreeStar). In some embodiments, positive binding can be defined by differential staining by antibody of SARS-CoV-2-expressing cells versus control (e.g., mock) cells.

[0068] In certain embodiments, an antibody of the present disclosure is capable of neutralizing infection by SARS-CoV-2. As used herein, a "neutralizing antibody" is one that can neutralize, i.e., prevent, inhibit, reduce, impede, or interfere with, the ability of a pathogen to initiate and/or perpetuate an infection in a host. The terms "neutralizing antibody" and "an antibody that neutralizes" or "antibodies that neutralize" are used interchangeably herein. In any of the presently disclosed embodiments, the antibody or antigen-binding fragment is capable of preventing and/or neutralizing a SARS-CoV-2 infection in an in vitro model of infection and/or in an in vivo animal model of infection and/or in a human.

[0069] In certain embodiments, the antibody or antigen-binding fragment (i) recognizes an epitope in the ACE2 receptor binding motif (RBM, SEQ ID NO.:390) of SARS-CoV-2; (ii) is capable of blocking an interaction between SARS-CoV-2 and ACE2; (ii) is capable of binding to SARS-CoV-2 S protein with greater avidity than to SARS coronavirus S protein; (iv) is capable of staining about 30%, about 35%, about 40%, about 50%, about 55%, about 56%,

about 57%, about 58%, about 59%, about 60%, or more of target cells expressing SARS-CoV-2 surface glycoprotein in a sample comprising about 50,000 of the target cells (e.g., ExpiCHO cells) in approximately 100 μL when the antibody or antigen-binding fragment is present at 10 μg/ml (e.g., staining as determined by a flow cytometry ELISA); (v) recognizes an epitope that is conserved in the ACE2 RBM of SARS-CoV-2 and in an ACE2 RBM of SARS coronavirus; (vi) is cross-reactive against SARS-CoV-2 and SARS coronavirus; (vii) recognizes an epitope in the SARS-CoV-2 \surface glycoprotein that is not in the ACE2 RBM; or (viii) any combination of (i)-(vii).

[0070] Terms understood by those in the art of antibody technology are each given the meaning acquired in the art, unless expressly defined differently herein. For example, the term "antibody" refers to an intact antibody comprising at least two heavy (H) chains and two light (L) chains interconnected by disulfide bonds, as well as any antigen-binding portion or fragment of an intact antibody that has or retains the ability to bind to the antigen target molecule recognized by the intact antibody, such as an scFv, Fab, or Fab'2 fragment. Thus, the term "antibody" herein is used in the broadest sense and includes polyclonal and monoclonal antibodies, including intact antibodies and functional (antigen-binding) antibody fragments thereof, including fragment antigen binding (Fab) fragments, F(ab')2 fragments, Fab' fragments, Fv fragments, recombinant IgG (rIgG) fragments, single chain antibody fragments, including single chain variable fragments (scFv), and single domain antibodies (e.g., sdAb, sdFv, nanobody) fragments. The term encompasses genetically engineered and/or otherwise modified forms of immunoglobulins, such as intrabodies, peptibodies, chimeric antibodies, fully human antibodies, humanized antibodies, and heteroconjugate antibodies, multispecific, e.g., bispecific antibodies, diabodies, triabodies, tetrabodies, tandem di-scFv, and tandem tri-scFv. Unless otherwise stated, the term "antibody" should be understood to encompass functional antibody fragments thereof. The term also encompasses intact or full-length antibodies, including antibodies of any class or sub-class, including IgG and sub-classes thereof (IgG1, IgG2, IgG3, IgG4), IgM, IgE, IgA, and IgD.

[0071] The terms "VL" or "VL" and "VH" or "VH" refer to the variable binding region from an antibody light chain and an antibody heavy chain, respectively. In certain embodiments, a VL is a kappa (κ) class (also "VK" herein). In certain embodiments, a VL is a lambda (k) class. The variable binding regions comprise discrete, well-defined sub-regions known as "complementarity determining regions" (CDRs) and "framework regions" (FRs). The terms "complementarity determining region," and "CDR," are synonymous with "hypervariable region" or "HVR," and refer to sequences of amino acids within antibody variable regions, which, in general, together confer the antigen specificity and/or binding affinity of the antibody, wherein consecutive CDRs (i.e., CDR1 and CDR2, CDR2 and CDR3) are separated from one another in primary structure by a framework region. There are three CDRs in each variable region (HCDR1, HCDR2, HCDR3; LCDR1, LCDR2, LCDR3; also referred to as CDRHs and CDRLs, respectively). In certain embodiments, an antibody VH comprises four FRs and three CDRs as follows: FR1-HCDR1-FR2-HCDR2-FR3-HCDR3-FR4; and an antibody VL comprises four FRs and three CDRs as follows: FR1-LCDR1-FR2-LCDR2-FR3-LCDR3-FR4. In general, the VH and the VL together form the antigen-binding site through their respective CDRs.

[0072] As used herein, a "variant" of a CDR refers to a functional variant of a CDR sequence having up to 1-3 amino acid substitutions (e.g., conservative or non-conservative substitutions), deletions, or combinations thereof.

[0073] Numbering of CDR and framework regions may be according to any known method or scheme, such as the Kabat, Chothia, EU, IMGT, and AHo numbering schemes (see, e.g., Kabat et al., "Sequences of Proteins of Immunological Interest, US Dept. Health and Human Services, Public Health Service National Institutes of Health, 1991, 5th ed.; Chothia and Lesk, *J. Mol. Biol.* 196:901-917 (1987)); Lefranc et al., *Dev. Comp. Immunol.* 27:55, 2003; Honegger and Pluckthun, *J. Mol. Bio.* 309:657-670 (2001)). Equivalent residue positions can be annotated and for different molecules to be compared using Antigen receptor Numbering And Receptor Classification (ANARCI) software tool (2016, Bioinformatics 15:298-300). Accordingly, identification of CDRs of an exemplary variable domain (VH or VL) sequence as provided herein according to one numbering scheme is not exclusive of an antibody comprising CDRs of the same variable domain as determined using a different numbering scheme. In certain embodiments, an antibody or antigen-binding fragment is provided that comprises the three CDRs of a VH sequence according to any one of SEQ ID NOs.: 5, 21, 37, 53, 69, 85, 101, 117, 133, 149, 165, 181, 197, 213, 229, 245, 261, 277, 293, 309, 325, 341, 357, 374, 377, 395, or 415, and/or the three CDRs of a VL sequence according to any one of SEQ ID NOs.: 13, 29, 45, 61, 77, 93, 109, 125, 141, 157, 173, 189, 205, 221, 237, 253, 269, 285, 301, 317, 333, 349, 365, 380, 383, 385, 388, 392, 393, 400, 402, 404, and 406-414, as determined using any known CDR numbering method, including the Kabat, Chothia, EU, IMGT, Martin (Enhanced Chothia), Contact, and AHo numbering methods. In certain embodiments, CDRs are according to the IMGT numbering method. In certain embodiments, CDRs are according to the antibody numbering method developed by the Chemical Computing Group (CCG); e.g., using Molecular Operating Environment (MOE) software (www.chemcomp.com).

[0074] In certain embodiments, an antibody or an antigen-binding fragment is provided that comprises a heavy chain variable domain (VH) comprising a CDRH1, a CDRH2, and a CDRH3, and a light chain variable domain (VL) comprising a CDRL1, a CDRL2, and a CDRL3, wherein: (i) the CDRH1 comprises or consists of the amino acid sequence according to any one of SEQ ID NOs.: 6, 22, 38, 54, 70, 86, 102, 118, 134, 150, 166, 182, 198, 214, 230, 246, 262, 278, 294, 310, 326, 342, or 358, ora sequence variant thereof comprising one, two, or three acid substitutions, one or more of which substitutions is optionally a conservative substitution and/or is a substitution to a germline-encoded amino acid; (ii) the CDRH2 comprises or consists of the amino acid sequence according to any one of SEQ ID NOs.: 7, 23, 39, 55, 71, 87, 103, 119, 135, 151, 167, 183, 199, 215, 231, 247, 263, 279, 295, 311, 327, 343, 359, or 416, or a sequence variant thereof comprising one, two, or three amino acid substitutions, one or more of which substitutions is optionally a conservative substitution and/or is a substitution to a germline-encoded amino acid; (iii) the CDRH3 comprises or consists of the amino acid sequence according to any one of SEQ ID NOs.: 8, 24, 40, 56, 72, 88, 104, 120, 136, 152, 168,

184, 200, 216, 232, 248, 264, 280, 296, 312, 328, 344, 360, 375, 378, or 397, or a sequence variant thereof comprising one, two, or three amino acid substitutions, one or more of which substitutions is optionally a conservative substitution and/or is a substitution to a germline-encoded amino acid; (iv) the CDRL1 comprises or consists of the amino acid sequence according to any one of SEQ ID NOs.: 14, 30, 46, 62, 78, 94, 110, 126, 142, 158, 174, 190, 206, 222, 238, 254, 270, 286, 302, 318, 334, 350, 366, 398, 399, 401, 403, or 405, or a sequence variant thereof comprising one, two, or three amino acid substitutions, one or more of which substitutions is optionally a conservative substitution and/or is a substitution to a germline-encoded amino acid; (v) the CDRL2 comprises or consists of the amino acid sequence according to any one of SEQ ID NOs.: 15, 31, 47, 63, 79, 95, 111, 127, 143, 159, 175, 191, 207, 223, 239, 255, 271, 287, 303, 319, 335, 351, or 367, orasequence variant thereof comprising one, two, or three amino acid substitutions, one or more of which substitutions is optionally a conservative substitution and/or is a substitution to a germline-encoded amino acid; and/or (vi) the CDRL3 comprises or consists of the amino acid sequence according to any one of SEQ ID NOs.: 16, 32, 48, 64, 80, 96, 112, 128, 144, 160, 176, 192, 208, 224, 240, 256, 272, 288, 304, 320, 336, 352, 358, 386, or 394, or a sequence variant thereof comprising having one, two, or three amino acid substitutions, one or more of which substitutions is optionally a conservative substitution and/or is a substitution to a germline-encoded amino acid, wherein the antibody or antigen binding fragment is capable of binding to a surface glycoprotein of SARS-CoV-2 expressed on a cell surface of a host cell.

[0075] In any of the presently disclosed embodiments, the antibody or antigen-binding fragment is capable of preventing and/or neutralizing a SARS-CoV-2 infection in an in vitro model of infection and/or in an in vivo animal model of infection and/or in a human.

[0076] In any of the presently disclosed embodiments, the antibody or antigen-binding fragment comprises CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 amino acid sequences according to SEQ ID NOs.: (i) 6-8 and 14-16, respectively; (ii) 22-24 and 30-32, respectively; (iii) 22-24, 398, 31, and 32, respectively; (iv) 22-24, 399, 31, and 32, respectively; (v) 22-24, 401, 31, and 32, respectively; (vi) 22-24, 403, 31, and 32, respectively; (v) 22-24, 405, 31, and 32, respectively; (vi) 38-40 and 46-48, respectively; (vii) 38-40, 398, 47, and 48, respectively; (viii) 38-40, 399, 47, and 48, respectively; (viv) 38-40, 401, 47, and 48, respectively; (x) 38-40, 403, 47, and 48, respectively; (xi) 38-40, 405, 47, and 48, respectively; (xii) 54-56 and 62-64, respectively; (xiii) 70-72 and 78-80, respectively; (xiv) 86-88 and 94-96, respectively; (xv) 102-104 and 110-112, respectively; (xvi) 118-120 and 126-128, respectively; (xvii) 134-136 and 142-144, respectively; (xviii) 150-152 and 158-160, respectively; (xix) 166-168 and 174-176, respectively; (xx) 182-184 and 190-192, respectively; (xxi) 198-200 and 206-208, respectively; (xxii) 214-216 and 222-224, respectively; (xxiii) 230-232 and 238-240, respectively; (xxiv) 246-248 and 254-256, respectively; (xxv) 262-264 and 270-272, respectively; (xxxvi) 278-280 and 286-288, respectively; (xxvii) 294-296 and 302-304, respectively; (xxviii) 310-312 and 318-320, respectively; (xxix) 326-328 and 334-336, respectively; (xxx) 342-344 and 350-352, respectively; (xxxi) 358-360 and 366-368, respectively; (xxxii) 22, 23, 375, and 30-32, respectively; (xxxiii) 22, 23, 375, 398, 31, and 32, respectively; (xxxiv) 22, 23, 375, 399, 31, and 32, respectively; (xxxv) 22, 23, 375, 401, 31, and 32, respectively; (xxxvi) 22, 23, 375, 403, 31, and 32, respectively; (xxxvii) 22, 23, 375, 405, 31, and 32, respectively; (xxxviii) 22, 23, 378, and 30-32, respectively; (xxxix) 22, 23, 378, 398, 31, and 32, respectively; (xl) 22, 23, 378, 399, 31, and 32, respectively; (xli) 22, 23, 378, 401, 31, and 32, respectively; (xlii) 22, 23, 378, 403, 31, and 32, respectively; (xliii) 22, 23, 378, 405, 31, and 32, respectively; (xliv) 22-24, 30, 31, and 386, respectively; (xlv) 22-24, 398, 31, and 386, respectively; (xlvi) 22-24, 399, 31, and 386, respectively; (xlvii) 22-24, 401, 31, and 386, respectively; (xlviii) 22-24, 403, 31, and 386, respectively; (xlix) 22-24, 405, 31, and 386, respectively; (1) 38-40, 46, 47, and 386, respectively; (li) 38-40, 398, 47, and 386, respectively; (lii) 38-40, 399, 47, and 386, respectively; (liii) 38-40, 401, 47, and 386, respectively; (liv) 38-40, 403, 47, and 386, respectively; (lv) 38-40, 405, 47, and 386, respectively; (lvi) 22-24, 30, 31, and 394, respectively; (lvii) 22-24, 398, 31, and 394, respectively; (lviii) 22-24, 399, 31, and 394, respectively; (lix) 22-24, 401, 31, and 394, respectively; (lx) 22-24, 403, 31, and 394, respectively; (lxi) 22-24, 405, 31, and 394, respectively; (lxii) 22, 23, 375, 30, 31, and 394, respectively; (lxiii) 22, 23, 375, 30, 31, and 386, respectively; (lxiv) 22, 23, 375, 398, 31, and 386, respectively; (lxv) 22, 23, 375, 399, 31, and 386, respectively; (lxvi) 22, 23, 375, 401, 31, and 386, respectively; (lxvii) 22, 23, 375, 403, 31, and 386, respectively; (lxviii) 22, 23, 375, 405, 31, and 386, respectively; (lxix) 22, 23, 378, 30, 31, and 394, respectively; (lxx) 22, 23, 378, 398, 31, and 394, respectively; (lxxi) 22, 23, 378, 399, 31, and 394, respectively; (lxxii) 22, 23, 378, 401, 31, and 394, respectively; (lxxiii) 22, 23, 378, 403, 31, and 394, respectively; (lxxiv) 22, 23, 378, 405, 31, and 394, respectively; (lxxv) 22, 23, 378, 30, 31, and 386, respectively; (lxxvi) 22, 23, 378, 398, 31, and 386, respectively; (lxxvii) 22, 23, 378, 399, 31, and 386, respectively; (lxxviii) 22, 23, 378, 401, 31, and 386, respectively; (lxxix) 22, 23, 378, 403, 31, and 386, respectively; (lxxx) 22, 23, 378, 405, 31, and 386, respectively; (lxxxi) 22, 23, 397, and 30-32, respectively; (lxxxii) 22, 23, 397, 398, 31, and 32, respectively; (lxxxiii) 22, 23, 397, 399, 31, and 32, respectively; (lxxxiv) 22, 23, 397, 401, 31, and 32, respectively; (lxxxv) 22, 23, 397, 403, 31, and 32, respectively; (lxxxvi) 22, 23, 397, 405, 31, and 32, respectively; (lxxxvii) 22, 23, 397, 30, 31, and 386, respectively; (lxxxviii) 22, 23, 397, 398, 31, and 386, respectively; (lxxxix) 22, 23, 397, 399, 31, and 386, respectively; (xc) 22, 23, 397, 401, 31, and 386, respectively; (xci) 22, 23, 397, 403, 31, and 386, respectively; (xcii) 22, 23, 397, 405, 31, and 386, respectively; (xciii) 22, 23, 397, 30, 31, and 394, respectively; (xciv) 22, 23, 397, 398, 31, and 394, respectively; (xcv) 22, 23, 397, 399, 31, and 394, respectively; (xcvi) 22, 23, 397, 401, 31, and 394, respectively; (xcvii) 22, 23, 397, 403, 31, and 394, respectively; (xcviii) 22, 23, 397, 405, 31, and 394, respectively; (xcix) 22, 416, 24, 30, 31, and 32, respectively; (c) 22, 416, 24, 30, 31, and 386, respectively; (ci) 22, 416, 24, 30, 31, and 394, respectively; (cii) 22, 416, 24, 398, 31, and 32, respectively; (ciii) 22, 416, 24, 398, 31, and 386, respectively; (civ) 22, 416, 24, 398, 31, and 394, respectively; (cv) 22, 416, 24, 399, 31, and 32, respectively; (cvi) 22, 416, 24, 399, 31, and 386, respectively; (cvii) 22, 416, 24, 399, 31, and 394, respectively; (cviii) 22, 416, 24, 401, 31, and 32, respectively; (cix) 22, 416, 24, 401, 31, and 386, respectively; (cx) 22, 416, 24, 401, 31, and 394, respectively; (cxi)

22, 416, 24, 403, 31, and 32, respectively; (cxii) 22, 416, 24, 403, 31, and 386, respectively; (cxiii) 22, 416, 24, 403, 31, and 394, respectively; (cxiv) 22, 416, 24, 405, 31, and 32, respectively; (cxv) 22, 416, 24, 405, 31, and 386, respectively; (cxvi) 22, 416, 24, 405, 31, and 394, respectively; (cxvii) 22, 416, 375, 30, 31, and 32, respectively; (cxviii) 22, 416, 375, 398, 31, and 386, respectively; (cxix) 22, 416, 375, 398, 31, and 394, respectively; (cxx) 22, 416, 375, 399, 31, and 386, respectively; (cxxi) 22, 416, 375, 399, 31, and 394, respectively; (cxxii) 22, 416, 375, 401, 31, and 386, respectively; (cxxiii) 22, 416, 375, 401, 31, and 394, respectively; (cxxiv) 22, 416, 375, 403, 31, and 386, respectively; (cxxv) 22, 416, 375, 403, 31, and 394, respectively; (cxxvi) 22, 416, 375, 405, 31, and 386, respectively; (cxxvii) 22, 416, 375, 405, 31, and 394, respectively; (cxxviii) 22, 416, 378, 30, 31, and 32, respectively; (cxxix) 22, 416, 378, 398, 31, and 386, respectively; (cxxx) 22, 416, 378, 398, 31, and 394, respectively; (cxxxi) 22, 416, 378, 399, 31, and 386, respectively; (cxxxii) 22, 416, 378, 399, 31, and 394, respectively; (cxxxiii) 22, 416, 378, 401, 31, and 386, respectively; (cxxxiv) 22, 416, 378, 401, 31, and 394, respectively; (cxxxv) 22, 416, 375, 403, 31, and 386, respectively; (cxxxvi) 22, 416, 378, 403, 31, and 394, respectively; (cxxxvii) 22, 416, 378, 405, 31, and 386, respectively; (cxxxviii) 22, 416, 378, 405, 31, and 394, respectively; (cxxxix) 22, 416, 397, 30, 31, and 32, respectively; (cxl) 22, 416, 397, 398, 31, and 386, respectively; (cxli) 22, 416, 397, 398, 31, and 394, respectively; (cxlii) 22, 416, 397, 399, 31, and 386, respectively; (ccxliii) 22, 416, 397, 399, 31, and 394, respectively; (cxliv) 22, 416, 397, 401, 31, and 386, respectively; (cxlv) 22, 416, 397, 401, 31, and 394, respectively; (cxlvi) 22, 416, 375, 403, 31, and 386, respectively; (cxlvii) 22, 416, 397, 403, 31, and 394, respectively; (cxlviii) 22, 416, 397, 405, 31, and 386, respectively; or (cxlix) 22, 416, 397, 405, 31, and 394, respectively.

In certain embodiments, an antibody or an antigen-binding fragment of the present disclosure comprises a CDRH1, a CDRH2, a CDRH3, a CDRL1, a CDRL2, and a CDRL3, wherein each CDR is independently selected from a corresponding CDR of nCoV-3 mAb, nCoV-17 mAb, nCoV-6 mAb, nCoV-16 mAb, nCoV-20 mAb, nCoV-4 mAb, nCoV-4-v2 mAb, nCoV-4-v3 mAb, nCoV-15 mAb, nCoV-12 mAb, nCoV-5 mAb, nCoV-14 mAb, nCoV-9 mAb, nCoV-18 mAb, nCoV-8 mAb, nCoV-7 mAb, nCoV-2 mAb, nCoV-19 mAb, nCoV-1 mAb, nCoV-11 mAb, nCoV-13 mAb, nCoV-10 mAb, nCoV-10-v2 mAb, nCoV-10 mAb VL-v3, nCoV-10 mAb VL-v4, nCoV-10 mAb VL-v5, nCoV-10 mAb VL-v6, nCoV-10 mAb VL-v7, nCoV-10 mAb VL-v8, nCoV-10 mAb VL-v9, nCoV-10 mAb VL-v10, nCoV-10 mAb VL-v11, nCoV-10 mAb VL-v12, nCoV-10 mAb VL-v13, nCoV-10 mAb VL-v14, nCoV-10 mAb VL-v15, nCoV-10 mAb VL-v16, nCoV-10 mAb VL-v17, nCoV-10 mAb VL-v18, nCoV-10 mAb VL-v19, nCoV-10 mAb VL-v20, nCoV-10 mAb VH-v3, nCoV-10 mAb VH-v4, nCoV-10 mAb VH-v5, or nCoV-10 mAb VH-v21, as provided in Table 1. That is, all combinations of CDRs from the SARS-CoV-2 mAbs and the variant sequences thereof provided in Table 1 are contemplated. Several different naming conventions for antibodies may be used herein. For example, antibody nCoV-x mAb can also be referred to as nCoV-x, nCoVx, or nCoVx mAb. Antibody nCoV-x-v2 mAb can also be referred to as nCoV-x-v2, nCoVx-v2, nCoVx-v2 mAb, nCoV-x mAb v2, or nCoVx mAb v2. Antibody nCoV-x mAb VH-v2 can also be referred to as nCoV-x VH-v2 or nCoV-x VH-v2 mAb.

[0077] The term "CL" refers to an "immunoglobulin light chain constant region" or a "light chain constant region," i.e., a constant region from an antibody light chain. The term "CH" refers to an "immunoglobulin heavy chain constant region" or a "heavy chain constant region," which is further divisible, depending on the antibody isotype into CH1, CH2, and CH3 (IgA, IgD, IgG), or CH1, CH2, CH3, and CH4 domains (IgE, IgM). The Fc region of an antibody heavy chain is described further herein. In any of the presently disclosed embodiments, an antibody or antigen-binding fragment of the present disclosure comprises any one or more of CL, a CH1, a CH2, and a CH3. In certain embodiments, a CL comprises an amino acid sequence having 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to the amino acid sequence of SEQ ID NO.:391. In certain embodiments, a CH1-CH2-CH3 comprises an amino acid sequence having 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to the amino acid sequence of SEQ ID NO.:395.

[0078] A "Fab" (fragment antigen binding) is the part of an antibody that binds to antigens and includes the variable region and CH1 of the heavy chain linked to the light chain via an inter-chain disulfide bond. Each Fab fragment is monovalent with respect to antigen binding, i.e., it has a single antigen-binding site. Pepsin treatment of a full-length antibody yields a single large F(ab')2 fragment that roughly corresponds to two disulfide linked Fab fragments having divalent antigen-binding activity and is still capable of cross-linking antigen. Both the Fab and F(ab')2 are examples of "antigen-binding fragments." Fab' fragments differ from Fab fragments by having additional few residues at the carboxy terminus of the CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. F(ab')2 antibody fragments can be produced as pairs of Fab' fragments that have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

[0079] "Fv" is a small antibody fragment that contains a complete antigen-recognition and antigen-binding site. This fragment consists of a dimer of one heavy-chain variable domain and one light-chain variable domain in tight, non-covalent association. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although typically at a lower affinity than the entire binding site. "Fd" refers to VH+CH1.

[0080] "Single-chain Fv" also abbreviated as "sFv" or "scFv", are antibody fragments that comprise the VH and VL antibody domains preferably connected into a single polypeptide chain. Preferably, the sFv polypeptide further comprises a polypeptide linker between the VH and VL domains that enables the sFv to form the desired structure for antigen binding. Additionally or alternatively, Fv can have a disulfide bond formed between the VH and the VL. For a review of sFv, see Pluckthun in The Pharmacology of Monoclonal Antibodies, vol. 113, Rosenburg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994); Borrebaeck 1995, infra.

[0081] During antibody development, DNA in the germline variable (V), joining (J), and diversity (D) gene loci may

be rearranged and insertions and/or deletions of nucleotides in the coding sequence may occur. Somatic mutations may be encoded by the resultant sequence, and can be identified by reference to a corresponding known germline sequence. In some contexts, somatic mutations that are not critical to a desired property of the antibody (e.g., binding to a SARS-CoV-2 antigen), or that confer an undesirable property upon the antibody (e.g., an increased risk of immunogenicity in a subject administered the antibody), or both, may be replaced by the corresponding germline-encoded amino acid, or by a different amino acid, so that a desirable property of the antibody is improved or maintained and the undesirable property of the antibody is reduced or abrogated. Thus, in some embodiments, the antibody or antigen-binding fragment of the present disclosure comprises at least one more germline-encoded amino acid in a variable region as compared to a parent antibody or antigen-binding fragment, provided that the parent antibody or antigen binding fragment comprises one or more somatic mutations. Variable region and CDR amino acid sequences of exemplary anti-SARS-CoV-2 antibodies of the present disclosure are provided in Table 1 herein.

[0082] In certain embodiments, an antibody or antigen-binding fragment comprises an amino acid modification (e.g., a substitution mutation) to remove an undesired risk of oxidation, deamidation, and/or isomerization.

[0083] Also provided herein are variant antibodies that comprise one or more amino acid alterations (e.g. substitutions) in a variable region (e.g., VH, VL, framework or CDR) as compared to a presently disclosed ("parent" or "reference") antibody, wherein the variant antibody is capable of binding to a SARS-CoV-2 antigen.

[0084] In certain embodiments, the VH comprises or consists of an amino acid sequence having at least 85% (i.e., 85%, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100%) identity to the amino acid sequence according to any one of SEQ ID NOs.: 5, 21, 37, 53, 69, 85, 101, 117, 133, 149, 165, 181, 197, 213, 229, 245, 261, 277, 293, 309, 325, 341, 357, 374, 377, 396, or 415, wherein the variation as compared to the reference VH SEQ ID NO., if present, is optionally limited to one or more framework regions and/or the variation, if present, comprises one or more substitution to a germline-encoded amino acid; and/or (ii) the VL comprises or consists of an amino acid sequence having at least 85% (i.e., 85%, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100%) identity to the amino acid sequence according to any one of SEQ ID NOs.: 13, 29, 45, 61, 77, 93, 109, 125, 141, 157, 173, 189, 205, 221, 237, 253, 269, 285, 301, 317, 333, 349, 365, 380, 383, 385, 388, 392, 393, 400, 402, 404, and 406-414, wherein the variation as compared to the reference VL SEQ ID NO., if present, is optionally limited to one or more framework regions and/or the variation, if present, comprises one or more substitution to a germline-encoded amino acid.

[0085] In some embodiments, the VH and the VL comprise or consist of an amino acid sequence having at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% to the amino acid sequence set forth in SEQ ID NOs.: (i) 5 and 13, respectively; (ii) 21 and any one of 29, 45, 380, 383, 385, 388, 392, 393, 400, 402, 404, 406, 407, 408, 409, 410, 411, 412, 413, and 414, respectively; (iii) 415 and any one of 29, 45, 380, 383, 385, 388, 392, 400, 402, 404, 406, 407, 408, 409, 410, 411, 412, 413, and 414, respectively; (iv) 37 and any one of 29, 45, 380, 383, 385, 388, 392, 400, 402, 404, 406, 407, 408, 409, 410, 411, 412, 413, and 414, respectively; (v) 53 and 61, respectively; (vi) 69 and 77, respectively; (vii) 85 and 93, respectively; (viii) 101 and 109, respectively; (ix) 117 and any one of 125, 141, and 157, respectively; (x) 133 and any one of 125, 141, and 157, respectively; (xi) 149 and any one of 125, 141, and 157, respectively; (xii) 165 and 173, respectively; (xiii) 181 and 189, respectively; (xiv) 197 and 205, respectively; (xv) 213 and 221, respectively; (xvi) 229 and 237, respectively; (xvii) 245 and 253, respectively; (xviii) 261 and 269, respectively; (xix) 277 and 285, respectively; (xx) 293 and 301, respectively; (xxi) 309 and 317, respectively; (xxii) 325 and 333, respectively; (xxiii) 341 and 349, respectively; (xxiv) 357 and 365, respectively; (xxv) 374 and any one of 29, 45, 380, 383, 385, 392, 393, 400, 402, 404, 406, 407, 408, 409, 410, 411, 412, 413, and 414, respectively; (xxvi) 377 and any one of 29, 45, 380, 383, 385, 392, 393, 400, 402, 404, 406, 407, 408, 409, 410, 411, 412, 413, and 414, respectively; (xxvii) 415 and any one of 29, 45, 380, 383, 385, 392, 393, 400, 402, 404, 406, 407, 408, 409, 410, 411, 412, 413, and 414, respectively; or (xxviii) 396 and any one of 29, 37, 45, 380, 383, 385, 388, 392, 393, 400, 402, 404, 406, 407, 408, 409, 410, 411, 412, 413, and 414, respectively.

[0086] In certain embodiments, the VH comprises or consists of any VH amino acid sequence set forth in Table 1, and the VL comprises or consists of any VL amino acid sequence set forth in Table 1. In particular embodiments, the VH and the VL comprise or consist of the amino acid sequences according to SEQ ID NOs.: (i) 5 and 13, respectively; (ii) 21 and any one of 29, 45, 380, 383, 385, 388, 392, 393, 400, 402, 404, 406, 407, 408, 409, 410, 411, 412, 413, and 414, respectively; (iii) 415 and any one of 29, 45, 380, 383, 385, 388, 392, 400, 402, 404, 406, 407, 408, 409, 410, 411, 412, 413, and 414, respectively; (iv) 37 and any one of 29, 45, 380, 383, 385, 388, 392, 400, 402, 404, 406, 407, 408, 409, 410, 411, 412, 413, and 414, respectively; (v) 53 and 61, respectively; (vi) 69 and 77, respectively; (vii) 85 and 93, respectively; (viii) 101 and 109, respectively; (ix) 117 and any one of 125, 141, and 157, respectively; (x) 133 and any one of 125, 141, and 157, respectively; (xi) 149 and any one of 125, 141, and 157, respectively; (xii) 165 and 173, respectively; (xiii) 181 and 189, respectively; (xiv) 197 and 205, respectively; (xv) 213 and 221, respectively; (xvi) 229 and 237, respectively; (xvii) 245 and 253, respectively; (xviii) 261 and 269, respectively; (xix) 277 and 285, respectively; (xx) 293 and 301, respectively; (xxi) 309 and 317, respectively; (xxii) 325 and 333, respectively; (xxiii) 341 and 349, respectively; (xxiv) 357 and 365, respectively; (xxv) 374 and any one of 29, 45, 380, 383, 385, 392, 393, 400, 402, 404, 406, 407, 408, 409, 410, 411, 412, 413, and 414, respectively; (xxvi) 377 and any one of 29, 45, 380, 383, 385, 392, 393, 400, 402, 404, 406, 407, 408, 409, 410, 411, 412, 413, and 414, respectively; (xxvii) 415 and any one of 29, 45, 380, 383, 385, 392, 393, 400, 402, 404, 406, 407, 408, 409, 410, 411, 412, 413, and 414, respectively; or (xxviii) 396 and any one of 29, 37, 45, 380, 383, 385, 388, 392, 393, 400, 402, 404, 406, 407, 408, 409, 410, 411, 412, 413, and 414, respectively.

[0087] In certain embodiments, an antibody or antigen-binding fragment of the present disclosure is a multispecific antibody, such as a bispecific or trispecific antibody. Formats for bispecific antibodies are disclosed in, for example, Spiess et al., Mol. Immunol. 67(2):95 (2015), and in Brink-

mann and Kontermann, mAbs 9(2):182-212 (2017), which bispecific formats and methods of making the same are incorporated herein by reference and include, for example, Bispecific T cell Engagers (BiTEs), DARTs, Knobs-Into-Holes (KIH) assemblies, scFv-CH3-KIH assemblies, KIH Common Light-Chain antibodies, TandAbs, Triple Bodies, TriBi Minibodies, Fab-scFv, scFv-CH-CL-scFv, F(ab')2-scFv2, tetravalent HCabs, Intrabodies, CrossMabs, Dual Action Fabs (DAFs) (two-in-one or four-in-one), DutaMabs, DT-IgG, Charge Pairs, Fab-arm Exchange, SEEDbodies, Triomabs, LUZ-Y assemblies, Fcabs, k-bodies, orthogonal Fabs, DVD-Igs (e.g., U.S. Pat. No. 8,258,268, which formats are incorporated herein by reference in their entirety), IgG(H)-scFv, scFv-(H)IgG, IgG(L)-scFv, scFv-(L)IgG, IgG (L,H)-Fv, IgG(H)-V, V(H)-IgG, IgG(L)-V, V(L)-IgG, KIH IgG-scFab, 2scFv-IgG, IgG-2scFv, scFv4-Ig, Zybody, and DVI-IgG (four-in-one), as well as so-called FIT-Ig (e.g., PCT Publication No. WO 2015/103072, which formats are incorporated herein by reference in their entirety), so-called WuxiBody formats (e.g., PCT Publication No. WO 2019/057122, which formats are incorporated herein by reference in their entirety), and so-called In-Elbow-Insert Ig formats (IEI-Ig; e.g., PCT Publication Nos. WO 2019/024979 and WO 2019/025391, which formats are incorporated herein by reference in their entirety).

[0088] A bispecific or multispecific antibody may comprise one, two, or more SARS-CoV-2 antigen-binding domains or sequences (e.g., CDRS, and/or a VH and a VL) of the instant disclosure, optionally in combination with another SARS-CoV-2 binding domain of the instant disclosure, or in combination with a different binding domain that specifically binds to SARS-CoV-2 (e.g., at a same or a different epitope), or with a binding domain that binds to a different antigen.

[0089] In any of the presently disclosed embodiments, the antibody or antigen-binding fragment can be multispecific; e.g., bispecific, trispecific, or the like.

[0090] In certain embodiments, the antibody or antigen-binding fragment comprises: (i) a first VH and a first VL; and (ii) a second VH and a second VL, wherein the first VH and the second VH are different and each independently comprise an amino acid sequence having at least 85% (i.e., 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%) identity to the amino acid sequence set forth in any one of SEQ ID NOs.: 5, 21, 37, 53, 69, 85, 101, 117, 133, 149, 165, 181, 197, 213, 229, 245, 261, 277, 293, 309, 325, 341, 357, 374, 377, 396, or 415, and wherein the first VL and the second VL are different and each independently comprise an amino acid sequence having at least 85% (i.e., 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%) identity to the amino acid sequence set forth in any one of SEQ ID NOs.: 13, 29, 45, 61, 77, 93, 109, 125, 141, 157, 173, 189, 205, 221, 237, 253, 269, 285, 301, 317, 333, 349, 365, 380, 383, 385, 388, 392, 393, 400, 402, 404, and 406-414, and wherein the first VH and the first VL together form a first antigen-binding site, and wherein the second VH and the second VL together form a second antigen-binding site.

[0091] In particular embodiments, (i) the first VH comprises or consists of the amino acid sequence set forth in any one of SEQ ID NOs.:21, 37, 374, 377, 396, and 415, and the first VL comprises or consists of the amino acid sequence set forth in any one of SEQ ID NOs.:29, 45, 380, 383, 385, 388, 392, 393, 400, 402, 404, and 406-414, and (ii) the second VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:69 and the second VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:77.

[0092] In certain embodiments, the antibody or antigen-binding fragment comprises an Fc polypeptide, or a fragment thereof. The "Fc" fragment or Fc polypeptide comprises the carboxy-terminal portions (i.e., the CH2 and CH3 domains of IgG) of both antibody H chains held together by disulfides. Antibody "effector functions" refer to those biological activities attributable to the Fc region (a native sequence Fc region or amino acid sequence variant Fc region) of an antibody, and vary with the antibody isotype. Examples of antibody effector functions include: Clq binding and complement dependent cytotoxicity; Fc receptor binding; antibody-dependent cell-mediated cytotoxicity (ADCC); phagocytosis; down regulation of cell surface receptors (e.g., B cell receptor); and B cell activation. As discussed herein, modifications (e.g., amino acid substitutions) may be made to an Fc domain in order to modify (e.g., improve, reduce, or ablate) one or more functionality of an Fc-containing polypeptide (e.g., an antibody of the present disclosure). Such functions include, for example, Fc receptor (FcR) binding, antibody half-life modulation (e.g., by binding to FcRn), ADCC function, protein A binding, protein G binding, and complement binding. Amino acid modifications that modify (e.g., improve, reduce, or ablate) Fc functionalities include, for example, the T250Q/M428L, M252Y/S254T/T256E, H433K/N434F, M428L/N434S, E233P/L234V/L235A/G236+A327G/A330S/P331S, E333A, S239D/A330L/I332E, P257I/Q311, K326W/E333S, S239D/I332E/G236A, N297Q, K322A, S228P, L235E+E318A/K320A/K322A, L234A/L235A (also referred to herein as "LALA"), and L234A/L235A/P329G mutations, which mutations are summarized and annotated in "Engineered Fe Regions", published by InvivoGen (2011) and available online at invivogen.com/PDF/review/review-Engineered-Fc-Regions-invivogen.pdf?utm_source=review&utm_medium=pdf&utm_campaign=review&utm_content=Engineered-Fc-Regions, and are incorporated herein by reference.

[0093] For example, to activate the complement cascade, the Clq protein complex can bind to at least two molecules of IgG1 or one molecule of IgM when the immunoglobulin molecule(s) is attached to the antigenic target (Ward, E. S., and Ghetie, V., *Ther. Immunol.* 2 (1995) 77-94). Burton, D. R., described (*Mol. Immunol.* 22 (1985) 161-206) that the heavy chain region comprising amino acid residues 318 to 337 is involved in complement fixation. Duncan, A. R., and Winter, G. (*Nature* 332 (1988) 738-740), using site directed mutagenesis, reported that Glu318, Lys320 and Lys322 form the binding site to C1q. The role of Glu318, Lys320 and Lys 322 residues in the binding of C1q was confirmed by the ability of a short synthetic peptide containing these residues to inhibit complement mediated lysis.

[0094] For example, FcR binding can be mediated by the interaction of the Fc moiety (of an antibody) with Fc receptors (FcRs), which are specialized cell surface receptors on cells including hematopoietic cells. Fc receptors belong to the immunoglobulin superfamily, and shown to mediate both the removal of antibody-coated pathogens by phagocytosis of immune complexes, and the lysis of erythrocytes and various other cellular targets (e.g. tumor cells)

coated with the corresponding antibody, via antibody dependent cell mediated cytotoxicity (ADCC; Van de Winkel, J. G., and Anderson, C. L., *J. Leukoc. Biol.* 49 (1991) 511-524). FcRs are defined by their specificity for immunoglobulin classes; Fc receptors for IgG antibodies are referred to as FcγR, for IgE as FcR, for IgA as FcαR and so on and neonatal Fc receptors are referred to as FcRn. Fc receptor binding is described for example in Ravetch, J. V., and Kinet, J. P., *Annu. Rev. Immunol.* 9 (1991) 457-492; Capel, P. J., et al., *Immunomethods* 4 (1994) 25-34; de Haas, M., et al., *JLab. Clin. Med.* 126 (1995) 330-341; and Gessner, J. E., et al., *Ann. Hematol.* 76 (1998) 231-248.

[0095] Cross-linking of receptors by the Fc domain of native IgG antibodies (FcγR) triggers a wide variety of effector functions including phagocytosis, antibody-dependent cellular cytotoxicity, and release of inflammatory mediators, as well as immune complex clearance and regulation of antibody production. Fc moieties providing cross-linking of receptors (e.g., FcγR) are contemplated herein. In humans, three classes of FcγR have been characterized to-date, which are: (i) FcγRI (CD64), which binds monomeric IgG with high affinity and is expressed on macrophages, monocytes, neutrophils and eosinophils; (ii) FcγRII (CD32), which binds complexed IgG with medium to low affinity, is widely expressed, in particular on leukocytes, is believed to be a central player in antibody-mediated immunity, and which can be divided into FcγRIIA, FcγRIIB and FcγRIIC, which perform different functions in the immune system, but bind with similar low affinity to the IgG-Fc, and the ectodomains of these receptors are highly homologous; and (iii) FcγRIII (CD16), which binds IgG with medium to low affinity and has been found in two forms: FcγRIIIA, which has been found on NK cells, macrophages, eosinophils, and some monocytes and T cells, and is believed to mediate ADCC; and FcγRIIIB, which is highly expressed on neutrophils.

[0096] FcγRIIA is found on many cells involved in killing (e.g. macrophages, monocytes, neutrophils) and seems able to activate the killing process. FcγRIIB seems to play a role in inhibitory processes and is found on B-cells, macrophages and on mast cells and eosinophils. Importantly, it has been shown that 75% of all FcγRIIB is found in the liver (Ganesan, L. P. et al., 2012: "FcγRIIb on liver sinusoidal endothelium clears small immune complexes," *Journal of Immunology* 189: 4981-4988). FcγRIIB is abundantly expressed on Liver Sinusoidal Endothelium, called LSEC, and in Kupffer cells in the liver and LSEC are the major site of small immune complexes clearance (Ganesan, L. P. et al., 2012: FcγRIIb on liver sinusoidal endothelium clears small immune complexes. *Journal of Immunology* 189: 4981-4988).

[0097] In some embodiments, the antibodies disclosed herein and the antigen-binding fragments thereof comprise an Fc polypeptide or fragment thereof for binding to FcγRIIb, in particular an Fc region, such as, for example IgG-type antibodies. Moreover, it is possible to engineer the Fc moiety to enhance FcγRIIB binding by introducing the mutations S267E and L328F as described by Chu, S. Y. et al., 2008: Inhibition of B cell receptor-mediated activation of primary human B cells by coengagement of CD19 and FcgammaRIIb with Fc-engineered antibodies. Molecular Immunology 45, 3926-3933. Thereby, the clearance of immune complexes can be enhanced (Chu, S., et al., 2014: Accelerated Clearance of IgE In Chimpanzees Is Mediated By Xmab7195, An Fc-Engineered Antibody With Enhanced Affinity For Inhibitory Receptor FcγRIIb. Am J Respir Crit, American Thoracic Society International Conference Abstracts). In some embodiments, the antibodies of the present disclosure, or the antigen binding fragments thereof, comprise an engineered Fc moiety with the mutations S267E and L328F, in particular as described by Chu, S. Y. et al., 2008: Inhibition of B cell receptor-mediated activation of primary human B cells by coengagement of CD19 and FcgammaRIIb with Fc-engineered antibodies. Molecular Immunology 45, 3926-3933.

[0098] On B cells, FcγRIIB may function to suppress further immunoglobulin production and isotype switching to, for example, the IgE class. On macrophages, FcγRIIB is thought to inhibit phagocytosis as mediated through FcγRIIA. On eosinophils and mast cells, the B form may help to suppress activation of these cells through IgE binding to its separate receptor.

[0099] Regarding FcγRI binding, modification in native IgG of at least one of E233-G236, P238, D265, N297, A327 and P329 reduces binding to FcγRI. IgG2 residues at positions 233-236, substituted into corresponding positions IgG1 and IgG4, reduces binding of IgG1 and IgG4 to FcγRI by 10^3-fold and eliminated the human monocyte response to antibody-sensitized red blood cells (Armour, K. L., et al. *Eur. J. Immunol.* 29 (1999) 2613-2624).

[0100] Regarding FcγRII binding, reduced binding for FcγRIIA is found, e.g., for IgG mutation of at least one of E233-G236, P238, D265, N297, A327, P329, D270, Q295, A327, R292 and K414.

[0101] Two allelic forms of human FcγRIIA are the "H131" variant, which binds to IgG1 Fc with high affinity, and the "R131" variant, which binds to IgG1 Fc with low affinity. See, e.g., Bruhns et al., *Blood* 113:3716-3725 (2009).

[0102] Regarding FcγRIII binding, reduced binding to FcγRIIIA is found, e.g., for mutation of at least one of E233-G236, P238, D265, N297, A327, P329, D270, Q295, A327, S239, E269, E293, Y296, V303, A327, K338 and D376. Mapping of the binding sites on human IgG1 for Fc receptors, the above-mentioned mutation sites, and methods for measuring binding to FcγRI and FcγRIIA, are described in Shields, R. L., et al., *J. Biol. Chem.* 276 (2001) 6591-6604.

[0103] Two allelic forms of human FcγRIIIA are the "F158" variant, which binds to IgG1 Fc with low affinity, and the "V158" variant, which binds to IgG1 Fc with high affinity. See, e.g., Bruhns et al., *Blood* 113:3716-3725 (2009).

[0104] Regarding binding to FcγRII, two regions of native IgG Fc appear to be involved in interactions between FcγRIIs and IgGs, namely (i) the lower hinge site of IgG Fc, in particular amino acid residues L, L, G, G (234-237, EU numbering), and (ii) the adjacent region of the CH2 domain of IgG Fc, in particular a loop and strands in the upper CH2 domain adjacent to the lower hinge region, e.g. in a region of P331 (Wines, B. D., et al., J. Immunol. 2000; 164: 5313-5318). Moreover, FcγRI appears to bind to the same site on IgG Fc, whereas FcRn and Protein A bind to a different site on IgG Fc, which appears to be at the CH2-CH3 interface (Wines, B. D., et al., J. Immunol. 2000; 164: 5313-5318).

[0105] Also contemplated are mutations that increase binding affinity of an Fc polypeptide or fragment thereof of

the present disclosure to a (i.e., one or more) Fc7 receptor (e.g., as compared to a reference Fc polypeptide or fragment thereof or containing the same that does not comprise the mutation(s)). See, e.g., Delillo and Ravetch, Cell 161(5): 1035-1045 (2015) and Ahmed et al., J. Struc. Biol. 194(1):78 (2016), the Fc mutations and techniques of which are incorporated herein by reference.

[0106] In any of the herein disclosed embodiments, an antibody or antigen-binding fragment can comprise a Fc polypeptide or fragment thereof comprising a mutation selected from G236A; S239D; A330L; and I332E; or a combination comprising any two or more of the same; e.g., S239D/I332E; S239D/A330L/I332E; G236A/S239D/I332E; G236A/A330L/I332E (also referred to herein as "GAALIE"); or G236A/S239D/A330L/I332E. In some embodiments, the Fc polypeptide or fragment thereof does not comprise S239D. In some embodiments, the Fc polypeptide or fragment comprises a Ser at position 239 (EU numbering).

[0107] In certain embodiments, the Fc polypeptide or fragment thereof may comprise or consist of at least a portion of an Fc polypeptide or fragment thereof that is involved in binding to FcRn binding. In certain embodiments, the Fc polypeptide or fragment thereof comprises one or more amino acid modifications that improve binding affinity for (e.g., enhance binding to) FcRn (e.g., at a pH of about 6.0) and, in some embodiments, thereby extend in vivo half-life of a molecule comprising the Fc polypeptide or fragment thereof (e.g., as compared to a reference Fc polypeptide or fragment thereof or antibody that is otherwise the same but does not comprise the modification(s)). In certain embodiments, the Fc polypeptide or fragment thereof comprises or is derived from a IgG Fe and a half-life-extending mutation comprises any one or more of: M428L; N434S; N434H; N434A; N434S; M252Y; S254T; T256E; T250Q; P257I Q311I; D376V; T307A; E380A (EU numbering). In certain embodiments, a half-life-extending mutation comprises M428L/N434S (also referred to herein as "MLNS"). In certain embodiments, a half-life-extending mutation comprises M252Y/S254T/T256E. In certain embodiments, a half-life-extending mutation comprises T250Q/M428L. In certain embodiments, a half-life-extending mutation comprises P257I/Q311I. In certain embodiments, a half-life-extending mutation comprises P257I/N434H. In certain embodiments, a half-life-extending mutation comprises D376V/N434H. In certain embodiments, a half-life-extending mutation comprises T307A/E380A/N434A.

[0108] In some embodiments, an antibody or antigen-binding fragment includes an Fc moiety that comprises the substitution mutations M428L/N434S. In some embodiments, an antibody or antigen-binding fragment includes an Fc polypeptide or fragment thereof that comprises the substitution mutations G236A/A330L/I332E. In certain embodiments, an antibody or antigen-binding fragment includes a (e.g., IgG) Fc moiety that comprises a G236A mutation, an A330L mutation, and an I332E mutation (GAALIE), and does not comprise a S239D mutation (e.g., comprises a native S at position 239). In particular embodiments, an antibody or antigen-binding fragment includes an Fc polypeptide or fragment thereof that comprises the substitution mutations: M428L/N434S and G236A/A330L/I332E, and optionally does not comprise S239D (e.g., comprises a Ser at position 239). In certain embodiments, an antibody or antigen-binding fragment includes a Fc polypeptide or fragment thereof that comprises the substitution mutations: M428L/N434S and G236A/S239D/A330L/I332E, and, optionally, does comprise any further other substitution mutations.

[0109] In certain embodiments, the antibody or antigen-binding fragment comprises a mutation that alters glycosylation, wherein the mutation that alters glycosylation comprises N297A, N297Q, or N297G, and/or the antibody or antigen-binding fragment is partially or fully aglycosylated and/or is partially or fully afucosylated. Host cell lines and methods of making partially or fully aglycosylated or partially or fully afucosylated antibodies and antigen-binding fragments are known (see, e.g., PCT Publication No. WO 2016/181357; Suzuki et al. *Clin. Cancer Res.* 13(6):1875-82 (2007); Huang et al. *MAbs* 6:1-12 (2018)).

[0110] In certain embodiments, the antibody or antigen-binding fragment is capable of eliciting continued protection in vivo in a subject even once no detectable levels of the antibody or antigen-binding fragment can be found in the subject (i.e., when the antibody or antigen-binding fragment has been cleared from the subject following administration). Such protection is referred to herein as a vaccinal effect. Without wishing to be bound by theory, it is believed that dendritic cells can internalize complexes of antibody and antigen and thereafter induce or contribute to an endogenous immune response against antigen. In certain embodiments, an antibody or antigen-binding fragment comprises one or more modifications, such as, for example, mutations in the Fc comprising G236A, A330L, and I332E, that are capable of activating dendritic cells that may induce, e.g., T cell immunity to the antigen.

[0111] In any of the presently disclosed embodiments, the antibody or antigen-binding fragment comprises a Fc polypeptide or a fragment thereof, including a CH2 (or a fragment thereof, a CH3 (or a fragment thereof), or a CH2 and a CH3, wherein the CH2, the CH3, or both can be of any isotype and may contain amino acid substitutions or other modifications as compared to a corresponding wild-type CH2 or CH3, respectively. In certain embodiments, an Fc polypeptide of the present disclosure comprises two CH2-CH3 polypeptides that associate to form a dimer.

[0112] In any of the presently disclosed embodiments, the antibody or antigen-binding fragment can be monoclonal. The term "monoclonal antibody" (mAb) as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., individual antibodies comprising the population are identical except for possible naturally occurring mutations that may be present, in some cases in minor amounts. Monoclonal antibodies are highly specific, being directed against a single antigenic site. Furthermore, in contrast to polyclonal antibody preparations that include different antibodies directed against different epitopes, each monoclonal antibody is directed against a single epitope of the antigen. In addition to their specificity, the monoclonal antibodies are advantageous in that they may be synthesized uncontaminated by other antibodies. The term "monoclonal" is not to be construed as requiring production of the antibody by any particular method. For example, monoclonal antibodies useful in the present invention may be prepared by the hybridoma methodology first described by Kohler et al., *Nature* 256:495 (1975), or may be made using recombinant DNA methods in bacterial, eukaryotic animal, or plant cells (see, e.g., U.S. Pat. No.

4,816,567). Monoclonal antibodies may also be isolated from phage antibody libraries using the techniques described in Clackson et al., *Nature,* 352:624-628 (1991) and Marks et al., *J. Mol. Biol.,* 222:581-597 (1991), for example. Monoclonal antibodies may also be obtained using methods disclosed in PCT Publication No. WO 2004/076677A2.

[0113] Antibodies and antigen-binding fragments of the present disclosure include "chimeric antibodies" in which a portion of the heavy chain and/or the light chain is identical with or homologous to a corresponding sequence or sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments of such antibodies, so long as they exhibit the desired biological activity (see, U.S. Pat. Nos. 4,816,567; 5,530,101 and 7,498,415; and Morrison et al., Proc. Natl. Acad. Sci. USA, 81:6851-6855 (1984)). For example, chimeric antibodies may comprise human and non-human residues. Furthermore, chimeric antibodies may comprise residues that are not found in the recipient antibody or in the donor antibody. These modifications are made to further refine antibody performance. For further details, see Jones et al., *Nature* 321:522-525 (1986); Riechmann et al., *Nature* 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.* 2:593-596 (1992). Chimeric antibodies also include primatized and humanized antibodies.

[0114] A "humanized antibody" is generally considered to be a human antibody that has one or more amino acid residues introduced into it from a source that is non-human. These non-human amino acid residues are typically taken from a variable domain. Humanization may be performed, for example, following the method of Winter and co-workers (Jones et al., *Nature,* 321:522-525 (1986); Reichmann et al., *Nature,* 332:323-327 (1988); Verhoeyen et al., *Science,* 239:1534-1536 (1988)), by substituting non-human variable sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (e.g., U.S. Pat. Nos. 4,816,567; 5,530,101 and 7,498,415) wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In some instances, a "humanized" antibody is one which is produced by a non-human cell or animal and comprises human sequences, e.g., Hc domains.

[0115] A "human antibody" is an antibody containing only sequences that are present in an antibody that is produced by a human. However, as used herein, human antibodies may comprise residues or modifications not found in a naturally occurring human antibody (e.g., an antibody that is isolated from a human), including those modifications and variant sequences described herein. These may be made to further refine or enhance antibody performance. In some instances, human antibodies are produced by transgenic animals. For example, see U.S. Pat. Nos. 5,770,429; 6,596,541 and 7,049,426.

[0116] In certain embodiments, an antibody or antigen-binding fragment of the present disclosure is chimeric, humanized, or human.

Polynucleotides, Vectors, and Host Cells

[0117] In another aspect, the present disclosure provides isolated polynucleotides that encode any of the presently disclosed antibodies or an antigen-binding fragment thereof, or a portion thereof (e.g., a CDR, a VH, a VL, a heavy chain, or a light chain). In certain embodiments, the polynucleotide is codon-optimized for expression in a host cell. Once a coding sequence is known or identified, codon optimization can be performed using known techniques and tools, e.g., using the GenScript® OptimiumGene™ tool; see also Scholten et al., *Clin. Immunol.* 119:135, 2006). Codon-optimized sequences include sequences that are partially codon-optimized (i.e., one or more codon is optimized for expression in the host cell) and those that are fully codon-optimized.

[0118] It will also be appreciated that polynucleotides encoding antibodies and antigen-binding fragments of the present disclosure may possess different nucleotide sequences while still encoding a same antibody or antigen-binding fragment due to, for example, the degeneracy of the genetic code, splicing, and the like.

[0119] In certain embodiments, the polynucleotide comprises a polynucleotide having at least 50% (i.e., 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%) identity to the polynucleotide sequence according to any one or more of SEQ ID NOs.:1-4, 9-12, 17-20, 25-28, 33-36, 41-44, 49-52, 57-60, 65-68, 73-76, 81-84, 89-92, 97-100, 105-108, 113-116, 121-124, 129-132, 137-140, 145-148, 153-156, 161-164, 169-172, 177-180, 185-188, 193-196, 201-204, 209-212, 217-220, 225-228, 233-236, 241-244, 249-252, 257-260, 265-268, 273-276, 281-284, 289-292, 297-300, 305-308, 313-316, 321-324, 329-332, 337-340, 345-348, 353-356, 361-364, 372, 373, 376, 379, 381, 384, 387, 389, and 417.

[0120] In any of the presently disclosed embodiments, the polynucleotide can comprise deoxyribonucleic acid (DNA) or ribonucleic acid (RNA). In some embodiments, the RNA comprises messenger RNA (mRNA).

[0121] Vectors are also provided, wherein the vectors comprise or contain a polynucleotide as disclosed herein (e.g., a polynucleotide that encodes an antibody or antigen-binding fragment that binds to SARS-CoV-2). A vector can comprise any one or more of the vectors disclosed herein. In particular embodiments, a vector is provided that comprises a DNA plasmid construct encoding the antibody or antigen-binding fragment, or a portion thereof (e.g., so-called "DMAb"; see, e.g., Muthumani et al., *J Infect Dis.* 214(3): 369-378 (2016); Muthumani et al., *Hum Vaccin Immunother* 9:2253-2262 (2013)); Flingai et al., *Sci Rep.* 5:12616 (2015); and Elliott et al., *NPJ Vaccines* 18 (2017), which antibody-coding DNA constructs and related methods of use, including administration of the same, are incorporated herein by reference). In certain embodiments, a DNA plasmid construct comprises a single open reading frame encoding a heavy chain and a light chain (or a VH and a VL) of the antibody or antigen-binding fragment, wherein the sequence encoding the heavy chain and the sequence encoding the light chain are optionally separated by polynucleotide encoding a protease cleavage site and/or by a polynucleotide encoding a self-cleaving peptide. In some embodiments, the substituent components of the antibody or antigen-binding fragment are encoded by a polynucleotide comprised in a single plasmid. In other embodiments, the substituent components of the antibody or antigen-binding fragment are encoded by a polynucleotide comprised in two or more plasmids (e.g., a first plasmid comprises a poly-

nucleotide encoding a heavy chain, VH, or VH+CH, and a second plasmid comprises a polynucleotide encoding the cognate light chain, VL, or VL+CL). In certain embodiments, a single plasmid comprises a polynucleotide encoding a heavy chain and/or a light chain from two or more antibodies or antigen-binding fragments of the present disclosure. An exemplary expression vector is pVax1, available from Invitrogen®. A DNA plasmid of the present disclosure can be delivered to a subject by, for example, electroporation (e.g., intramuscular electroporation), or with an appropriate formulation (e.g., hyaluronidase).

[0122] In a further aspect, the present disclosure also provides a host cell expressing an antibody or antigen-binding fragment according to the present disclosure; or comprising or containing a vector or polynucleotide according the present disclosure.

[0123] Examples of such cells include but are not limited to, eukaryotic cells, e.g., yeast cells, animal cells, insect cells, plant cells; and prokaryotic cells, including *E. coli*. In some embodiments, the cells are mammalian cells. In certain such embodiments, the cells are a mammalian cell line such as CHO cells (e.g., DHFR- CHO cells (Urlaub et al., *PNAS* 77:4216 (1980)), human embryonic kidney cells (e.g., HEK293T cells), PER.C6 cells, Y0 cells, Sp2/0 cells. NS0 cells, human liver cells, e.g. Hepa RG cells, myeloma cells or hybridoma cells. Other examples of mammalian host cell lines include mouse sertoli cells (e.g., TM4 cells); monkey kidney CV1 line transformed by SV40 (COS-7); baby hamster kidney cells (BHK); African green monkey kidney cells (VERO-76); monkey kidney cells (CV1); human cervical carcinoma cells (HELA); human lung cells (W138); human liver cells (Hep G2); canine kidney cells (MDCK; buffalo rat liver cells (BRL 3A); mouse mammary tumor (MMT 060562); TRI cells; MRC 5 cells; and FS4 cells. Mammalian host cell lines suitable for antibody production also include those described in, for example, Yazaki and Wu, *Methods in Molecular Biology*, Vol. 248 (B. K. C. Lo, ed., Humana Press, Totowa, N.J.), pp. 255-268 (2003).

[0124] In certain embodiments, a host cell is a prokaryotic cell, such as an *E. coli*. The expression of peptides in prokaryotic cells such as *E. coli* is well established (see, e.g., Pluckthun, A. *Bio/Technology* 9:545-551 (1991). For example, antibodies may be produced in bacteria, in particular when glycosylation and Fc effector function are not needed. For expression of antibody fragments and polypeptides in bacteria, see, e.g., U.S. Pat. Nos. 5,648,237; 5,789,199; and 5,840,523.

[0125] In particular embodiments, the cell may be transfected with a vector according to the present description with an expression vector. The term "transfection" refers to the introduction of nucleic acid molecules, such as DNA or RNA (e.g. mRNA) molecules, into cells, such as into eukaryotic cells. In the context of the present description, the term "transfection" encompasses any method known to the skilled person for introducing nucleic acid molecules into cells, such as into eukaryotic cells, including into mammalian cells. Such methods encompass, for example, electroporation, lipofection, e.g., based on cationic lipids and/or liposomes, calcium phosphate precipitation, nanoparticle based transfection, virus based transfection, or transfection based on cationic polymers, such as DEAE-dextran or polyethylenimine, etc. In certain embodiments, the introduction is non-viral.

[0126] Moreover, host cells of the present disclosure may be transfected stably or transiently with a vector according to the present disclosure, e.g. for expressing an antibody, or an antigen-binding fragment thereof, according to the present disclosure. In such embodiments, the cells may be stably transfected with the vector as described herein. Alternatively, cells may be transiently transfected with a vector according to the present disclosure encoding an antibody or antigen-binding fragment as disclosed herein. In any of the presently disclosed embodiments, a polynucleotide may be heterologous to the host cell.

[0127] Accordingly, the present disclosure also provides recombinant host cells that heterologously express an antibody or antigen-binding fragment of the present disclosure. For example, the cell may be of a species that is different to the species from which the antibody was fully or partially obtained (e.g., CHO cells expressing a human antibody or an engineered human antibody). In some embodiments, the cell type of the host cell does not express the antibody or antigen-binding fragment in nature. Moreover, the host cell may impart a post-translational modification (PTM; e.g., glycosylation or fucosylation, or reduced glycosylation or fucosylation) on the antibody or antigen-binding fragment that is not present in a native state of the antibody or antigen-binding fragment (or in a native state of a parent antibody from which the antibody or antigen binding fragment was engineered or derived). Such a PTM may result in a functional difference (e.g., reduced immunogenicity). Accordingly, an antibody or antigen-binding fragment of the present disclosure that is produced by a host cell as disclosed herein may include one or more post-translational modification that is distinct from the antibody (or parent antibody) in its native state (e.g., a human antibody produced by a CHO cell can comprise one or more post-translational modification that is distinct from the antibody when isolated from the human and/or produced by the native human B cell or plasma cell).

[0128] Insect cells useful expressing an antibody or antigen-binding fragment of the present disclosure are known in the art and include, for example, *Spodoptera frugipera* Sf9 cells, *Trichoplusia ni* BTI-TN5B1-4 cells, and *Spodoptera frugipera* SfSWT01 "Mimic™" cells. See, e.g., Palmberger et al., *J. Biotechnol.* 153(3-4):160-166 (2011). Numerous baculoviral strains have been identified which may be used in conjunction with insect cells, particularly for transfection of Spodopterafrugiperda cells.

[0129] Eukaryotic microbes such as filamentous fungi or yeast are also suitable hosts for cloning or expressing protein-encoding vectors, and include fungi and yeast strains with "humanized" glycosylation pathways, resulting in the production of an antibody with a partially or fully human glycosylation pattern. See Gerngross, *Nat. Biotech.* 22:1409-1414 (2004); Li et al., *Nat. Biotech.* 24:210^{-215} (2006).

[0130] Plant cells can also be utilized as hosts for expressing an antibody or antigen-binding fragment of the present disclosure. For example, PLANTIBODIES™ technology (described in, for example, U.S. Pat. Nos. 5,959,177; 6,040,498; 6,420,548; 7,125,978; and 6,417,429) employs transgenic plants to produce antibodies.

[0131] In certain embodiments, the host cell comprises a mammalian cell. In particular embodiments, the host cell is

a CHO cell, a HEK293 cell, a PER.C6 cell, a Y0 cell, a Sp2/0 cell, a NS0 cell, a human liver cell, a myeloma cell, or a hybridoma cell.

[0132] In a related aspect, the present disclosure provides methods for producing an antibody, or antigen-binding fragment, wherein the methods comprise culturing a host cell of the present disclosure under conditions and for a time sufficient to produce the antibody, or the antigen-binding fragment. Methods useful for isolating and purifying recombinantly produced antibodies, by way of example, may include obtaining supernatants from suitable host cell/vector systems that secrete the recombinant antibody into culture media and then concentrating the media using a commercially available filter. Following concentration, the concentrate may be applied to a single suitable purification matrix or to a series of suitable matrices, such as an affinity matrix or an ion exchange resin. One or more reverse phase HPLC steps may be employed to further purify a recombinant polypeptide. These purification methods may also be employed when isolating an immunogen from its natural environment. Methods for large scale production of one or more of the isolated/recombinant antibody or antigen-binding fragment described herein include batch cell culture, which is monitored and controlled to maintain appropriate culture conditions. Purification of soluble antibodies may be performed according to methods described herein and known in the art and that comport with laws and guidelines of domestic and foreign regulatory agencies.

Compositions

[0133] Also provided herein are compositions that comprise any one or more of the presently disclosed antibodies, antigen-binding fragments, polynucleotides, vectors, or host cells, singly or in any combination, and can further comprise a pharmaceutically acceptable carrier, excipient, or diluent. Carriers, excipients, and diluents are discussed in further detail herein.

[0134] In certain embodiments, a composition comprises two or more different antibodies or antigen-binding fragments according to the present disclosure. In some embodiments, comprising a first antibody or antigen-binding fragment and a second antibody or antigen-binding fragment, wherein: (i) the first antibody or antigen-binding fragment comprises a VH comprising or consisting of the amino acid sequence set forth in any one of SEQ ID NOs.:21, 37, 374, 377, 396, and 415, and a VL comprising or consisting of the amino acid sequence set forth in any one of SEQ ID NOs.:29, 45, 380, 383, 385, 388, 392, 393, 400, 402, 404, and 406-414; and (ii) the second antibody or antigen-binding fragment comprises a VH comprising or consisting of the amino acid sequence set forth in SEQ ID NO.:69, and a VL comprising or consisting of the amino acid sequence set forth in SEQ ID NO.:77.

[0135] In certain embodiments, a composition comprises a first vector comprising a first plasmid, and a second vector comprising a second plasmid, wherein the first plasmid comprises a polynucleotide encoding a heavy chain, VH, or VH+CH, and a second plasmid comprises a polynucleotide encoding the cognate light chain, VL, or VL+CL of the antibody or antigen-binding fragment thereof.

[0136] In certain embodiments, a composition comprises a polynucleotide (e.g., mRNA) coupled to a suitable delivery vehicle or carrier. Exemplary vehicles or carriers for administration to a human subject include a lipid or lipid-derived delivery vehicle, such as a liposome, solid lipid nanoparticle, oily suspension, submicron lipid emulsion, lipid microbubble, inverse lipid micelle, cochlear liposome, lipid microtubule, lipid microcylinder, or lipid nanoparticle (LNP) or a nanoscale platform (see, e.g., Li et al. *Wilery Interdiscip Rev. Nanomed Nanobiotechnol.* 11(2):e1530 (2019)). Principles, reagents, and techniques for designing appropriate mRNA and formulating mRNA-LNP and delivering the same are described in, for example, Pardi et al. (*J Control Release* 217345-351 (2015)); Thess et al. (*Mol Ther* 23: 1456-1464 (2015)); Thran et al. (*EMBO Mol Med* 9(10):1434-1448 (2017); Kose et al. (*Sci. Immunol.* 4 eaaw6647 (2019); and Sabnis et al. (*Mol. Ther.* 26:1509-1519 (2018)), which techniques, include capping, codon optimization, nucleoside modification, purification of mRNA, incorporation of the mRNA into stable lipid nanoparticles (e.g., ionizable cationic lipid/phosphatidylcholine/cholesterol/PEG-lipid; ionizable lipid:distearoyl PC:cholesterol: polyethylene glycol lipid), and subcutaneous, intramuscular, intradermal, intravenous, intraperitoneal, and intratracheal administration of the same, are incorporated herein by reference.

Methods and Uses

[0137] Also provided herein are methods for use of an antibody or antigen-binding fragment, nucleic acid, vector, cell, or composition of the present disclosure in the diagnosis of sarbecovirus and/or SARS-CoV-2 infection (e.g., in a human subject, or in a sample obtained from a human subject).

[0138] Methods of diagnosis (e.g., in vitro, ex vivo) may include contacting an antibody, antibody fragment (e.g., antigen binding fragment) with a sample. Such samples may be isolated from a subject, for example an isolated tissue sample taken from, for example, nasal passages, sinus cavities, salivary glands, lung, liver, pancreas, kidney, ear, eye, placenta, alimentary tract, heart, ovaries, pituitary, adrenals, thyroid, brain, skin or blood. The methods of diagnosis may also include the detection of an antigen/antibody complex, in particular following the contacting of an antibody or antibody fragment with a sample. Such a detection step can be performed at the bench, i.e. without any contact to the human or animal body. Examples of detection methods are well-known to the person skilled in the art and include, e.g., ELISA (enzyme-linked immunosorbent assay), including direct, indirect, and sandwich ELISA.

[0139] Also provided herein are methods of treating a subject using an antibody or antigen-binding fragment of the present disclosure, or a composition comprising the same, wherein the subject has, is believed to have, or is at risk for having an infection by SARS-CoV-2. "Treat," "treatment," or "ameliorate" refers to medical management of a disease, disorder, or condition of a subject (e.g., a human or non-human mammal, such as a primate, horse, cat, dog, goat, mouse, or rat). In general, an appropriate dose or treatment regimen comprising an antibody or composition of the present disclosure is administered in an amount sufficient to elicit a therapeutic or prophylactic benefit. Therapeutic or prophylactic/preventive benefit includes improved clinical outcome; lessening or alleviation of symptoms associated with a disease; decreased occurrence of symptoms; improved quality of life; longer disease-free status; diminishment of extent of disease, stabilization of disease state; delay or prevention of disease progression; remission; sur-

vival; prolonged survival; or any combination thereof. In certain embodiments, therapeutic or prophylactic/preventive benefit includes reduction or prevention of hospitalization for treatment of a SARS-CoV-2 infection (i.e., in a statistically significant manner). In certain embodiments, therapeutic or prophylactic/preventive benefit includes a reduced duration of hospitalization for treatment of a SARS-CoV-2 infection (i.e., in a statistically significant manner). In certain embodiments, therapeutic or prophylactic/preventive benefit includes a reduced or abrogated need for respiratory intervention, such as intubation and/or the use of a respirator device. In certain embodiments, therapeutic or prophylactic/preventive benefit includes reversing a late-stage disease pathology and/or reducing mortality.

[0140] A "therapeutically effective amount" or "effective amount" of an antibody, antigen-binding fragment, polynucleotide, vector, host cell, or composition of this disclosure refers to an amount of the composition or molecule sufficient to result in a therapeutic effect, including improved clinical outcome; lessening or alleviation of symptoms associated with a disease; decreased occurrence of symptoms; improved quality of life; longer disease-free status; diminishment of extent of disease, stabilization of disease state; delay of disease progression; remission; survival; or prolonged survival in a statistically significant manner. When referring to an individual active ingredient, administered alone, a therapeutically effective amount refers to the effects of that ingredient or cell expressing that ingredient alone. When referring to a combination, a therapeutically effective amount refers to the combined amounts of active ingredients or combined adjunctive active ingredient with a cell expressing an active ingredient that results in a therapeutic effect, whether administered serially, sequentially, or simultaneously. A combination may comprise, for example, two different antibodies that specifically bind a SARS-CoV-2 antigen, which in certain embodiments, may be the same or different SARS-CoV-2 antigen, and/or can comprise the same or different epitopes.

[0141] Accordingly, in certain embodiments, methods are provided for treating a SARS-CoV-2 infection in a subject, wherein the methods comprise administering to the subject an effective amount of an antibody, antigen-binding fragment, polynucleotide, vector, host cell, or composition as disclosed herein, or any combination thereof.

[0142] Subjects that can be treated by the present disclosure are, in general, human and other primate subjects, such as monkeys and apes for veterinary medicine purposes. Other model organisms, such as mice and rats, may also be treated according to the present disclosure. In any of the aforementioned embodiments, the subject may be a human subject. The subjects can be male or female and can be any suitable age, including infant, juvenile, adolescent, adult, and geriatric subjects.

[0143] A number of criteria are believed to contribute to high risk for severe symptoms or death associated with a SARS CoV-2 infection. These include, but are not limited to, age, occupation, general health, pre-existing health conditions, and lifestyle habits. In some embodiments, a subject treated according to the present disclosure comprises one or more risk factors.

[0144] In certain embodiments, a human subject treated according to the present disclosure is an infant, a child, a young adult, an adult of middle age, or an elderly person. In certain embodiments, a human subject treated according to the present disclosure is less than 1 year old, or is 1 to 5 years old, or is between 5 and 125 years old (e.g., 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, or 125 years old, including any and all ages therein or therebetween). In certain embodiments, a human subject treated according to the present disclosure is 0-19 years old, 20-44 years old, 45-54 years old, 55-64 years old, 65-74 years old, 75-84 years old, or 85 years old, or older. Persons of middle, and especially of elderly age are believed to be at particular risk. In particular embodiments, the human subject is 45-54 years old, 55-64 years old, 65-74 years old, 75-84 years old, or 85 years old, or older. In some embodiments, the human subject is male. In some embodiments, the human subject is female.

[0145] In certain embodiments, a human subject treated according to the present disclosure is a resident of a nursing home or a long-term care facility, is a hospice care worker, is a healthcare provider or healthcare worker, is a first responder, is a family member or other close contact of a subject diagnosed with or suspected of having a SARS-CoV-2 infection, is overweight or clinically obese, is or has been a smoker, has or had chronic obstructive pulmonary disease (COPD), is asthmatic (e.g., having moderate to severe asthma), has an autoimmune disease or condition (e.g., diabetes), and/or has a compromised or depleted immune system (e.g., due to AIDS/HIV infection, a cancer such as a blood cancer, a lymphodepleting therapy such as a chemotherapy, a bone marrow or organ transplantation, or a genetic immune condition), has chronic liver disease, has cardiovascular disease, has a pulmonary or heart defect, works or otherwise spends time in close proximity with others, such as in a factory, shipping center, hospital setting, or the like.

[0146] In certain embodiments, a subject treated according to the present disclosure has received a vaccine for SARS-CoV-2 and the vaccine is determined to be ineffective, e.g., by post-vaccine infection or symptoms in the subject, by clinical diagnosis or scientific or regulatory criteria.

[0147] In certain embodiments, treatment is administered as peri-exposure prophylaxis. In certain embodiments, treatment is administered to a subject with mild-to-moderate disease, which may be in an outpatient setting. For example, human subjects with mild COVID-19 can include individuals who have any of various signs and symptoms, e.g., fever, cough, sore throat, malaise, headache, muscle pain, without shortness of breath, dyspnea, or abnormal imaging. Human subjects with moderate COVID-19 can include individuals who have evidence of lower respiratory disease by clinical assessment or imaging and a saturation of oxygen (SaO2) greater than (>) 93 percent (%) on room air at sea level. In some embodiments, the subject is at risk for contracting COVID-19. In some embodiments, the subject has COVID-19, e.g., a subject who has a positive SARS-CoV-2 viral testing result. In some embodiments, the human subject is at high risk for progressing to severe COVID-19 and/or hospitalization, e.g., the human subject (i) is 65 years of age or older (≥65); (ii) has a body mass index (BMI) of 35 or greater (≥35); (iii) has chronic kidney disease; (iv) has diabetes; (v) has immunosuppressive disease, (vi) is receiving immunosuppressive treatment; (vii) is 55 years of age or older (≥55) and has cardiovascular disease, hypertension, chronic obstructive pulmonary disease, or other chronic respiratory disease; or (viii) is 12-17 years of age and have a BMI≥85% for their age and gender, or sickle cell disease,

congenital or acquired heart disease, neurodevelopmental disorders (e.g., cerebral palsy), a medical-related technological dependence (e.g., tracheostomy, gastrostomy, or positive pressure ventilation not related to COVID-19), or asthma, reactive airway or other chronic respiratory disease that requires daily medication for control.

[0148] In certain embodiments, treatment is administered to a subject with moderate-to-severe disease, such as requiring hospitalization.

[0149] Typical routes of administering the presently disclosed compositions thus include, without limitation, oral, topical, transdermal, inhalation, parenteral, sublingual, buccal, rectal, vaginal, and intranasal. The term "parenteral", as used herein, includes subcutaneous injections, intravenous, intramuscular, intrasternal injection or infusion techniques. In certain embodiments, administering comprises administering by a route that is selected from oral, intravenous, parenteral, intragastric, intrapleural, intrapulmonary, intrarectal, intradermal, intraperitoneal, intratumoral, subcutaneous, topical, transdermal, intracisternal, intrathecal, intranasal, and intramuscular. In particular embodiments, a method comprises orally administering the antibody, antigen-binding fragment, polynucleotide, vector, host cell, or composition to the subject.

[0150] Pharmaceutical compositions according to certain embodiments of the present invention are formulated so as to allow the active ingredients contained therein to be bioavailable upon administration of the composition to a patient. Compositions that will be administered to a subject or patient may take the form of one or more dosage units, where for example, a tablet may be a single dosage unit, and a container of a herein described an antibody or antigen-binding in aerosol form may hold a plurality of dosage units. Actual methods of preparing such dosage forms are known, or will be apparent, to those skilled in this art; for example, see Remington: The Science and Practice of Pharmacy, 20th Edition (Philadelphia College of Pharmacy and Science, 2000). The composition to be administered will, in any event, contain an effective amount of an antibody or antigen-binding fragment, polynucleotide, vector, host cell, or composition of the present disclosure, for treatment of a disease or condition of interest in accordance with teachings herein.

[0151] A composition may be in the form of a solid or liquid. In some embodiments, the carrier(s) are particulate, so that the compositions are, for example, in tablet or powder form. The carrier(s) may be liquid, with the compositions being, for example, an oral oil, injectable liquid or an aerosol, which is useful in, for example, inhalatory administration. When intended for oral administration, the pharmaceutical composition is preferably in either solid or liquid form, where semi solid, semi liquid, suspension and gel forms are included within the forms considered herein as either solid or liquid.

[0152] As a solid composition for oral administration, the pharmaceutical composition may be formulated into a powder, granule, compressed tablet, pill, capsule, chewing gum, wafer or the like. Such a solid composition will typically contain one or more inert diluents or edible carriers. In addition, one or more of the following may be present: binders such as carboxymethylcellulose, ethyl cellulose, microcrystalline cellulose, gum tragacanth or gelatin; excipients such as starch, lactose or dextrins, disintegrating agents such as alginic acid, sodium alginate, Primogel, corn starch and the like; lubricants such as magnesium stearate or Sterotex; glidants such as colloidal silicon dioxide; sweetening agents such as sucrose or saccharin; a flavoring agent such as peppermint, methyl salicylate or orange flavoring; and a coloring agent. When the composition is in the form of a capsule, for example, a gelatin capsule, it may contain, in addition to materials of the above type, a liquid carrier such as polyethylene glycol or oil.

[0153] The composition may be in the form of a liquid, for example, an elixir, syrup, solution, emulsion or suspension. The liquid may be for oral administration or for delivery by injection, as two examples. When intended for oral administration, preferred compositions contain, in addition to the present compounds, one or more of a sweetening agent, preservatives, dye/colorant and flavor enhancer. In a composition intended to be administered by injection, one or more of a surfactant, preservative, wetting agent, dispersing agent, suspending agent, buffer, stabilizer and isotonic agent may be included.

[0154] Liquid pharmaceutical compositions, whether they be solutions, suspensions or other like form, may include one or more of the following adjuvants: sterile diluents such as water for injection, saline solution, preferably physiological saline, Ringer's solution, isotonic sodium chloride, fixed oils such as synthetic mono or diglycerides which may serve as the solvent or suspending medium, polyethylene glycols, glycerin, propylene glycol or other solvents; antibacterial agents such as benzyl alcohol or methyl paraben; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates and agents for the adjustment of tonicity such as sodium chloride or dextrose. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic. Physiological saline is a preferred adjuvant. An injectable pharmaceutical composition is preferably sterile.

[0155] A liquid composition intended for either parenteral or oral administration should contain an amount of an antibody or antigen-binding fragment as herein disclosed such that a suitable dosage will be obtained. Typically, this amount is at least 0.01% of the antibody or antigen-binding fragment in the composition. When intended for oral administration, this amount may be varied to be between 0.1 and about 70% of the weight of the composition. Certain oral pharmaceutical compositions contain between about 4% and about 75% of the antibody or antigen-binding fragment. In certain embodiments, pharmaceutical compositions and preparations according to the present invention are prepared so that a parenteral dosage unit contains between 0.01 to 10% by weight of antibody or antigen-binding fragment prior to dilution.

[0156] The composition may be intended for topical administration, in which case the carrier may suitably comprise a solution, emulsion, ointment or gel base. The base, for example, may comprise one or more of the following: petrolatum, lanolin, polyethylene glycols, bee wax, mineral oil, diluents such as water and alcohol, and emulsifiers and stabilizers. Thickening agents may be present in a composition for topical administration. If intended for transdermal administration, the composition may include a transdermal patch or iontophoresis device. The pharmaceutical composition may be intended for rectal administration, in the form, for example, of a suppository, which will melt in the rectum and release the drug. The composition for rectal administration may contain an oleaginous base as a suitable nonir-

ritating excipient. Such bases include, without limitation, lanolin, cocoa butter and polyethylene glycol.

[0157] A composition may include various materials which modify the physical form of a solid or liquid dosage unit. For example, the composition may include materials that form a coating shell around the active ingredients. The materials that form the coating shell are typically inert, and may be selected from, for example, sugar, shellac, and other enteric coating agents. Alternatively, the active ingredients may be encased in a gelatin capsule. The composition in solid or liquid form may include an agent that binds to the antibody or antigen-binding fragment of the disclosure and thereby assists in the delivery of the compound. Suitable agents that may act in this capacity include monoclonal or polyclonal antibodies, one or more proteins or a liposome. The composition may consist essentially of dosage units that can be administered as an aerosol. The term aerosol is used to denote a variety of systems ranging from those of colloidal nature to systems consisting of pressurized packages. Delivery may be by a liquefied or compressed gas or by a suitable pump system that dispenses the active ingredients. Aerosols may be delivered in single phase, bi phasic, or tri phasic systems in order to deliver the active ingredient(s). Delivery of the aerosol includes the necessary container, activators, valves, subcontainers, and the like, which together may form a kit. One of ordinary skill in the art, without undue experimentation, may determine preferred aerosols.

[0158] It will be understood that compositions of the present disclosure also encompass carrier molecules for polynucleotides, as described herein (e.g., lipid nanoparticles, nanoscale delivery platforms, and the like).

[0159] The pharmaceutical compositions may be prepared by methodology well known in the pharmaceutical art. For example, a composition intended to be administered by injection can be prepared by combining a composition that comprises an antibody, antigen-binding fragment thereof, or antibody conjugate as described herein and optionally, one or more of salts, buffers and/or stabilizers, with sterile, distilled water so as to form a solution. A surfactant may be added to facilitate the formation of a homogeneous solution or suspension. Surfactants are compounds that non-covalently interact with the peptide composition so as to facilitate dissolution or homogeneous suspension of the antibody or antigen-binding fragment thereof in the aqueous delivery system.

[0160] In general, an appropriate dose and treatment regimen provide the composition(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit (such as described herein, including an improved clinical outcome (e.g., a decrease in frequency, duration, or severity of diarrhea or associated dehydration, or inflammation, or longer disease-free and/or overall survival, or a lessening of symptom severity). For prophylactic use, a dose should be sufficient to prevent, delay the onset of, or diminish the severity of a disease associated with disease or disorder. Prophylactic benefit of the compositions administered according to the methods described herein can be determined by performing pre-clinical (including in vitro and in vivo animal studies) and clinical studies and analyzing data obtained therefrom by appropriate statistical, biological, and clinical methods and techniques, all of which can readily be practiced by a person skilled in the art.

[0161] Compositions are administered in an effective amount (e.g., to treat a SARS-CoV-2 infection), which will vary depending upon a variety of factors including the activity of the specific compound employed; the metabolic stability and length of action of the compound; the age, body weight, general health, sex, and diet of the subject; the mode and time of administration; the rate of excretion; the drug combination; the severity of the particular disorder or condition; and the subject undergoing therapy. In certain embodiments, following administration of therapies according to the formulations and methods of this disclosure, test subjects will exhibit about a 10% up to about a 99% reduction in one or more symptoms associated with the disease or disorder being treated as compared to placebo-treated or other suitable control subjects.

[0162] Generally, a therapeutically effective daily dose of an antibody or antigen binding fragment is (for a 70 kg mammal) from about 0.001 mg/kg (i.e., 0.07 mg) to about 100 mg/kg (i.e., 7.0 g); preferably a therapeutically effective dose is (for a 70 kg mammal) from about 0.01 mg/kg (i.e., 0.7 mg) to about 50 mg/kg (i.e., 3.5 g); more preferably a therapeutically effective dose is (for a 70 kg mammal) from about 1 mg/kg (i.e., 70 mg) to about 25 mg/kg (i.e., 1.75 g). For polynucleotides, vectors, host cells, and related compositions of the present disclosure, a therapeutically effective dose may be different than for an antibody or antigen-binding fragment.

[0163] In certain embodiments, a method comprises administering the antibody, antigen-binding fragment, polynucleotide, vector, host cell, or composition to the subject at 2, 3, 4, 5, 6, 7, 8, 9, 10 times, or more.

[0164] In certain embodiments, a method comprises administering the antibody, antigen-binding fragment, or composition to the subject a plurality of times, wherein a second or successive administration is performed at about 6, about 7, about 8, about 9, about 10, about 11, about 12, about 24, about 48, about 74, about 96 hours, or more, following a first or prior administration, respectively.

[0165] In certain embodiments, a method comprises administering the antibody, antigen-binding fragment, polynucleotide, vector, host cell, or composition at least one time prior to the subject being infected by SARS-CoV-2.

[0166] Compositions comprising an antibody, antigen-binding fragment, polynucleotide, vector, host cell, or composition of the present disclosure may also be administered simultaneously with, prior to, or after administration of one or more other therapeutic agents. Such combination therapy may include administration of a single pharmaceutical dosage formulation which contains a compound of the invention and one or more additional active agents, as well as administration of compositions comprising an antibody or antigen-binding fragment of the disclosure and each active agent in its own separate dosage formulation. For example, an antibody or antigen-binding fragment thereof as described herein and the other active agent can be administered to the patient together in a single oral dosage composition such as a tablet or capsule, or each agent administered in separate oral dosage formulations. Similarly, an antibody or antigen-binding fragment as described herein and the other active agent can be administered to the subject together in a single parenteral dosage composition such as in a saline solution or other physiologically acceptable solution, or each agent administered in separate parenteral dosage formulations. Where separate dosage formulations are used, the compo-

sitions comprising an antibody or antigen-binding fragment and one or more additional active agents can be administered at essentially the same time, i.e., concurrently, or at separately staggered times, i.e., sequentially and in any order; combination therapy is understood to include all these regimens.

[0167] In certain embodiments, a combination therapy is provided that comprises one or more anti-SARS-CoV-2 antibody or antigen-binding fragment (or one or more nucleic acid, host cell, vector, or composition) of the present disclosure and one or more anti-inflammatory agent and/or one or more anti-viral agent. In particular embodiments, the one or more anti-inflammatory agent comprises a corticosteroid such as, for example, dexamethasone, prednisone, or the like. In some embodiments, the one or more anti-inflammatory agents comprise a cytokine antagonist such as, for example, an antibody or antigen-binding fragment that binds to IL6 (such as siltuximab), or to IL-6R (such as tocilizumab), or to IL-1β, IL-7, IL-8, IL-9, IL-10, FGF, G-CSF, GM-CSF, IFN-7, IP-10, MCP-1, MIP-1A, MIP1-B, PDGR, TNF-α, or VEGF. In some embodiments, anti-inflammatory agents such as ruxolitinib and/or anakinra are used. In some embodiments, the one or more anti-viral agents comprise nucleotide analogs or nucleotide analog prodrugs such as, for example, remdesivir, sofosbuvir, acyclovir, and zidovudine. In particular embodiments, an anti-viral agent comprises lopinavir, ritonavir, favipiravir, leronlimab or any combination thereof. Other anti-inflammatory agents for use in a combination therapy of the present disclosure include non-steroidal anti-inflammatory drugs (NSAIDS). It will be appreciated that in such a combination therapy, the one or more antibody or antigen-binding fragment (or one or more nucleic acid, host cell, vector, or composition) and the one or more anti-inflammatory agent and/or one or the more antiviral agent can be administered in any order and any sequence, or together.

[0168] In some embodiments, an antibody or antigen-binding fragment (or one or more nucleic acid, host cell, vector, or composition) is administered to a subject who has previously received one or more anti-inflammatory agent and/or one or more antiviral agent. In some embodiments, one or more anti-inflammatory agent and/or one or more antiviral agent is administered to a subject who has previously received an antibody (or one or more nucleic acid, host cell, vector, or composition).

[0169] In certain embodiments, a combination therapy is provided that comprises one or more anti-SARS-CoV-2 antibody or antigen-binding fragment thereof (or one or more nucleic acid, host cell, vector, or composition) of the present disclosure and an anti-CCR5 antibody or antigen binding fragments, such as leronlimab.

[0170] In certain embodiments, a combination therapy is provided that comprises two or more anti-SARS-CoV-2 antibodies of the present disclosure. A method can comprise administering a first antibody to a subject who has received a second antibody, or can comprise administering two or more antibodies together. For example, in particular embodiments, a method is provided that comprises administering to the subject (a) a first antibody or antigen-binding fragment, when the subject has received a second antibody or antigen-binding fragment; (b) the second antibody or antigen-binding fragment, when the subject has received the first antibody or antigen-binding fragment; or (c) the first antibody or antigen-binding fragment, and the second antibody or antigen-binding fragment. In certain further embodiments, (i) the first antibody or antigen-binding fragment comprises a VH comprising or consisting of the amino acid sequence set forth in any one of SEQ ID NOs.:21, 37, 374, 377, 396, and 415, and a VL comprising or consisting of the amino acid sequence set forth in any one of SEQ ID NOs.:29, 45, 380, 383, 385, 388, 392, 393, 400, 402, 404, and 406-414; and (ii) the second antibody or antigen-binding fragment comprises a VH comprising or consisting of the amino acid sequence set forth in SEQ ID NO.:69, and a VL comprising or consisting of the amino acid sequence set forth in SEQ ID NO.:77. In certain embodiments, the first antibody or antigen-binding fragment comprises three heavy chain CDRs and three light chain CDRS of a first antibody disclosed herein, and the second antibody or antigen-binding fragment independently comprises three heavy chain CDRs and three light chain CDRs of a second, different antibody disclosed herein.

[0171] In a related aspect, uses of the presently disclosed antibodies, antigen-binding fragments, vectors, host cells, and compositions are provided.

[0172] In certain embodiments, an antibody, antigen-binding fragment, polynucleotide, vector, host cell, or composition is provided for use in a method of treating a SARS-CoV-2 infection in a subject.

[0173] In certain embodiments, an antibody, antigen-binding fragment, or composition is provided for use in a method of manufacturing or preparing a medicament for treating a SARS-CoV-2 infection in a subject.

TABLE 1

Sequences

Sequence Description	SEQ ID NO.	Sequence
nCoV-3 mAb VH (nt)	1	gaagtgcagttgttggagtctgggggaggcttggttcagccgggggg gtccctgagactctcctgtacagcctct**ggattcacctttgccagctat** **gcc**atgacctgggtccgccaggctccaggcaaggggctggagtgggt ctcaact**attagtggtggtggtggtgacaca**tactccgcagactccgt gaagggccggttcaccatctccagagacaattccaagagcacgctgta tttgcaaatgaacagcctgagagccgcggacacggccctatattactgt gcgagattggaaagcgcgac**gcagcccctcggctactatttctacg** **gtatggacgtc**tggggccaagggactacggtcaccgtctcctcag
nCoV-3 mAb CDRH1 (nt)	2	**ggattcacctttgccagctatgcc**

TABLE 1-continued

Sequences		
Sequence Description	SEQ ID NO.	Sequence
nCoV-3 mAb CDRH2 (nt)	3	**attagtggtggtggtggtgacaca**
nCoV-3 mAb CDRH3 (nt)	4	**gcgagattggaaagcgcgacgcagcccctcggctactatttctacggt atggacgtc**
nCoV-3 mAb VH (aa)	5	EVQLLESGGGLVQPGGSLRLSCTAS**GFTFASYA** MTWVRQAPGKGLEWVST**ISGGGGDT**YSADSV KGRFTISRDNSKSTLYLQMNSLRAADTALYYC **ARLESATQPLGYYFYGMDV**WGQGTTVTVSS
nCoV-3 mAb CDRH1 (aa)	6	**GFTFASYA**
nCoV-3 mAb CDRH2 (aa)	7	**ISGGGGDT**
nCoV-3 mAb CDRH3 (aa)	8	**ARLESATQPLGYYFYGMDV**
nCoV-3 mAb VL (nt)	9	tcctatgagctgacacagccaccctcggtgtcagtgtccccaggacagac ggccaggatcacctgctctggagat**gcattgccaaagcaatat**gctttttg gtaccagcagaggccaggccaggcccctgtgttggtgatatctaaagac agtgagaggccctcagggatccctgagcgattctctggctccagctcagg gacaacagtcacgttgaccatcagtggagtccaggcagaagacgaggct gactattactgt**cattcagcagacatcagtgctacttcttgggtt**ttcggc ggagggaccaagctgaccgtcgtt
nCoV-3 mAb CDRL1 (nt)	10	**gcattgccaaagcaatat**
nCoV-3 mAb CDRL2 (nt)	11	**aaagacagt**
nCoV-3 mAb CDRL3 (nt)	12	**cattcagcagacatcagtgctacttcttgggtt**
nCoV-3 mAb VL (aa)	13	SYELTQPPSVSVSPGQTARITCSGD**ALPKQY**AF WYQQRPGQAPVLVIS**KDS**ERPSGIPERFSGSSSG TTVTLTISGVQAEDEADYYC**HSADISATSWV**FG GGTKLTVV
nCoV-3 mAb CDRL1 (aa)	14	**ALPKQY**
nCoV-3 mAb CDRL2 (aa)	15	**KDS**
nCoV-3 mAb CDRL3 (aa)	16	**HSADISATSWV**
nCoV-10 mAb VH (nt-WT)	17	caggtgcagctggtggagtctgggggaggcgtggtccagcctgggaggt ccctgagactctcctgtgcagcctct**ggattcaccttcagtaactatggc**a tgcactgggtccgccaggctccaggcaaggggctggagtggctggcagt **tatatcatctgatggaagaattaag**ttctatgcagactccgtgaagggcc gattcaccatgtccagagacagttccaagaacacgctgtatctgcaaatga acagcctgagagctgaggacacggctgtgtattactgt**gcgaaagatcg gttccagtttgccagaagctggtacggtgactactttgactac**tggggc cagggaacccaggtcaccgtctcctcag
nCoV-10 mAb CDRH1 (nt)	18	**ggattcaccttcagtaactatggc**
nCoV-10 mAb CDRH2 (nt)	19	**atatcatctgatggaagaattaag**
nCoV-10 mAb CDRH3 (nt)	20	**gcgaaagatcggttccagtttgccagaagctggtacggtgactacttt gactac**

TABLE 1-continued

Sequences		
Sequence Description	SEQ ID NO.	Sequence
nCoV-10 mAb VH (aa)	21	QVQLVESGGGVVQPGRSLRLSCAAS**GFTFSNY** **G**MHWVRQAPGKGLEWLAV**ISSDGRIK**FYADS VKGRFTMSRDSSKNTLYLQMNSLRAEDTAVYY C**AKDRFQFARSWYGDYFDY**WGQGTQVTVSS
nCoV-10 mAb CDRH1 (aa)	22	**GFTFSNYG**
nCoV-10 mAb CDRH2 (aa)	23	**ISSDGRIK**
nCoV-10 mAb CDRH3 (aa)	24	**AKDRFQFARSWYGDYFDY**
nCoV-10 mAb VL (Vk) (nt)	25	gctgttgcgatgactcagtctccactctccctgcccgtcacccttggacagc cggcctccatctcctgcaggtctaatcaaagcctcgtatacagtgatgga aacatctacttgaattggtttcaacagaggccaggccaatctccaatgcgc ctaatttat**agggtttct**aaccgggactctggggtcccagacagattcagc ggcagtgggtcaggcactgatttcacactgaaaatcagcagggtggaggc tgaagatgttgggatttattactgc**atgcaagggacacactggcctccga** **ct**ttcggcggagggaccaaggtggagatcaaac
nCoV-10 mAb CDRL1 (nt)	26	**caaagcctcgtatacagtgatggaaacatctac**
nCoV-10 mAb CDRL2 (nt)	27	**agggtttct**
nCoV-10 mAb CDRL3 (nt)	28	**atgcaagggacacactggcctccgact**
nCoV-10 mAb VL (Vk) (aa)	29	AVAMTQSPLSLPVTLGQPASISCRSN**QSLVYSD** **GNIY**LNWFQQRPGQSPMRLIY**RVS**NRDSGVPD RFSGSGSGTDFTLKISRVEAEDVGIYYC**MQGTH** **WPPT**FGGGTKVEIK
nCoV-10 mAb CDRL1 (aa)	30	**QSLVYSDGNIY**
nCoV-10 mAb CDRL2 (aa)	31	**RVS**
nCoV-10 mAb CDRL3 (aa)	32	**MQGTHWPPT**
nCoV-10-v2 mAb VH (nt)	33	caggtgcagctggtggagtctgggggaggcgtggtccagcctgggaggt ccctgagactctcctgtgcagcctct**ggattcaccttcagtaactatggc**a tgcactgggtccgccaggctccaggcaaggggctggagtggctggcagt t**atatcatctgatggaagaattaag**ttctatgcagactccgtgaagggcc gattcaccatgtccagagacagttccaagaacacgctgtatctgcaaatga acagcctgagagctgaggacacggctgtgtattactgt**gcgaaagatcg** **gttccagtttgccagaagctggtacggtgactactttgactac**tggggc cagggaacccaggtcaccgtctcctcag
nCoV-10-v2 mAb CDRH1 (nt)	34	**ggattcaccttcagtaactatggc**
nCoV-10-v2 mAb CDRH2 (nt	35	**atatcatctgatggaagaattaag**

TABLE 1-continued

Sequences		
Sequence Description	SEQ ID NO.	Sequence
nCoV-10-v2 mAb CDRH3 (nt)	36	**gcgaaagatcggttccagtttgccagaagctggtacggtgactacttt gactac**
nCoV-10-v2 mAb VH (aa)	37	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNY GMHWVRQAPGKGLEWLAV**ISSDGRIK**FYADS VKGRFTMSRDSSKNTLYLQMNSLRAEDTAVYY C**AKDRFQFARSWYGDYFDY**WGQGTQVTVSS
nCoV-10-v2 mAb CDRH1 (aa)	38	**GFTFSNYG**
nCoV-10-v2 mAb CDRH2 (aa)	39	**ISSDGRIK**
nCoV-10-v2 mAb CDRH3 (aa)	40	**AKDRFQFARSWYGDYFDY**
nCoV-10-v2 (N→S) mAb VL (Vk) (nt)	41	gctgttgcgatgactcagtctccactctccctgcccgtcacccttggacagc cggcctccatctcctgcaggtctagt**caaagcctcgtatacagtgatgga aacatctac**ttgaattggtttcaacagaggccaggccaatctccaatgcgc ctaatttat**agggtttct**aaccgggactctggggtcccagacagattcagc ggcagtgggtcaggcactgatttcacactgaaaatcagcagggtggaggc tgaagatgttgggatttattactgc**atgcaagggacacactggcctccga ct**ttcggcggagggaccaaggtggagatcaaac
nCoV-10-v2 mAb CDRL1 (nt)	42	**caaagcctcgtatacagtgatggaaacatctac**
nCoV-10-v2 mAb CDRL2 (nt)	43	**agggtttct**
nCoV-10-v2 mAb CDRL3 (nt)	44	**atgcaagggacacactggcctccgact**
nCoV-10-v2 (N→S) mAb VL (Vk) (aa)	45	AVAMTQSPLSLPVTLGQPASISCRSS**QSLVYSD GNIY**LNWFQQRPGQSPMRLIY**RVS**NRDSGVPD RFSGSGSGTDFTLKISRVEAEDVGIYYC**MQGTH WPPT**FGGGTKVEIK
nCoV-10-v2 mAb CDRL1 (aa)	46	**QSLVYSDGNIY**
nCoV-10-v2 mAb CDRL2 (aa)	47	**RVS**
nCoV-10-v2 mAb CDRL3 (aa)	48	**MQGTHWPPT**
nCoV-17 mAb VH (nt)	49	caggtgcagctggtggagtcgggggggaggcgtggtccagcctgggagg tccctgagactctcctgtgcagcctct**ggattcactttcagttcctatgct**at acactgggtccgccaggctccaggcaagggtctggagtggctggcagtt **atatcatttgatggaagacataaa**tactacgcagactccgtgaagggcc gattcaccatctccagagacaattccaagaacacggtgtatctgcaaatga acagcctgagagttgaggacacggctgtctattcctgt**gcgagagatattc gtcatttgatagtagtggtttccgatatggacgtc**tggggccaagggac cacggtcaccgtctcctcag
nCoV-17 mAb CDRH1 (nt)	50	**ggattcactttcagttcctatgct**

TABLE 1-continued

Sequences		
Sequence Description	SEQ ID NO.	Sequence
nCoV-17 mAb CDRH2 (nt)	51	**atatcatttgatggaagacataaa**
nCoV-17 mAb CDRH3 (nt)	52	**gcgagagatattcgtcatttgatagtagtggtttccgatatggacgtc**
nCoV-17 mAb VH (aa)	53	QVQLVESGGGVVQPGRSLRLSCAAS**GFTFSSY** **A**IHWVRQAPGKGLEWLAV**ISFDGRHK**YYADS VKGRFTISRDNSKNTVYLQMNSLRVEDTAVYS C**ARDIRHLIVVVSDMDV**WGQGTTVTVSS
nCoV-17 mAb CDRH1 (aa)	54	**GFTFSSYA**
nCoV-17 mAb CDRH2 (aa)	55	**ISFDGRHK**
nCoV-17 mAb CDRH3 (aa)	56	**ARDIRHLIVVVSDMDV**
nCoV-17 mAb VL (Vk) (nt)	57	gatgttgtgatgactcagtctccactctccctgcccgtcacccttggacagc cggcctccatctcctgcaggtctagt**caaagcctcgtaaacagtgatgg** **agacacctcc**ttgaattggtttcagcagaggccaggccaatctccaaggc gcctgatttataaggtttctaaccgggactctggggtcccagacagaatca gcggcagtgggtcaggcactgatttcacactgaaaatcagcagggtggag gctgaggatgttggggtttattactgcatgcaaggtacacactggcctcc gacttttggccaggggaccaagctggagatcaaac
nCoV-17 mAb CDRL1 (nt)	58	**caaagcctcgtaaacagtgatggagacacctcc**
nCoV-17 mAb CDRL2 (nt)	59	**caaagcctcgtaaacagtgatggagacacctcc**
nCoV-17 mAb CDRL3 (nt)	60	atgcaaggtacacactggcctccgact
nCoV-17 mAb VL (Vk) (aa)	61	DVVMTQSPLSLPVTLGQPASISCRSS**QSLVNSD** G**DTS**LNWFQQRPGQSPRRLIY**KVS**NRDSGVPD RISGSGSGTDFTLKISRVEAEDVGVYYC**MQGT** **HWPPT**FGQGTKLEIK
nCoV-17 mAb CDRL1 (aa)	62	**QSLVNSDGDTS**
nCoV-17 mAb CDRL2 (aa)	63	**KVS**
nCoV-17 mAb CDRL3 (aa)	64	**MQGTHWPPT**
nCoV-6 mAb VH (nt)	65	caggtcaccttgaaggagtctggtcctgtgctggtgaaacccacagagac cctcacgctgacctgcaccgtctct**gtgttctcactcagcaatgctagaat** **gggt**gtgagctggatccgtcagccccagggaaggccctggagtggctt gcacac**atttttcgagtgaccaaaaa**tcctacagcacatctctgaagag caggctcaccatctccaaggacacctccaaaagccaggtggtccttaccat gaccaacatggaccctgaggacacaggcacatattactgt**gcacgaata** **aacacggcggcgtatgattatgatagtaccacctttgatatc**tggggcc aagggacaatggtcaccgtctcttcag

TABLE 1-continued

Sequences		
Sequence Description	SEQ ID NO.	Sequence
nCoV-6 mAb CDRH1 (nt)	66	**gtgttctcactcagcaatgctagaatgggt**
nCoV-6 mAb CDRH2 (nt)	67	**atttttcgagtgaccaaaaa**
nCoV-6 mAb CDRH3 (nt)	68	**gcacgaataaacacggcggcgtatgattatgatagtaccacctttgat atc**
nCoV-6 mAb VH (aa)	69	QVTLKESGPVLVKPTETLTLTCTVS**VFSLSNAR** **MG**VSWIRQPPGKALEWLAH**IFSSDQK**SYSTSL KSRLTISKDTSKSQVVLTMTNMDPEDTGTYYC **ARINTAAYDYDSTTFDI**WGQGTMVTVSS
nCoV-6 mAb CDRH1 (aa)	70	**VFSLSNARMG**
nCoV-6 mAb CDRH2 (aa)	71	**IFSSDQK**
nCoV-6 mAb CDRH3 (aa)	72	**ARINTAAYDYDSTTFDI**
nCoV-6 mAb VL (Vk) (nt)	73	gacatccagatgacccagtctccatcctccctgtctgcatctgtaggagaca gagtcaccatcacttgccgggcaagt**cagaccattagcaactat**ttaaatt ggtatcagcagaaaccagggaaagcccctaagctcctgctctat**gctgca tcc**agtttgcaaagtggggtcccatcaaggttcagtggcagtggatctggg acagatttcactctcaccatcagcagtctgcaacttgaagattttgcaacttac tactgt**caacagagttacagtacccctcccact**ttcggcggagggacca aggtggagatcaaac
nCoV-6 mAb CDRL1 (nt)	74	**cagaccattagcaactat**
nCoV-6 mAb CDRL2 (nt)	75	**gctgcatcc**
nCoV-6 mAb CDRL3 (nt)	76	**caacagagttacagtacccctcccact**
nCoV-6 mAb VL (Vk) (aa)	77	DIQMTQSPSSLSASVGDRVTITCRAS**QTISNY**LN WYQQKPGKAPKLLLY**AAS**SLQSGVPSRFSGSGS GTDFTLTISSLQLEDFATYYC**QQSYSTPPT**FGG GTKVEIK
nCoV-6 mAb CDRL1 (aa)	78	**QTISNY**
nCoV-6 mAb CDRL2 (aa)	79	**AAS**
nCoV-6 mAb CDRL3 (aa)	80	**QQSYSTPPT**
nCoV-16 mAb VH (nt)	81	caggtgcagctggtggagtctgggggaggcgtggtccagcctgggaggt ccctgagactctcctgtgcagcctct**ggattcaccttcagtagctatggc**a tgcactgggtccgccaggctccaggcaaggggctggagtgggtggcattt **atatcatatgatggaagtaatata**cagtatgcagactccgtgcagggcc gattcaccatctccagagacaattccaagaccacgttgtatctgcaaatgaa cagcctgagagttgaggacacggctatgtactactgt**gcgaaagatctttt cggatattgtaggagtaccagctgcgagtctcttgacgac**tggggcca gggagccctggtcaccgtctcctcag
nCoV-16 mAb CDRH1 (nt)	82	**ggattcaccttcagtagctatggc**
nCoV-16 mAb CDRH2 (nt)	83	**atatcatatgatggaagtaatata**

TABLE 1-continued

Sequences		
Sequence Description	SEQ ID NO.	Sequence
nCoV-16 mAb CDRH3 (nt)	84	**gcgaaagatcttttcggatattgtaggagtaccagctgcgagtctcttg acgac**
nCoV-16 mAb VH (aa)	85	QVQLVESGGGVVQPGRSLRLSCAAS**GFTFSSY** **G**MHWVRQAPGKGLEWVAF**ISYDGSNI**QYADS VQGRFTISRDNSKTTLYLQMNSLRVEDTAMYY C**AKDLFGYCRSTSCESLDD**WGQGALVTVSS
nCoV-16 mAb CDRH1 (aa)	86	**GFTFSSYG**
nCoV-16 mAb CDRH2 (aa)	87	**ISYDGSNI**
nCoV-16 mAb CDRH3 (aa)	88	**AKDLFGYCRSTSCESLDD**
nCoV-16 mAb VL (Vk) (nt)	89	gacatccagttgacccagtctccatccttcctgtctgcatctgtaggagaca gagtcaccatcacttgccgggccagt**cagggcattagcagttat**ttagcc tggtatcagcaaaaaccagggaaagcccctaagctcctgatctat**gctgca tcca**ctttgcaaagtggggtcccatcaaggttcagcggcactggatatggg acagaattcactctcacaatcagcagcctgcagcctgaagattttgcaactt attactgt**caacagcttaataattaccctctcact**ttcggcggagggacc aaggtggagatcaaac
nCoV-16 mAb CDRL1 (nt)	90	**cagggcattagcagttat**
nCoV-16 mAb CDRL2 (nt)	91	**gctgcatcc**
nCoV-16 mAb CDRL3 (nt)	92	**caacagcttaataattaccctctcact**
nCoV-16 mAb VL (Vk) (aa)	93	DIQLTQSPSFLSASVGDRVTITCRAS**QGISSY**LA WYQQKPGKAPKLLIY**AAS**TLQSGVPSRFSGTGY GTEFTLTISSLQPEDFATYYC**QQLNNYPLT**FGG GTKVEIK
nCoV-16 mAb CDRL1 (aa)	94	**QGISSY**
nCoV-16 mAb CDRL2 (aa)	95	**AAS**
nCoV-16 mAb CDRL3 (aa)	96	**QQLNNYPLT**
nCoV-20 mAb VH (nt)	97	caggtcaccttgcgggagtctggtcctgcgctggtgaaacccacacagac cctcacactgacctgcaccttctct**gggttctcactcaccactactgaaat gt**gtgtgggctggatccgtcagcccccagggaaggccctggagtggctt gcactc**attgattgggatgatgataaa**tactacagcacatctctgaggac caggctcaccatctccaaggacacctccaaaaaccaggtggtccttaccat gaccaacatggaccctgtggacacagccacatattactgt**gcacggatgt tcgggcgaaagcgtctggcaccaactgggttcgaccccc**tggggccag ggaaccctggtcaccgtctcctcag
nCoV-20mAb CDRH1 (nt)	98	**gggttctcactcaccactactgaaatgtgt**

TABLE 1-continued

Sequences		
Sequence Description	SEQ ID NO.	Sequence
nCoV-20 mAb CDRH2 (nt)	99	**attgattgggatgatgataaa**
nCoV-20 mAb CDRH3 (nt)	100	**gcacggatgttcgggcgaaagcgtctggcaccaactgggttcgaccc c**
nCoV-20 mAb VH (aa)	101	QVTLRESGPALVKPTQTLTLTCTFS**GFSLTTTE** **MC**VGWIRQPPGKALEWLAL**IDWDDDK**YYSTS LRTRLTISKDTSKNQVVLTMTNMDPVDTATYY C**ARMFGRKRLAPTGFDP**WGQGTLVTVSS
nCoV-20 mAb CDRH1 (aa)	102	**GFSLTTTEMC**
nCoV-20mAb CDRH2 (aa)	103	**IDWDDDK**
nCoV-20 mAb CDRH3 (aa)	104	**ARMFGRKRLAPTGFDP**
nCoV-20 mAb VL (Vk) (nt)	105	gatattgtgatgactcagtctccactctccctgcccgtcacccctggagagc cggcctccatctcctgcaggtctagt**cagagcctcctgcatagtaatgga aagaactat**ttggattggtacctgcagaagccagggcagtctccacagct cctgatctgt**ttgggttct**tatcgggcctccggggtccctgacaggttcagt ggcagtggatcaggcacagattttacactgaaaatcagcagagtggaggc tgaagatgttggggtttattactgc**atgcaagctctacaaactccctggac g**ttcggccaagggaccaaggtggaaatcaaac
nCoV-20 mAb CDRL1 (nt)	106	**cagagcctcctgcatagtaatggaaagaactat**
nCoV-20 mAb CDRL2 (nt)	107	**ttgggttct**
nCoV-20 mAb CDRL3 (nt)	108	**atgcaagctctacaaactccctggacg**
nCoV-20 mAb VL (Vk) (aa)	109	DIVMTQSPLSLPVTPGEPASISCRSS**QSLLHSNG** **KNY**LDWYLQKPGQSPQLLIC**LGS**YRASGVPDR FSGSGSGTDFTLKISRVEAEDVGVYYC**MQALQ** **TPWT**FGQGTKVEIK
nCoV-20 mAb CDRL1 (aa)	110	**QSLLHSNGKNY**
nCoV-20 mAb CDRL2 (aa)	111	**LGS**
nCoV-20 mAb CDRL3 (aa)	112	**MQALQTPWT**
nCoV-4 mAb VH (nt)	113	caggtgcaactggtggagtctgggggaggcgtggtccagcctgggaggt ccctgagactctcctgtgaagcctct**ggattcaccctcagaaccagtagt** ctccactgggtccgccaggctccaggcaaggggctggagtgggtggca gtt**atatcaaatgatggagccactaaa**ttctacgcagacgccgtgaagg gccgattcaccatctccagagacaactccaacaacaaaatatatctgcaact gaacggcctgaaacctgaggacacggctgtctattactgt**gcgagagaa acacgtcattacagccatggtttgaactggttcgacccc**tggggccag ggaaccctggtcaacgtctcctcag
nCoV-4 mAb CDRH1 (nt)	114	**ggattcaccctcagaaccagtagt**

TABLE 1-continued

Sequences		
Sequence Description	SEQ ID NO.	Sequence
nCoV-4 mAb CDRH2 (nt)	115	**atatcaaatgatggagccactaaa**
nCoV-4 mAb CDRH3 (nt)	116	**gcgagagaaacacgtcattacagccatggtttgaactggttcgacccc**
nCoV-4 mAb VH (aa)	117	**GFTLRTSS**LHWVRQAPGKGLEWVAV**ISNDGA** **TK**FYADAVKGRFTISRDNSNNKIYLQLNGLKPE DTAVYYC**ARETRHYSHGLNWFDP**WGQGTLV NVSS
nCoV-4 mAb CDRHI (aa)	118	**GFTLRTSS**
nCoV-4 mAb CDRH2 (aa)	119	**ISNDGATK**
nCoV-4 mAb CDRH3 (aa)	120	**ARETRHYSHGLNWFDP**
nCoV-4 mAb VL (Vk) (nt)	12	gaaagagtgatgacgcagtctccagtcaccctgtctgtgtctccaggggaa agagccaccctctcctgcagggccagt**cagagtgttagcagcgac**ttag cctggtaccagcagaaacctggccaggctcccaggctcctcatctat**ggt** **gcatcc**accagggccactggtatcccagccaggttcagtggcagtgggtc tgggacagagttcactctcaccatcagcagcctgcagtctgaagattttgca gtttattactgt**cagcagtataataactggccgaccacc**ttcggccaagg gacacgactggacattaaac
nCoV-4 mAb CDRL1 (nt)	122	**cagagtgttagcagcgac**
nCoV-4 mAb CDRL2 (nt)	123	**ggtgcatcc**
nCoV-4 mAb CDRL3 (nt)	124	**cagcagtataataactggccgaccacc**
nCoV-4 mAb VL (Vk) (aa)	125	ERVMTQSPVTLSVSPGERATLSCRAS**QSVSSD**L AWYQQKPGQAPRLLIY**GAS**TRATGIPARFSGSG SGTEFTLTISSLQSEDFAVYYC**QQYNNWPTT**FG QGTRLDIK
nCoV-4 mAb CDRL1 (aa)	126	**QSVSSD**
nCoV-4 mAb CDRL2 (aa)	127	**GAS**
nCoV-4 mAb CDRL3 (aa)	128	**QQYNNWPTT**
nCoV-4-v2 (N→T) mAb VH(nt)	129	caggtgcaactggtggagtctgggggaggcgtggtccagcctgggaggt ccctgagactctcctgtgaagcctct**ggattcaccctcagaaccagtagt** ctccactgggtccgccaggctccaggcaaggggctggagtgggtggca gtt**atatcaaatgatggagccactaaa**ttctacgcagacgccgtgaaggg ccgattcaccatctccagagacaactccaacaacaaaatatatctgcaac tgaacggcctgaaacctgaggacacggctgtctattactgt**gcgagagaa** **acacgtcattacagccatggtttgaactggttcgacccc**tggggccag ggaaccctggtcaccgtctcctcag
nCoV-4-v2 mAb CDRH1 (nt)	130	**ggattcaccctcagaaccagtagt**
nCoV-4-v2 mAb CDRH2 (nt)	131	**atatcaaatgatggagccactaaa**
nCoV-4-v2 mAb CDRH3 (nt)	132	**gcgagagaaacacgtcattacagccatggtttgaactggttcgacccc**

TABLE 1-continued

Sequences		
Sequence Description	SEQ ID NO.	Sequence
nCoV-4-v2 (NVS→ TVS) mAb VH (aa)	133	QVQLVESGGGVVQPGRSLRLSCEAS**GFTLRTSS** LHWVRQAPGKGLEWVAV**ISNDGATK**FYADAV KGRFTISRDNSNNKIYLQLNGLKPEDTAVYYC**A** **RETRHYSHGLNWFDP**WGQGTLVTVSS
nCoV-4-v2 mAb CDRH1 (aa)	134	**GFTLRTSS**
nCoV-4-v2 mAb CDRH2 (aa)	135	**ISNDGATK**
nCoV-4-v2 mAb CDRH3 (aa)	136	**ARETRHYSHGLNWFDP**
nCoV-4-v2 mAb VL (Vk) (nt)	137	gaaagagtgatgacgcagtctccagtcaccctgtctgtgtctccaggggaa agagccaccctctcctgcagggccagt**cagagtgttagcagcgac**ttag cctggtaccagcagaaacctggccaggctcccaggctcctcatctatggt gcatccaccagggccactggtatcccagccaggttcagtggcagtgggtc tgggacagagttcactctcaccatcagcagcctgcagtctgaagattttgca gtttattactgtcagcagtataataactggccgaccaccttcggccaagg gacacgactggacattaaac
nCoV-4-v2 mAb CDRL1 (nt)	138	**cagagtgttagcagcgac**
nCoV-4-v2 mAb CDRL2 (nt)	139	**ggtgcatcc**
nCoV-4-v2 mAb CDRL3 (nt)	140	**cagcagtataataactggccgaccacc**
nCoV-4-v2 mAb VL (Vk) (aa)	141	ERVMTQSPVTLSVSPGERATLSCRAS**QSVSSD**L AWYQQKPGQAPRLLIY**GAS**TRATGIPARFSGSG SGTEFTLTISSLQSEDFAVYYC**QQYNNWPTT**FG QGTRLDIK
nCoV-4-v2 mAb CDRL1 (aa)	142	**QSVSSD**
nCoV-4-v2 mAb CDRL2 (aa)	143	**GAS**
nCoV-4-v2 mAb CDRL3 (aa)	144	**QQYNNWPTT**
nCoV-4-v3 (N→T) mAb VH (nt)	145	caggtgcaactggtggagtctgggggaggcgtggtccagcctgggaggt ccctgagactctcctgtgaagcctct**ggattcaccctcagaaccagtagt** ctccactgggtccgccaggctccaggcaaggggctggagtgggtggca gtt**atatcaaatgatggagccactaaa**ttctacgcagacgccgtgaagg gccgattcaccatctccagagacaactccaacaacaaaatatatctgcaact gaacggcctgaaacctgaggacacggctgtctattactgt**gcgagagaa** **acacgtcattacagccatggtttgaactggttcgacccc**tggggccag ggaaccctggtcaccgtctcctcag
nCoV-4-v3 mAb CDRH1 (nt)	146	**ggattcaccctcagaaccagtagt**
nCoV-4-v3 mAb CDRH2 (nt)	147	**atatcaaatgatggagccactaaa**

TABLE 1-continued

Sequences		
Sequence Description	SEQ ID NO.	Sequence
nCoV-4-v3 mAb CDRH3 (nt)	148	**gcgagagaaacacgtcattacagccatggtttgaactggttegacccc**
nCoV-4-v3 (N=>T) mAb VH (aa)	149	QVQLVESGGGVVQPGRSLRLSCEAS**GFTLRTSS** LHWVRQAPGKGLEWVAV**ISNDGATK**FYADAV KGRFTISRDNSNNKIYLQLNGLKPEDTAVYYC**A** **RETRHYSHGLNWFDP**WGQGTLVTVSS
nCoV-4-v3 mAb CDRH1 (aa)	150	**GFTLRTSS**
nCoV-4-v3 mAb CDRH2 (aa)	151	**ISNDGATK**
nCoV-4-v3 mAb CDRH3 (aa)	152	**ARETRHYSHGLNWFDP**
nCoV-4-v3 (W→F) mAb VL (Vk) (nt)	153	gaaagagtgatgacgcagtctccagtcaccctgtctgtgtctccaggggaa agagccaccctctcctgcagggccagt**cagagtgttagcagcgac**ttag cctggtaccagcagaaacctggccaggctcccaggctcctcatctat**ggt** **gcatcc**accagggccactggtatcccagccaggttcagtggcagtgggtc tgggacagagttcactctcaccatcagcagcctgcagtctgaagattttgca gtttattactgt**cagcagtataataacttcccgaccacc**ttcggccaaggg acacgactggacattaaac
nCoV-4-v3 mAb CDRL1 (nt)	154	**cagagtgttagcagcgac**
nCoV-4-v3 mAb CDRL2 (nt)	155	**ggtgcatcc**
nCoV-4-v3 mAb CDRL3 (nt)	156	**cagcagtataataacttcccgaccacc**
nCoV-4-v3 (W→F) mAb VL (Vk) (aa)	157	ERVMTQSPVTLSVSPGERATLSCRAS**QSVSSD**L AWYQQKPGQAPRLLIY**GAS**TRATGIPARFSGSG SGTEFTLTISSLQSEDFAVYYC**QQYNNFPTT**FG QGTRLDIK
nCoV-4-v3 mAb CDRL1 (aa)	158	QSVSSD
nCoV-4-v3 mAb CDRL2 (aa)	159	GAS
nCoV-4-v3 mAb CDRL3 (aa)	160	QQYNNFPTT
nCoV-15 mAb VH (nt)	161	gaggtgcagctggtggagtctgggggaggcttggtaacgccagggcggt ccctgagactctcctgtacagcttct**ggattcacgtttggtgattatgct**ct gagctggttccgccaggctccagggaaggggctggagtgggtagctttc **attagaagcaaagcttatggtgggacaaca**gaatacgccgcgtctgtg aaaggcagattcaccatctcaagagatgattcgcaaatcattgtctatctgca aatggacagcctgaaaaccgaagacacagccgtatattattgt**agttggat** **acaccggatagtctcct**ggggccagggaaccctggtcaccgtctcctca g
nCoV-15 mAb CDRH1 (nt)	162	**ggattcacgtttggtgattatgct**

TABLE 1-continued

Sequences		
Sequence Description	SEQ ID NO.	Sequence
nCoV-15 mAb CDRH2 (nt)	163	**attagaagcaaagcttatggtgggacaaca**
nCoV-15 mAb CDRH3 (nt)	164	**agttggatacaccggatagtctcc**
nCoV-15 mAb VH (aa)	165	EVQLVESGGGLVTPGRSLRLSCTAS**GFTFGDY** **A**LSWFRQAPGKGLEWVAF**IRSKAYGGTT**EYA ASVKGRFTISRDDSQIIVYLQMDSLKTEDTAVY YC**SWIHRIVS**WGQGTLVTVSS
nCoV-15 mAb CDRH1 (aa)	166	GFTFGDYA
nCoV-15 mAb CDRH2 (aa)	167	IRSKAYGGTT
nCoV-15 mAb CDRH3 (aa)	168	SWIHRIVS
nCoV-15 mAb VL (Vk) (nt)	169	gacatccagatgacccagtctccatcctccctgtctgcatctgaaggagac agagtcaccatcacttgccaggcgagt**caggacattagcatctat**ttaaat tggtttcagcagaaaccagggaaagcccctaagctcctgatctac**gaggc** **atcc**aatttgaaaacaggggtcccatcaaggttcagtggaagtggatctgg gacagattttactttcaccatcagcagcctgcagcctgaagatattgcaacat attactgt**caacagtatgataatctcccctacact**tttggccaggggacca agctggagatcaaac
nCoV-15 mAb CDRL1 (nt)	170	**caggacattagcatctat**
nCoV-15 mAb CDRL2 (nt)	171	**gaggcatcc**
nCoV-15 mAb CDRL3 (nt)	172	**caacagtatgataatctcccctacact**
nCoV-15 mAb VL (Vk) (aa)	173	DIQMTQSPSSLSASEGDRVTITCQAS**QDISIY**LN WFQQKPGKAPKLLIY**EAS**NLKTGVPSRFSGSGS GTDFTFTISSLQPEDIATYYC**QQYDNLPYT**FGQ GTKLEIK
nCoV-15 mAb CDRL1 (aa)	174	**QDISIY**
nCoV-15 mAb CDRL2 (aa)	175	**EAS**
nCoV-15 mAb CDRL3 (aa)	176	**QQYDNLPYT**
nCoV-12 mAb VH (nt)	177	caggtgcagctggtggagtctgggggaggcgtggtccagcctgggaggt ccctgagactctcctgtgcaggctct**ggattcaccttcagtagctttggt**tt gcactgggtccgccaggcgccaggcaagggactggagtggttggcactt **atttcagatgagggacgcattaaa**tactacgcaaactccgtgaagggcc gattctttatctccagagacaattccaagaacacgctgtatctgcaaatgaac agcctgagaggtgaggacacggctgtatattactgt**gcgagagatgtcaa** **aggacatattgtggtgatgacttctcttgactac**tggggccagggagcc ctggtcaccgtctcctcag

TABLE 1-continued

Sequences		
Sequence Description	SEQ ID NO.	Sequence
nCoV-12 mAb CDRH1 (nt)	178	**ggattcaccttcagtagctttggt**
nCoV-12 mAb CDRH2 (nt)	179	**atttcagatgagggacgcattaaa**
nCoV-12 mAb CDRH3 (nt)	180	**gcgagagatgtcaaaggacatattgtggtgatgacttctcttgactac**
nCoV-12 mAb VH (aa)	181	QVQLVESGGGVVQPGRSLRLSCAGS**GFTFSSF** **G**LHWVRQAPGKGLEWLAL**ISDEGRIK**YYANS VKGRFFISRDNSKNTLYLQMNSLRGEDTAVYY C**ARDVKGHIVVMTSLDY**WGQGALVTVSS
nCoV-12 mAb CDRH1 (aa)	182	**GFTFSSFG**
nCoV-12 mAb CDRH2 (aa)	183	**ISDEGRIK**
nCoV-12 mAb CDRH3 (aa)	184	**ARDVKGHIVVMTSLDY**
nCoV-12 mAb VL (Vk) (nt)	185	gatgttgtgatgactcagtctccactctccctgcccgtcacccttggacagc cggcctccatctcctgtaggtctagt**caaagcctcgtctccagtgatgga** **gacacctcc**ttgagttggtttcagcagaggccaggccaatctccaaggcg cctaatttat**gaggtttct**aaccgggactctggggtcccagacagattcag cggcagtgggtcaggcactgatttcacactgaaaatcagcagggtggagg ctgaggatgttggggtttattactgc**atgcaaggtacacactggcctccg** **acg**ttcggccaagggaccaaggtggaaatcaaac
nCoV-12 mAb CDRL1 (nt)	186	**caaagcctcgtctccagtgatggagacacctcc**
nCoV-12 mAb CDRL2 (nt)	187	**gaggtttct**
nCoV-12 mAb CDRL3 (nt)	188	**atgcaaggtacacactggcctccgacg**
nCoV-12 mAb VL (Vk) (aa)	189	DVVMTQSPLSLPVTLGQPASISCRSS**QSLVSSDG** **DTS**LSWFQQRPGQSPRRLIY**EVS**NRDSGVPDRF SGSGSGTDFTLKISRVEAEDVGVYYC**MQGTH** **WPPTF**GQGTKVEIK
nCoV-12 mAb CDRL1 (aa)	190	**QSLVSSDGDTS**
nCoV-12 mAb CDRL2 (aa)	191	**EVS**
nCoV-12 mAb CDRL3 (aa)	192	**MQGTHWPPT**
nCoV-5 mAb VH (nt)	193	caaatgcagctggtgcagtctgggcctgagatgaagaagcctgggacctc agtgaaggtctcctgcaaggcctct**ggattcacttttagtaaaactacc**tt gcagtgggtacgtcaggctcgtggacaacgccctgagtggataggatgg **atcgtccttggcagcggtaacaca**aactacgcacattacttccaggcaag agtcaccattaccagggacatgtccacgagcacagcctacatggaactga gcagcctgagttccgaggacacggccgtctattactgt**gcggcagagatg**

TABLE 1-continued

Sequences		
Sequence Description	SEQ ID NO.	Sequence
		gctacaattcagaattactattactactatggtatggacgtctggggcc aagggaccacggtcaccgtctcctcag
nCoV-5 mAb CDRH1 (nt)	194	**ggattcacttttagtaaaactacc**
nCoV-5 mAb CDRH2 (nt)	195	**atcgtccttggcagcggtaacaca**
nCoV-5 mAb CDRH3 (nt)	196	**gcggcagagatggctacaattcagaattactattactactatggtatgg acgtc**
nCoV-5 mAb VH (aa)	197	QMQLVQSGPEMKKPGTSVKVSCKAS**GFTFSKT** **T**LQWVRQARGQRPEWIGW**IVLGSGNT**NYAHY FQARVTITRDMSTSTAYMELSSLSSEDTAVYYC **AAEMATIQNYYYYYGMDV**WGQGTTVTVSS
nCoV-5 mAb CDRH1 (aa)	198	**GFTFSKTT**
nCoV-5 mAb CDRH2 (aa)	199	**IVLGSGNT**
nCoV-5 mAb CDRH3 (aa)	200	**AAEMATIQNYYYYYGMDV**
nCoV-5 mAb VL (Vk) (nt)	201	gacatccagatgacccagtctccatcctccctgtctgcatctgtcggggaca gagtcaccatcacttgccgggcaagt**cagagcattaactactat**ttaaatt ggtatcagcagaaacctgggaaagcccctaacctcctgatctat**gctgcat cc**agtttgcctggtggggtcccatcaaggttcagtggcagtggatctggga cagatttcactctcaccatcaccagtctgcaacctgaggattttgcaacttact tctgt**caacagagttacagtacccctccgact**tttggccaggggaccaa gctggagatcaaac
nCoV-5 mAb CDRL1 (nt)	202	**cagagcattaactactat**
nCoV-5 mAb CDRL2 (nt)	203	**gctgcatcc**
nCoV-5 mAb CDRL3 (nt)	204	**caacagagttacagtacccctccgact**
nCoV-5 mAb VL (Vk) (aa)	205	DIQMTQSPSSLSASVGDRVTITCRAS**QSINYY**LN WYQQKPGKAPNLLIY**AAS**SLPGGVPSRFSGSGS GTDFTLTITSLQPEDFATYFC**QQSYSTPPTF**GQG TKLEIK
nCoV-5 mAb CDRL1 (aa)	206	**QSINYY**
nCoV-5 mAb CDRL2 (aa)	207	**AAS**
nCoV-5 mAb CDRL3 (aa)	208	**QQSYSTPPT**
nCoV-14 mAb VH (nt)	209	caggtgcagctggtgcactctggggctgaggtgaagaagcctggggcct cagtgagggtctcctgcaaggcctct**ggatacacctacaccgcctactat** atacactggctgcggcaggcccctggacaagggcttgagtggatgggat gg**atcaacgctgacaatggtgacaca**cactctgtgcagaagtttcaggg cagggtcaccatgaccagggacacgtccatcaatacagcctacctggag gtgagcaggctgaagtctgacgacacggccgtctattattgt**gcgagagg agacgttccagttggtactggctgggtctttgacttc**tggggccaggga accctggtcaccgtctcctcag
nCoV-14 mAb CDRH1 (nt)	210	**ggatacacctacaccgcctactat**
nCoV-14 mAb CDRH2 (nt)	211	**atcaacgctgacaatggtgacaca**

TABLE 1-continued

Sequences		
Sequence Description	SEQ ID NO.	Sequence
nCoV-14 mAb CDRH3 (nt)	212	**gcgagaggagacgttccagttggtactggctgggtctttgacttc**
nCoV-14 mAb VH (aa)	213	QVQLVHSGAEVKKPGASVRVSCKAS**GYTYTA** **YY**IHWLRQAPGQGLEWMGW**INADNGDT**HSV QKFQGRVTMTRDTSINTAYLEVSRLKSDDTAV YYC**ARGDVPVGTGWVFDF**WGQGTLVTVSS
nCoV-14 mAb CDRH1 (aa)	214	**GYTYTAYY**
nCoV-14 mAb CDRH2 (aa)	215	**INADNGDT**
nCoV-14 mAb CDRH3 (aa)	216	**ARGDVPVGTGWVFDF**
nCoV-14 mAb VL (Vk) (nt)	217	gacatccagatgacccagtctccatcctccctgtctgcatctgtgggagaca gcgtcaccatcagttgccgggcaagt**cagaccattaacaactttt**taaatt ggtaccagcagaagccagggaaagcccctaacctcctgatctat**ggtgca** **tac**aatttgcaaagtggggtcccatcaaggttcagtggcagtggatccggg acagatttcactctcaccatcagcagcctgcaacctgaggatgttgcaattta ctattgt**caacagagtctcagtatggtcacc**ttcggccaagggacacgac tggacattaaac
nCoV-14 mAb CDRL1 (nt)	218	**cagaccattaacaacttt**
nCoV-14 mAb CDRL2 (nt)	219	**ggtgcatac**
nCoV-14 mAb CDRL3 (nt)	220	**caacagagtctcagtatggtcacc**
nCoV-14 mAb VL (Vk) (aa)	221	DIQMTQSPSSLSASVGDSVTISCRAS**QTINNF**LN WYQQKPGKAPNLLIY**GAY**NLQSGVPSRFSGSG SGTDFTLTISSLQPEDVAIYYC**QQSLSMVT**FGQ GTRLDIK
nCoV-14 mAb CDRL1 (aa)	222	**QTINNF**
nCoV-14 mAb CDRL2 (aa)	223	**GAY**
nCoV-14 mAb CDRL3 (aa)	224	**QQSLSMVT**
nCoV-9 mAb VH (nt)	225	caggtgcttctggtggagtctgggggaggcgtggtccagcctgggatgtc cctgagactctcctgtgcagcctct**ggattcaccttcagttcctatgct**atg cactgggtccgccaggctccaggcaaggggctggagtgggtggcagtt**a** **tctcatatgatggaagcactaaa**ttctacgcagactccgtgaggggccg attccccatctccagagacaattccaagaacacggtgtatctgcaaatgaac agcctgagacctgaggacacggcagtctattactgt**gcgacagttagtgt** **cgaggggtataccagtggctggtatttgggaacccttgacttc**tggggc cagggaaccccggtcaccgtctcctcag
nCoV-9 mAb CDRH1 (nt)	226	**ggattcaccttcagttcctatgct**
nCoV-9 mAb CDRH2 (nt)	227	**atctcatatgatggaagcactaaa**

TABLE 1-continued

Sequences		
Sequence Description	SEQ ID NO.	Sequence
nCoV-9 mAb CDRH3 (nt)	228	**gcgacagttagtgtcgaggggtataccagtggctggtatttgggaacc cttgacttc**
nCoV-9 mAb VH (aa)	229	QVLLVESGGGVVQPGMSLRLSCAAS**GFTFSSY** **A**MHWVRQAPGKGLEWVAV**ISYDGSTK**FYADS VRGRFPISRDNSKNTVYLQMNSLRPEDTAVYY C**ATVSVEGYTSGWYLGTLDF**WGQGTPVTVSS
nCoV-9 mAb CDRH1 (aa)	230	**GFTFSSYA**
nCoV-9 mAb CDRH2 (aa)	231	**ISYDGSTK**
nCoV-9 mAb CDRH3 (aa)	232	**CATVSVEGYTSGWYLGTLDF**
nCoV-9 mAb VL (Vk) (nt)	233	gaaagagtgatgacgcagtttccagccaccctgtctgtgtctccaggggaa agagccaccctctcctgcagggccagt**cagagtgttagtagcaac**ttag cctggtaccagcagaaacctggccaggctcccaggctcctcatctat**ggt gcatcc**accagggccattggtgtcccagccaggttcagtggcagtgggtc tgggacagagttcactctcaccatcagcagcctgcagtctgaagattttgca gtttattactgt**cagcagtataataactggccgggaact**tttggccaggg gaccaagctggagatcaaac
nCoV-9 mAb CDRL1 (nt)	234	**cagagtgttagtagcaac**
nCoV-9 mAb CDRL2 (nt)	235	**ggtgcatcc**
nCoV-9 mAb CDRL3 (nt)	236	**cagcagtataataactggccgggaact**
nCoV-9 mAb VL (Vk) (aa)	237	ERVMTQFPATLSVSPGERATLSCRAS**QSVSSN**L AWYQQKPGQAPRLLIY**GAS**TRAIGVPARFSGSG SGTEFTLTISSLQSEDFAVYYC**QQYNNWPGT**FG QGTKLEIK
nCoV-9 mAb CDRL1 (aa)	238	**QSVSSN**
nCoV-9 mAb CDRL2 (aa)	239	**GAS**
nCoV-9 mAb CDRL3 (aa)	240	**QQYNNWPGT**
nCoV-18 mAb VH (nt)	241	caggttcagctggtgcagtctggagctgaggtgaggcagcctgggacctc agtgaaggtctcctgcaaggcttct**ggttacacctttatgaataatgat**at cacctgggtgcgacaggcccctggacaggtgcttcagtggatggggtgg **atcaggccttccaatggaaacaca**aactacgcacagaagttccagggc agagtcaccctgaccacagacacatccacgaacacagcccacatggaac tgaggagcctgaaatctgacgacacggccgtgtattattgt**gcgagacaa tctcattcgacgcggggtggctggcacttcagcccc**tggggccaggga accctggtcaccgtctcctcag
nCoV-18 mAb CDRH1 (nt)	242	**ggttacacctttatgaataatgat**
nCoV-18 mAb CDRH2 (nt)	243	**atcaggccttccaatggaaacaca**
nCoV-18 mAb CDRH3 (nt)	244	**gcgagacaatctcattcgacgcgggggctggcacttcagcccc**
nCoV-18 mAb VH (aa)	245	QVQLVQSGAEVRQPGTSVKVSCKAS**GYTFMN** **ND**ITWVRQAPGQVLQWMGW**IRPSNGNT**NYA

TABLE 1-continued

Sequences		
Sequence Description	SEQ ID NO.	Sequence
		QKFQGRVTLTTDTSTNTAHMELRSLKSDDTAV YYC**ARQSHSTRGGWHFSP**WGQGTLVTVSS
nCoV-18 mAb CDRH1 (aa)	246	**GYTFMNND**
nCoV-18 mAb CDRH2 (aa)	247	**IRPSNGNT**
nCoV-18 mAb CDRH3 (aa)	248	**ARQSHSTRGGWHFSP**
nCoV-18 mAb VL (Vk) (nt)	249	gacatccagatgacccagtctccatcctccctgtctgcatctgtaggagaca gagtcaccatcacttgccggccaagt**caacccattagctactttt**taaattg gtatcagcagacaccagggaaagcccctaagctcctcatctat**gctgcatc** **c**agtttgcaaagtggggtcccatcaaggttcagtggcagtggatctgggac agatttcactctcaccatcagcagtctgcaacctgaagattctgcaacttact actgt**caacagagttatagtgtcccgtacact**tttggccaggggaccaa gctggagatcaaac
nCoV-18 mAb CDRL1 (nt)	250	**caacccattagctacttt**
nCoV-18 mAb CDRL2 (nt)	251	**gctgcatcc**
nCoV-18 mAb CDRL3 (nt)	252	**caacagagttatagtgtcccgtacact**
nCoV-18 mAb VL (Vk) (aa)	253	DIQMTQSPSSLSASVGDRVTITCRPS**QPISYF**LN WYQQTPGKAPKLLIY**AAS**SLQSGVPSRFSGSGS GTDFTLTISSLQPEDSATYYC**QQSYSVPYT**FGQ GTKLEIK
nCoV-18 mAb CDRL1 (aa)	254	**QPISYF**
nCoV-18 mAb CDRL2 (aa)	255	**AAS**
nCoV-18 mAb CDRL3 (aa)	256	**QQSYSVPYT**
nCoV-8 mAb VH (nt)	257	gaagtgctcctggtggagtctgggggaggcttggtacagcctggcaggtc cctgagactctcctgtgtagtctct**ggattcacctttgattattatgcc**atgc actgggtccggcaagctccagggaagggcctggagtgggtctcaggt**at** **tagttggaatagtgataacaca**gactatgcggactctgtgaagggccga ttcaccatctccagagacaacgccaagaactccctgtatctgcaaatgaac agtctgaaaactgaggacacggccttgtattactgt**gcaaaagatattagt** **ctagtttttggagtgttaaccctccccgtaacggaatggacgtc**tggg gccaagggaccacggtcaccgtctcctcag
nCoV-8 mAb CDRH1 (nt)	258	**ggattcacctttgattattatgcc**
nCoV-8 mAb CDRH2 (nt)	259	**attagttggaatagtgataacaca**
nCoV-8 mAb CDRH3 (nt)	260	**gcaaaagatattagtctagtttttggagtgttaaccctccccgtaacg** **gaatggacgtc**
nCoV-8 mAb VH (aa)	261	EVLLVESGGGLVQPGRSLRLSCVVS**GFTFDYY** **AM**HWVRQAPGKGLEWVSG**ISWNSDNT**DYAD

TABLE 1-continued

Sequences		
Sequence Description	SEQ ID NO.	Sequence
		SVKGRFTISRDNAKNSLYLQMNSLKTEDTALY YC**AKDISLVFWSVNPPRNGMDV**WGQGTTVT VSS
nCoV-8 mAb CDRH1 (aa)	262	**GFTFDYYAM**
nCoV-8 mAb CDRH2 (aa)	263	**ISWNSDNT**
nCoV-8 mAb CDRH3 (aa)	264	**AKDISLVFWSVNPPRNGMDV**
nCoV-8 mAb VL (Vk) (nt)	265	gacatccagatgacccagtctccatcctccctgtctgcatctgtaggagaca gagtcaccatcacttgccgggcaagt**cagagcattcgcagctat**ttaaatt ggtatcagcagaaaccagggaaagcccctaacctcctgatctat**actgca** **tcc**agtttgcaaagtggggtcccatcaaggttcagtggcagtggatctggg acagatttcactctcaccatcagcagtctgcaacctgaagattttgcgactta ctactgt**caacagagttacagttcccctctcact**ttcggcggagggacca aggtggagatcaaac
nCoV-8 mAb CDRL1 (nt)	266	**cagagcattcgcagctat**
nCoV-8 mAb CDRL2 (nt)	267	**actgcatcc**
nCoV-8 mAb CDRL3 (nt)	268	**caacagagttacagttcccctctcact**
nCoV-8 mAb VL (Vk) (aa)	269	DIQMTQSPSSLSASVGDRVTITCRAS**QSIRSY**LN WYQQKPGKAPNLLIY**TAS**SLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYC**QQSYSSPLT**FGGG TKVEIK
nCoV-8 mAb CDRL1 (aa)	270	**QSIRSY**
nCoV-8 mAb CDRL2 (aa)	271	**TAS**
nCoV-8 mAb CDRL3 (aa)	272	**QQSYSSPLT**
nCoV-7 mAb VH (nt)	273	caggagcaggtggtggagtctgggggaggcgtggtccagcctgggaag tccctgagactctcctgtgcagcctct**ggattcagcttgaatgactttgct**a tccactgggtccgccaggctccaggcaagaggctggagtgggtggcaat c**atatcatacgatggaagggttaaa**ttttacgcagactcagtgaagggc cgattcaccatctcccgagactcttccgtgcatctgcaaatggacagcctga gacctgaggacacgggtctgtattactgt**gcgagagactcttcgtggcag** **agcactgggtggcctataaactggttcgaccgc**tggggccggggaac cctggtcaccgtctcctcag
nCoV-7 mAb CDRH1 (nt)	274	**ggattcagcttgaatgactttgct**
nCoV-7 mAb CDRH2 (nt)	275	**atatcatacgatggaagggttaaa**
nCoV-7 mAb CDRH3 (nt)	276	**gcgagagactcttcgtggcagagcactgggggcctataaactggttc** **gaccgc**
nCoV-7 mAb VH (aa)	277	QEQVVESGGGVVQPGKSLRLSCAAS**GFSLNDF** **A**IHWVRQAPGKRLEWVAI**ISYDGRVK**FYADSV KGRFTISRDSSVHLQMDSLRPEDTGLYYC**ARDS** **SWQSTGWPINWFDR**WGRGTLVTVSS
nCoV-7 mAb CDRH1 (aa)	278	**GFSLNDFA**
nCoV-7 mAb CDRH2 (aa)	279	**ISYDGRVK**

TABLE 1-continued

Sequences		
Sequence Description	SEQ ID NO.	Sequence
nCoV-7 mAb CDRH3 (aa)	280	**ARDSSWQSTGWPINWFDR**
nCoV-7 mAb VL (Vk) (nt)	281	gaaattgtgttgacacagtctccagccaccctgtctttgtctccagggcaaa gagccaccctctcctgcagggccagt**cagagtgttctcagctcc**ttagcc tggtaccagcacaaacctggccaggctcccaggctcctcatctat**gatgc** **atcc**agcagggccactggcgtcccagccaggttcagtggcagtgggtct gagacagacttcactctcaccatcagcagcctagagcctgaagattttgca gtttattactgt**cagcagcgtagcaactggcctccgacg**ttcggccaagg gaccaaggtggaaatcaaac
nCoV-7 mAb CDRL1 (nt)	282	**cagagtgttctcagctcc**
nCoV-7 mAb CDRL2 (nt)	283	**gatgcatcc**
nCoV-7 mAb CDRL3 (nt)	284	**cagcagcgtagcaactggcctccgacg**
nCoV-7 mAb VL (Vk) (aa)	285	EIVLTQSPATLSLSPGQRATLSCRAS**QSVLSS**LA WYQHKPGQAPRLLIY**DAS**SRATGVPARFSGSGS ETDFTLTISSLEPEDFAVYYC**QQRSNWPPT**FGQ GTKVEIK
nCoV-7 mAb CDRL1 (aa)	286	**QSVLSS**
nCoV-7 mAb CDRL2 (aa)	287	**DAS**
nCoV-7 mAb CDRL3 (aa)	288	**QQRSNWPPT**
nCoV-2 mAb VH (nt)	289	gacgtgcagctgttggagtctgggggaggcttggtacagcctggggggtc cctgagactctcctgtgcagcctct**ggattcagctttagcagctatgcc**at gacctgggtccgccaggctccagggaaggggctggagtgggtcgcaac t**atgagtgctagtggggatagcaca**aacgacgcagactccgtgaaggg ccggttcaccatctccagagacaattccaagaacacgctgtttctgcaaatg aacagcctcagacccgaggacacggccgtatattactgtgcgtccccccct tcggaattatggtgacttgctctactggggccagggaaccctggtcacc gtctcctccg
nCoV-2 mAb CDRH1 (nt)	290	**ggattcagctttagcagctatgcc**
nCoV-2 mAb CDRH2 (nt)	291	**atgagtgctagtggggatagcaca**
nCoV-2 mAb CDRH3 (nt)	292	**gcgtcccccccttcggaattatggtgacttgctctac**
nCoV-2 mAb VH (aa)	293	DVQLLESGGGLVQPGGSLRLSCAAS**GFSFSSYA** MTWVRQAPGKGLEWVAT**MSASGDST**NDADS VKGRFTISRDNSKNTLFLQMNSLRPEDTAVYYC **ASPLRNYGDLLY**WGQGTLVTVSS
nCoV-2 mAb CDRH1 (aa)	294	**GFSFSSYA**
nCoV-2 mAb CDRH2 (aa)	295	**MSASGDST**
nCoV-2 mAb CDRH3 (aa)	296	**ASPLRNYGDLLY**
nCoV-2 mAb VL (Vk) (nt)	297	gacatccagatgacccagtctccttccaccctgtctgcatctgtaggagaca gagtcaccatcacttgccgggccagt**cagaatattcatcgtttt**ttggcct ggtatcagcagaaaccagggaaagcccctaaactcctgatctat**acggcg** **tct**agtttagaaagtggggtcccatcaaggttcagcggcagtggatttggg acagaattcactctcaccatcagcagcctgcagcctgatgattttgcaactta

TABLE 1-continued

Sequences		
Sequence Description	SEQ ID NO.	Sequence
		ttactgc**caacaatataatagttactcgtggacg**ttcggccaagggacc aaggtggaaatcaaac
nCoV-2 mAb CDRL1 (nt)	298	**cagaatattcatcgtttt**
nCoV-2 mAb CDRL2 (nt)	299	**acggcgtct**
nCoV-2 mAb CDRL3 (nt)	300	**caacaatataatagttactcgtggacg**
nCoV-2 mAb VL (Vk) (aa)	301	DIQMTQSPSTLSASVGDRVTITCRAS**QNIHRF**L AWYQQKPGKAPKLLIY**TAS**SLESGVPSRFSGSG FGTEFTLTISSLQPDDFATYYC**QQYNSYSWT**FG QGTKVEIK
nCoV-2 mAb CDRL1 (aa)	302	**QNIHRF**
nCoV-2 mAb CDRL2 (aa)	303	**TAS**
nCoV-2 mAb CDRL3 (aa)	304	**QQYNSYSWT**
nCoV-19 mAb VH (nt)	305	caggtgaagctggtggagtctgggggaggcgtggtccagcctgggaggt ccctgagactctcctgtgcagcctct**ggattcaccttcagtagcaatgct**a tgcactgggtccgccagactccaggcaaggggctggagtgggtggcact tatatcatatgatgaaaggaataaatactacgcagagtccgtgaagggc cgattcaccatctccagagacaattccaagaacacgctgtatctgcaaatga acagcctgagacatgaggacacggctgtgtattactgt**gcgagagatctg caaatgagagtagtggttgtttcaaactttgactact**ggggccagggaa ccctggtcaccgtctcctcag
nCoV-19 mAb CDRH1 (nt)	306	**ggattcaccttcagtagcaatgct**
nCoV-19 mAb CDRH2 (nt)	307	**atatcatatgatgaaaggaataaa**
nCoV-19 mAb CDRH3 (nt)	308	**gcgagagatctgcaaatgagagtagtggttgtttcaaactttgactact**
nCoV-19 mAb VH (aa)	309	QVKLVESGGGVVQPGRSLRLSCAAS**GFTFSSN** **A**MHWVRQTPGKGLEWVAL**ISYDERNK**YYAES VKGRFTISRDNSKNTLYLQMNSLRHEDTAVYY C**ARDLQMRVVVVSNFDY**WGQGTLVTVSS
nCoV-19 mAb CDRH1 (aa)	310	**GFTFSSNA**
nCoV-19 mAb CDRH2 (aa)	311	**ISYDERNK**
nCoV-19 mAb CDRH3 (aa)	312	**ARDLQMRVVVVSNFDY**
nCoV-19 mAb VL (Vk) (nt)	313	gatgttgtgatgactcagtctccactctccctgcccgtcacccttggacagc cggcctccatctcctgcaggtctagt**caaagcctcgtatacagtgatgga aacacctac**ttgaattggtttcagcagaggccaggccaatctccaaggcg cctaatttat**gaggtttct**aactgggactctggggtcccagacagattcagc ggcagtgggtcaggcactgatttcacactgaaaatcagcagggtggaggc tgaggatgttggggtttattactgc**atgcaagctacacactggcctcccac t**tttggccaggggaccaagctggagatcaaac

TABLE 1-continued

Sequences		
Sequence Description	SEQ ID NO.	Sequence
nCoV-19 mAb CDRL1 (nt)	314	**caaagcctcgtatacagtgatggaaacacctac**
nCoV-19 mAb CDRL2 (nt)	315	**gaggtttct**
nCoV-19 mAb CDRL3 (nt)	316	**atgcaagctacacactggcctcccact**
nCoV-19 mAb VL (Vk) (aa)	317	DVVMTQSPLSLPVTLGQPASISCRSS**QSLVYSD** **GNTY**LNWFQQRPGQSPRRLIY**EVS**NWDSGVPD RFSGSGSGTDFTLKISRVEAEDVGVYYC**MQAT** **HWPPT**FGQGTKLEIK
nCoV-19 mAb CDRL1 (aa)	318	**QSLVYSDGNTY**
nCoV-19 mAb CDRL2 (aa)	319	**EVS**
nCoV-19 mAb CDRL3 (aa)	320	**MQATHWPPT**
nCoV-1 mAb VH (nt)	321	caggcgcaactggtggagtctgggggagccttggtccagcctgggaggt ccctgagactctcctgtgcagcctct**ggattcaccttcaggaattatgct**a tgcactgggtccgccaggctccagccacggggctgcagtggctggcagt c**ataacatctgatggaaggaataaa**ttctatgcagactccgtgaagggc cgattcaccatctccagagaggattccaagaacacgctgtatctgcaaatg gatagcctgagaggagaggacacggctgtctactactgc**gtgacacagc** **gtgataatagtcgcgattacttcccccactacttccacg**acatggacgt **c**tggggccaagggaccacggtcgccgtctcctcag
nCoV-1 mAb CDRH1 (nt)	322	**ggattcaccttcaggaattatgct**
nCoV-1 mAb CDRH2 (nt)	323	**ataacatctgatggaaggaataaa**
nCoV-1 mAb CDRH3 (nt)	324	**gtgacacagcgtgataatagtcgcgattacttcccccactacttccacg** **acatggacgtc**
nCoV-1 mAb VH (aa)	325	QAQLVESGGALVQPGRSLRLSCAAS**GFTFRNY** **A**MHWVRQAPATGLQWLAV**ITSDGRNK**FYADS VKGRFTISREDSKNTLYLQMDSLRGEDTAVYY C**VTQRDNSRDYFPHYFHDMDV**WGQGTTVAV SS
nCoV-1 mAb CDRH1 (aa)	326	**GFTFRNYA**
nCoV-1 mAb CDRH2 (aa)	327	**ITSDGRNK**
nCoV-1 mAb CDRH3 (aa)	328	**VTQRDNSRDYFPHYFHDMDV**
nCoV-1 mAb VL (Vk) (nt)	329	gatgttgtgctgactcagtctccactctccctgcccgtcacccttggacagc cggcctccatctcctgcaggtctagt**caaagcctcgtttacagtgatgga** **gacacctac**ttgaattggtttcagcagaggccaggccaatctccaagggcg cctaatttat**caggtttc**taatcgggactctggggtcccagacagatttagc ggcagtgggtcaggcactgatttcacactgaaaatcagcagggtggaggc tgaggatgttggggtttattactg**catgcaaggttcacactggcctccgac** **g**ttcggccaagggaccaaggtggaaatcaaac
nCoV-1 mAb CDRL1 (nt)	330	**caaagcctcgtttacagtgatggagacacctac**

TABLE 1-continued

Sequences		
Sequence Description	SEQ ID NO.	Sequence
nCoV-1 mAb CDRL2 (nt)	331	**caggtttct**
nCoV-1 mAb CDRL3 (nt)	332	**atgcaaggttcacactggcctccgacg**
nCoV-1 mAb VL (Vk) (aa)	333	DVVLTQSPLSLPVTLGQPASISCRSS**QSLVYSDG** **DTY**LNWFQQRPGQSPRRLIY**QVS**NRDSGVPDR FSGSGSGTDFTLKISRVEAEDVGVYYC**MQGSH** **WPPT**FGQGTKVEIK
nCoV-1 mAb CDRL1 (aa)	334	**QSLVYSDGDTY**
nCoV-1 mAb CDRL2 (aa)	335	**QVS**
nCoV-1 mAb CDRL3 (aa)	336	**MQGSHWPPT**
nCoV-11 mAb VH (nt)	337	ctggtgcaactggtagagtctgggggaggcgtggtccagcctgggaggt ccctgagactctcctgtgcaggctct**ggattcacctttagcagctatggc**a tgcactgggtccgccagactccaggcaaggggctggagtgggtggcagt **tatatcgtttgatggaaggaacaaa**ttctacgcagaccccgtgaagggt cgattcaccatctccagagacaattccaagaacacggtgttcttggaattgg atagcctgacaactgaggacacggctttttattactgt**gcgagagacgaca** **acttggacagacactggccccttcgactcgggggttac**tggggccagg gaaccctggtcaccgtctcctcag
nCoV-11 mAb CDRH1 (nt)	338	**ggattcacctttagcagctatggc**
nCoV-11 mAb CDRH2 (nt)	339	**atatcgtttgatggaaggaacaaa**
nCoV-11 mAb CDRH3 (nt)	340	**gcgagagacgacaacttggacagacactggccccttcgactcggggg** **ttac**
nCoV-11 mAb VH (aa)	341	LVQLVESGGGVVQPGRSLRLSCAGS**GFTFSSY** **G**MHWVRQTPGKGLEWVAV**ISFDGRNK**FYADP VKGRFTISRDNSKNTVFLELDSLTTEDTAFYYC **ARDDNLDRHWPLRLGGY**WGQGTLVTVSS
nCoV-11 mAb CDRH1 (aa)	342	**GFTFSSYG**
nCoV-11 mAb CDRH2 (aa)	343	**ISFDGRNK**
nCoV-11 mAb CDRH3 (aa)	344	**ARDDNLDRHWPLRLGGY**
nCoV-11 mAb VL (Vk) (nt)	345	gaaattgtgatgactcagtctccactctccctgcccgtcacccttggacagc cggcctccatctcctgcaggtctagt **caagacctcctatacaatgatgga** **ggcaccgac**ttgaactggtttcagcagaggccaggccaatctccaaggc gcctaatttac**agggtttct**aaccgggactctggggtcccagacagattca gcggcagtgggtcaggcagtgatttcacactgaaaatcagcagggtgga ggctgaggatgttggaatttattactgc**atgcaaggtgcacactggcctcc** **gact**ttcggccctgggaccaaagtggagatcaaac
nCoV-11 mAb CDRL1 (nt)	346	**caagacctcctatacaatgatggaggcaccgac**

TABLE 1-continued

Sequences		
Sequence Description	SEQ ID NO.	Sequence
nCoV-11 mAb CDRL2 (nt)	347	**agggtttct**
nCoV-11 mAb CDRL3 (nt)	348	**atgcaaggtgcacactggcctccgact**
nCoV-11 mAb VL (Vk) (aa)	349	EIVMTQSPLSLPVTLGQPASISCRSS**QDLLYNDG** **GTD**LNWFQQRPGQSPRRLIY**RVS**NRDSGVPDR FSGSGSGSDFTLKISRVEAEDVGIYYC**MQGAH** **WPPT**FGPGTKVEIK
nCoV-11 mAb CDRL 1 (aa)	350	**QDLLYNDGGTD**
nCoV-11 mAb CDRL2 (aa)	351	**RVS**
nCoV-11 mAb CDRL3 (aa)	352	**MQGAHWPPT**
nCoV-13 mAb VH (nt)	353	gaggtgcagctggtggagtctgggggaggcctggtcaagcctgggggt ccctgagactctcctgtgcagcctct**ggattcaccttcagtaactataac**a tgaactgggtccgccaggctccagggaaggggctggagtgggtctcatc c**attggtagtagtagcacttacata**tactccgcagactcagtgaagggc cgattcaccatctccagagacaacgccatgaactcgctgtttctgcaaatga agagcctgagagccgaggacacggctgtgtattactgt**gcgagaggtttc** **gagaggtactactttgactcc**tggggccagggaaccctggtcaccgtct cctcag
nCoV-13 mAb CDRH1 (nt)	354	**ggattcaccttcagtaactataac**
nCoV-13 mAb CDRH2 (nt)	355	**attggtagtagtagcacttacata**
nCoV-13 mAb CDRH3 (nt)	356	**gcgagaggtttcgagaggtactactttgactcc**
nCoV-13 mAb VH (aa)	357	EVQLVESGGGLVKPGGSLRLSCAAS**GFTFSNY** NMNWVRQAPGKGLEWVSS**IGSSSTYI**YSADSV KGRFTISRDNAMNSLFLQMKSLRAEDTAVYYC **ARGFERYYFDS**WGQGTLVTVSS
nCoV-13 mAb CDRH1 (aa)	358	**GFTFSNYN**
nCoV-13 mAb CDRH2 (aa)	359	**IGSSSTYI**
nCoV-13 mAb CDRH3 (aa)	360	**ARGFERYYFDS**
nCoV-13 mAb VL (nt)	361	cagtctgtgctgactcagccaccctcagcgtctgggacccccgggcagag ggtcaccatctcttgttctggaagc**acctccaacatcggaactaatgtt**gt aaactggtaccagcagctcccaggaacggcccccaaactcctcatctat**a** **gtaataat**cagcggccctcttgggtccctgaccgattctctggctccaagt ctggcacctcagcctccctggccatcagtgggctccagtctgaggatgag gctgattattactgt**gtggcatgggatgacatcctgaatgctgtggtc**ttc gccggagggaccaagctgaccgtcctag

TABLE 1-continued

Sequences		
Sequence Description	SEQ ID NO.	Sequence
nCoV-13 mAb CDRL1 (nt)	362	**acctccaacatcggaactaatgtt**
nCoV-13 mAb CDRL2 (nt)	363	**agtaataat**
nCoV-13 mAb CDRL3 (nt)	364	**gtggcatgggatgacatcctgaatgctgtggtc**
nCoV-13 mAb VL (aa)	365	QSVLTQPPSASGTPGQRVTISCSGS**TSNIGTNV**V NWYQQLPGTAPKLLIY**SNN**QRPSWVPDRFSGS KSGTSASLAISGLQSEDEADYYC**VAWDDILNA** **VV**FAGGTKLTVL
nCoV-13 mAb CDRL1 (aa)	366	**TSNIGTNV**
nCoV-13 mAb CDRL2 (aa)	367	**SNN**
nCoV-13 mAb CDRL3 (aa)	368	**VAWDDILNAVV**
Wuhan seafood market pneumonia virus isolate Wuhan-Hu-1 genomic sequence (GenBank: MN908947.3; Jan. 23, 2020)	369	1 attaaaggtt tataccttcc caggtaacaa accaaccaac tttcgatctc ttgtagatct 61 gttctctaaa cgaactttaa aatctgtgtg gctgtcactc ggctgcatgc ttagtgcact 121 cacgcagtat aattaataac taattactgt cgttgacagg acacgagtaa ctcgtctatc 181 ttctgcaggc tgcttacggt ttcgtccgtg ttgcagccga tcatcagcac atctaggttt 241 cgtccgggtg tgaccgaaag gtaagatgga gagccttgtc cctggtttca acgagaaaac 301 acacgtccaa ctcagtttgc ctgttttaca ggttcgcgac gtgctcgtac gtggctttgg 361 agactccgtg gaggaggtct tatcagaggc cgtcaacat cttaaagatg gcacttgtgg 421 cttagtagaa gttgaaaaag gcgttttgcc tcaacttgaa cagccctatg tgttcatcaa 481 acgttcggat gctcgaactg cacctcatgg tcatgttatg gttgagctgg tagcagaact 541 cgaaggcatt cagtacggtc gtagtggtga gacacttggt gtccttgtcc ctcatgtggg 601 cgaaatacca gtggcttacc gcaaggttct tcttcgtaag aacggtaata aaggagctgg 661 tggccatagt tacggcgccg atctaaagtc atttgactta ggcgacgagc ttggcactga 721 tccttatgaa gattttcaag aaaactggaa cactaaacat agcagtggtg ttacccgtga 781 actcatgcgt gagcttaacg gaggggcata cactcgctat gtcgataaca acttctgtgg 841 ccctgatggc taccctcttg agtgcattaa agaccttcta gcacgtgctg gtaaagcttc 901 atgcactttg tccgaacaac tggactttat tgacactaag aggggtgtat actgctgccg 961 tgaacatgag catgaaattg cttggtacac ggaacgttct gaaaagagct atgaattgca 1021 gacacctttt gaaattaaat tggcaaagaa atttgacacc ttcaatgggg aatgtccaaa 1081 ttttgtattt cccttaaatt ccataatcaa gactattcaa ccaagggttg aaaagaaaaa 1141 gcttgatggc tttatgggta gaattcgatc tgtctatcca gttgcgtcac caaatgaatg 1201 caaccaaatg tgcctttcaa ctctcatgaa gtgtgatcat tgtggtgaaa cttcatggca 1261 gacgggcgat tttgttaaag ccacttgcga attttgtggc actgagaatt tgactaaaga 1321 aggtgccact acttgtggtt acttacccca aaatgctgtt gttaaaattt attgtccagc 1381 atgtcacaat tcagaagtag gacctgagca tagtcttgcc gaataccata atgaatctgg 1441 cttgaaaacc attcttcgta agggtggtcg cactattgcc tttggaggct gtgtgttctc 1501 ttatgttggt tgccataaca agtgtgccta ttgggttcca cgtgctagcg ctaacatagg 1561 ttgtaaccat acaggtgttg ttggagaagg ttccgaaggt cttaatgaca accttcttga 1621 aatactccaa aaagagaaag tcaacatcaa tattgttggt gactttaaac ttaatgaaga 1681 gatcgccatt attttggcat ctttttctgc ttccacaagt gcttttgtgg aaactgtgaa 1741 aggtttggat tataaagcat tcaaacaaat tgttgaatcc tgtggtaatt ttaaagttac 1801 aaaaggaaaa gctaaaaaag gtgcctggaa tattggtgaa cagaaatcaa tactgagtcc 1861 tctttatgca tttgcatcag aggctgctcg tgttgtacga tcaattttct cccgcactct 1921 tgaaactgct caaaattctg tgcgtgtttt acagaaggcc gctataacaa tactagatgg 1981 aatttcacag tattcactga gactcattga tgctatgatg ttcacatctg atttggctac 2041 taacaatcta gttgtaatgg cctacattac aggtggtgtt gttcagttga cttcgcagtg 2101 gctaactaac atctttggca ctgtttatga aaaactcaaa cccgtccttg attggcttga 2161 agagaagttt aaggaaggtg tagagtttct tagagacggt tgggaaattg ttaaatttat 2221 ctcaacctgt gcttgtgaaa ttgtcggtgg acaaattgtc acctgtgcaa aggaaattaa 2281 ggagagtgtt cagacattct ttaagcttgt aaataaattt ttggctttgt gtgctgactc 2341 tatcattatt ggtggagcta aacttaaagc cttgaattta ggtgaaacat ttgtcacgca 2401 ctcaaaggga ttgtacagaa agtgtgttaa atccagagaa gaaactggcc tactcatgcc 2461 tctaaaagcc ccaaaagaaa ttatcttctt agagggagaa acacttccca cagaagtgtt 2521 aacagaggaa gttgtcttga aaactggtga tttacaacca ttagaacaac ctactagtga

TABLE 1-continued

Sequences		
Sequence Description	SEQ ID NO.	Sequence
		2581 agctgttgaa gctccattgg ttggtacacc agtttgtatt aacgggctta tgttgctcga
		2641 aatcaaagac acagaaaagt actgtgccct tgcacctaat atgatggtaa caaacaatac
		2701 cttcacactc aaaggcggtg caccaacaaa ggttactttt ggtgatgaca ctgtgataga
		2761 agtgcaaggt tacaagagtg tgaatatcac ttttgaactt gatgaaagga ttgataaagt
		2821 acttaatgag aagtgctctg cctatacagt tgaactcggt acagaagtaa atgagttcgc
		2881 ctgtgttgtg gcagatgctg tcataaaaac tttgcaacca gtatctgaat tacttacacc
		2941 actgggcatt gatttagatg agtggagtat ggctacatac tacttatttg atgagtctgg
		3001 tgagtttaaa ttggcttcac atatgtattg ttctttctac cctccagatg aggatgaaga
		3061 agaaggtgat tgtgaagaag aagagtttga gccatcaact caatatgagt atggtactga
		3121 agatgattac caaggtaaac ctttggaatt tggtgccact tctgctgctc ttcaacctga
		3181 agaagagcaa gaagaagatt ggttagatga tgatagtcaa caaactgttg gtcaacaaga
		3241 cggcagtgag gacaatcaga caactactat tcaaacaatt gttgaggttc aacctcaatt
		3301 agagatggaa cttacaccag ttgttcagac tattgaagtg aatagtttta gtggttattt
		3361 aaaacttact gacaatgtat acattaaaaa tgcagacatt gtggaagaag ctaaaaaggt
		3421 aaaaccaaca gtggttgtta atgcagccaa tgtttacctt aaacatggag gaggtgttgc
		3481 aggagcctta aataaggcta ctaacaatgc catgcaagtt gaatctgatg attacatagc
		3541 tactaatgga ccacttaaag tgggtggtag ttgtgtttta agcggacaca atcttgctaa
		3601 acactgtctt catgttgtcg gcccaaatgt taacaaaggt gaagacattc aacttcttaa
		3661 gagtgcttat gaaaatttta atcagcacga agttctactt gcaccattat tatcagctgg
		3721 tatttttggt gctgacccta tacattcttt aagagtttgt gtagatactg ttcgcacaaa
		3781 tgtctactta gctgtctttg ataaaaatct ctatgacaaa cttgtttcaa gctttttgga
		3841 aatgaagagt gaaaagcaag ttgaacaaaa gatcgctgag attcctaaag aggaagttaa
		3901 gccatttata actgaaagta aaccttcagt tgaacagaga aaacaagatg ataagaaaat
		3961 caaagcttgt gttgaagaag ttacaacaac tctggaagaa actaagttcc tcacagaaaa
		4021 cttgttactt tatattgaca ttaatggcaa tcttcatcca gattctgcca ctcttgttag
		4081 tgacattgac atcactttct taaagaaaga tgctccatat atagtgggtg atgttgttca
		4141 agagggtgtt ttaactgctg tggttatacc tactaaaaag gctggtggca ctactgaaat
		4201 gctagcgaaa gctttgagaa aagtgccaac agacaattat ataaccactt acccgggtca
		4261 gggtttaaat ggttacactg tagaggaggc aaagacagtg cttaaaaagt gtaaaagtgc
		4321 cttttacatt ctaccatcta ttatctctaa tgagaagcaa gaaattcttg gaactgtttc
		4381 ttggaatttg cgagaaatgc ttgcacatgc agaagaaaca cgcaaattaa tgcctgtctg
		4441 tgtggaaact aaagccatag tttcaactat acagcgtaaa tataagggta ttaaaataca
		4501 agagggtgtg gttgattatg gtgctagatt ttacttttac accagtaaaa caactgtagc
		4561 gtcacttatc aacacactta acgatctaaa tgaaactctt gttacaatgc cacttggcta
		4621 tgtaacacat ggcttaaatt tggaagaagc tgctcggtat atgagatctc tcaaagtgcc
		4681 agctacagtt tctgtttctt cacctgatgc tgttacagcg tataatggtt atcttacttc
		4741 ttcttctaaa acacctgaag aacattttat tgaaaccatc tcacttgctg gttcctataa
		4801 agattggtcc tattctggac aatctacaca actaggtata gaatttctta agagaggtga
		4861 taaaagtgta tattacacta gtaatcctac cacattccac ctagatggtg aagttatcac
		4921 ctttgacaat cttaagacac ttctttcttt gagagaagtg aggactatta aggtgtttac
		4981 aacagtagac aacattaacc tccacacgca agttgtggac atgtcaatga catatggaca
		5041 acagtttggt ccaacttatt tggatggagc tgatgttact aaaataaaac ctcataattc
		5101 acatgaaggt aaaacatttt atgttttacc taatgatgac actctacgtg ttgaggcttt
		5161 tgagtactac cacacaactg atcctagttt tctgggtagg tacatgtcag cattaaatca
		5221 cactaaaaag tggaaatacc cacaagttaa tggtttaact tctattaaat gggcagataa
		5281 caactgttat cttgccactg cattgttaac actccaacaa atagagttga agtttaatcc
		5341 acctgctcta caagatgctt attacagagc aagggctggt gaagctgcta acttttgtgc
		5401 acttatctta gcctactgta ataagacagt aggtgagtta ggtgatgtta gagaaacaat
		5461 gagttacttg tttcaacatg ccaatttaga ttcttgcaaa agagtcttga acgtggtgtg
		5521 taaaacttgt ggacaacagc agacaaccct taagggtgta gaagctgtta tgtacatggg
		5581 cacactttct tatgaacaat ttaagaaagg tgttcagata ccttgtacgt gtggtaaaca
		5641 agctacaaaa tatctagtac aacaggagtc acctttttgtt atgatgtcag caccacctgc
		5701 tcagtatgaa cttaagcatg gtacatttac ttgtgctagt gagtacactg gtaattacca
		5761 gtgtggtcac tataaacata taacttctaa agaaactttg tattgcatag acggtgcttt
		5821 acttacaaag tcctcagaat acaaaggtcc tattacggat gttttctaca aagaaaacag
		5881 ttacacaaca accataaaac cagttactta taaattggat ggtgttgttt gtacagaaat
		5941 tgaccctaag ttggacaatt attataagaa agacaattct tatttcacag agcaaccaat
		6001 tgatcttgta ccaaaccaac catatccaaa cgcaagcttc gataatttta agtttgtatg
		6061 tgataatatc aaatttgctg atgatttaaa ccagttaact ggttataaga aacctgcttc
		6121 aagagagctt aaagttacat ttttccctga cttaaatggt gatgtggtgg ctattgatta
		6181 taaacactac acaccctctt ttaagaaagg agctaaattg ttacataaac ctattgtttg
		6241 gcatgttaac aatgcaacta ataaagccac gtataaacca aatacctggt gtatacgttg
		6301 tctttggagc acaaaaccag ttgaaacatc aaattcgttt gatgtactga agtcagagga
		6361 cgcgcaggga atggataatc ttgcctgcga agatctaaaa ccagtctctg aagaagtagt
		6421 ggaaaatcct accatacaga aagacgttct tgagtgtaat gtgaaaacta ccgaagttgt
		6481 aggagacatt atacttaaac cagcaaataa tagtttaaaa attacagaag aggttggcca
		6541 cacagatcta atggctgctt atgtagacaa ttctagtctt actattaaga aacctaatga
		6601 attatctaga gtattaggtt tgaaaaccct tgctactcat ggtttagctg ctgttaatag
		6661 tgtcccttgg gatactatag ctaattatgc taagcctttt cttaacaaag ttgttagtac
		6721 aactactaac atagttacac ggtgtttaaa ccgtgtttgt actaattata tgccttattt
		6781 ctttacttta ttgctacaat tgtgtacttt tactagaagt acaaattcta gaattaaagc
		6841 atctatgccg actactatag caaagaatac tgttaagagt gtcggtaaat tttgtctaga

TABLE 1-continued

Sequences		
Sequence Description	SEQ ID NO.	Sequence
		6901 ggcttcattt aattatttga agtcacctaa tttttctaaa ctgataaata ttataatttg 6961 gtttttacta ttaagtgttt gcctaggttc tttaatctac tcaaccgctg ctttaggtgt 7021 tttaatgtct aatttaggca tgccttctta ctgtactggt tacagagaag gctatttgaa 7081 ctctactaat gtcactattg caacctactg tactggttct ataccttgta gtgtttgtct 7141 tagtggttta gattctttag acacctatcc ttctttagaa actatacaaa ttaccatttc 7201 atcttttaaa tgggatttaa ctgcttttgg cttagttgca gagtggtttt tggcatatat 7261 tcttttcact aggtttttct atgtacttgg attggctgca atcatgcaat tgtttttcag 7321 ctattttgca gtacatttta ttagtaattc ttggcttatg tggttaataa ttaatcttgt 7381 acaaatggcc ccgatttcag ctatggttag aatgtacatc ttctttgcat cattttatta 7441 tgtatggaaa agttatgtgc atgttgtaga cggttgtaat tcatcaactt gtatgatgtg 7501 ttacaaacgt aatagagcaa caagagtcga atgtacaact attgttaatg gtgttagaag 7561 gtccttttat gtctatgcta atggaggtaa aggcttttgc aaactacaca attggaattg 7621 tgttaattgt gatacattct gtgctggtag tacatttatt agtgatgaag ttgcgagaga 7681 cttgtcacta cagtttaaaa gaccaataaa tcctactgac cagtcttctt acatcgttga 7741 tagtgttaca gtgaagaatg gttccatcca tctttacttt gataaagctg gtcaaaagac 7801 ttatgaaaga cattctctct ctcattttgt taacttagac aacctgagag ctaataacac 7861 taaaggttca ttgcctatta atgttatagt ttttgatggt aaatcaaaat gtgaagaatc 7921 atctgcaaaa tcagcgtctg tttactacag tcagcttatg tgtcaaccta tactgttact 7981 agatcaggca ttagtgtctg atgttggtga tagtgcggaa gttgcagtta aaatgtttga 8041 tgcttacgtt aatacgtttt catcaacttt taacgtacca atggaaaaac tcaaaacact 8101 agttgcaact gcagaagctg aacttgcaaa gaatgtgtcc ttagacaatg tcttatctac 8161 ttttatttca gcagctcggc aagggtttgt tgattcagat gtagaaacta aagatgttgt 8221 tgaatgtctt aaattgtcac atcaatctga catagaagtt actggcgata gttgtaataa 8281 ctatatgctc acctataaca aagttgaaaa catgacaccc cgtgaccttg gtgcttgtat 8341 tgactgtagt gcgcgtcata ttaatgcgca ggtagcaaaa agtcacaaca ttgctttgat 8401 atggaacgtt aaagatttca tgtcattgtc tgaacaacta cgaaaacaaa tacgtagtgc 8461 tgctaaaaag aataacttac cttttaagtt gacatgtgca actactagac aagttgttaa 8521 tgttgtaaca acaaagatag cacttaaggg tggtaaaatt gttaataatt ggttgaagca 8581 gttaattaaa gttacacttg tgttcctttt tgttgctgct attttctatt taataacacc 8641 tgttcatgtc atgtctaaac atactgactt ttcaagtgaa atcataggat acaaggctat 8701 tgatggtggt gtcactcgtg acatagcatc tacagatact tgttttgcta acaaacatgc 8761 tgattttgac acatggttta gccagcgtgg tggtagttat actaatgaca aagcttgccc 8821 attgattgct gcagtcataa caagagaagt gggttttgtc gtgcctggtt tgcctggca
Wuhan seafood market pneumonia virus isolate Wuhan-Hu-1 genomic sequence (GenBank: MN908947.3; Jan. 23, 2020)-amino acid translation	370	MESLVPGFNEKTHVQLSLPVLQVRDVLVRGFGDSV EEVLSEARQHLKDGTCGLVEVEKGVLPQLEQPYVF IKRSDARTAPHGHVMVELVAELEGIQYGRSGETLG VLVPHVGEIPVAYRKVLLRKNGNKGAGGHSYGADL KSFDLGDELGTDPYEDFQENWNTKHSSGVTRELMR ELNGGAYTRYVDNNFCGPDGYPLECIKDLLARAGK ASCTLSEQLDFIDTKRGVYCCREHEHEIAWYTERS EKSYELQTPFEIKLAKKFDTFNGECPNFVFPLNSI IKTIQPRVEKKKLDGFMGRIRSVYPVASPNECNQM CLSTLMKCDHCGETSWQTGDFVKATCEFCGTENLT KEGATTCGYLPQNAVVKIYCPACHNSEVGPEHSLA EYHNESGLKTILRKGGRTIAFGGCVFSYVGCHNKC AYWVPRASANIGCNHTGVVGEGSEGLNDNLLEILQ KEKVNINIVGDFKLNEEIAIILASFSASTSAFVET VKGLDYKAFKQIVESCGNFKVTKGKAKKGAWNIGE QKSILSPLYAFASEAARVVRSIFSRTLETAQNSVR VLQKAAITILDGISQYSLRLIDAMMFTSDLATNNL VVMAYITGGVVQLTSQWLTNIFGTVYEKLKPVLDW LEEKFKEGVEFLRDGWEIVKFISTCACEIVGGQIV TCAKEIKESVQTFFKLVNKFLALCADSIIIGGAKL KALNLGETFVTHSKGLYRKCVKSREETGLLMPLKA PKEIIFLEGETLPTEVLTEEVVLKTGDLQPLEQPT SEAVEAPLVGTPVCINGLMLLEIKDTEKYCALAPN MMVTNNTFTLKGGAPTKVTFGDDTVIEVQGYKSVN ITFELDERIDKVLNEKCSAYTVELGTEVNEFACVV ADAVIKTLQPVSELLTPLGIDLDEWSMATYYLFDE SGEFKLASHMYCSFYPPDEDEEEGDCEEEEFEPST QYEYGTEDDYQGKPLEFGATSAALQPEEEQEEDWL DDDSQQTVGQQDGSEDNQTTTIQTIVEVQPQLEME LTPVVQTIEVNSFSGYLKLTDNVYIKNADIVEEAK KVKPTVVVNAANVYLKHGGGVAGALNKATNNAMQV ESDDYIATNGPLKVGGSCVLSGHNLAKHCLHVVGP NVNKGEDIQLLKSAYENFNQHEVLLAPLLSAGIFG ADPIHSLRVCVDTVRTNVYLAVFDKNLYDKLVSSF LEMKSEKQVEQKIAEIPKEEVKPFITESKPSVEQR KODDKKIKACVEEVTTTLEETKFLTENLLLYIDIN GNLHPDSATLVSDIDITFLKKDAPYIVGDVVQEGV LTAVVIPTKKAGGTTEMLAKALRKVPTDNYITTYP

TABLE 1-continued

Sequences		
Sequence Description	SEQ ID NO.	Sequence
		GQGLNGYTVEEAKTVLKKCKSAFYILPSIISNEKQ EILGTVSWNLREMLAHAEETRKLMPVCVETKAIVS TIQRKYKGIKIQEGVVDYGARFYFYTSKTTVASLI NTLNDLNETLVTMPLGYVTHGLNLEEAARYMRSLK VPATVSVSSPDAVTAYNGYLTSSSKTPEEHFIETI SLAGSYKDWSYSGQSTQLGIEFLKRGDKSVYYTSN PTTFHLDGEVITFDNLKTLLSLREVRTIKVFTTVD NINLHTQVVDMSMTYGQQFGPTYLDGADVTKIKPH NSHEGKTFYVLPNDDTLRVEAFEYYHTTDPSFLGR YMSALNHTKKWKYPQVNGLTSIKWADNNCYLATAL LTLQQIELKFNPPALQDAYYRARAGEAANFCALIL AYCNKTVGELGDVRETMSYLFQHANLDSCKRVLNV VCKTCGQQQTTLKGVEAVMYMGTLSYEQFKKGVQI PCTCGKQATKYLVQQESPFVMMSAPPAQYELKHGT FTCASEYTGNYQCGHYKHITSKETLYCIDGALLTK SSEYKGPITDVFYKENSYTTTIKPVTYKLDGVVCT EIDPKLDNYYKKDNSYFTEQPIDLVPNQPYPNASF DNFKFVCDNIKFADDLNQLTGYKKPASRELKVTFF PDLNGDVVAIDYKHYTPSFKKGAKLLHKPIVWHVN NATNKATYKPNTWCIRCLWSTKPVETSNSFDVLKS EDAQGMDNLACEDLKPVSEEVVENPTIQKDVLECN VKTTEVVGDIILKPANNSLKITEEVGHTDLMAAYV DNSSLTIKKPNELSRVLGLKTLATHGLAAVNSVPW DTIANYAKPFLNKVVSTTTNIVTRCLNRVCTNYMP YFFTLLLQLCTFTRSTNSRIKASMPTTIAKNTVKS VGKFCLEASFNYLKSPNFSKLINIIIWFLLLSVCL GSLIYSTAALGVLMSNLGMPSYCTGYREGYLNSTN VTIATYCTGSIPCSVCLSGLDSLDTYPSLETIQIT ISSFKWDLTAFGLVAEWFLAYILFTRFFYVLGLAA IMQLFFSYFAVHFISNSWLMWLIINLVQMAPISAM VRMYIFFASFYYVWKSYVHVVDGCNSSTCMMCYKR NRATRVECTTIVNGVRRSFYVYANGGKGFCKLHNW NCVNCDTFCAGSTFISDEVARDLSLQFKRPINPTD QSSYIVDSVTVKNGSIHLYFDKAGQKTYERHSLSH FVNLDNLRANNTKGSLPINVIVFDGKSKCEESSAK SASVYYSQLMCQPILLLDQALVSDVGDSAEVAVKM FDAYVNTFSSTFNVPMEKLKTLVATAEAELAKNVS LDNVLSTFISAARQGFVDSDVETKDVVECLKLSHQ SDIEVTGDSCNNYMLTYNKVENMTPRDLGACIDCS ARHINAQVAKSHNIALIWNVKDFMSLSEQLRKQIR SAAKKNNLPFKLTCATTRQVVNVVTTKIALKGGKI VNNWLKQLIKVTLVFLFVAAIFYLITPVHVMSKHT DFSSEIIGYKAIDGGVTRDIASTDTCFANKHADFD TWFSQRGGSYTNDKACPLIAAVITREVGFVVPGLP GTILRTTNGDFLHFLPRVFSAVGNICYTPSKLIEY TDFATSACVLAAECTIFKDASGKPVPYCYDTNVLE GSVAYESLRPDTRYVLMDGSIIQFPNTYLEGSVRV VTTFDSEYCRHGTCERSEAGVCVSTSGRWVLNNDY YRSLPGVFCGVDAVNLLTNMFTPLIQPIGALDISA SIVAGGIVAIVVTCLAYYFMRFRRAFGEYSHVVAF NTLLFLMSFTVLCLTPVYSFLPGVYSVIYLYLTFY LTNDVSFLAHIQWMVMFTPLVPFWITIAYIICIST KHFYWFFSNYLKRRVVFNGVSFSTFEEAALCTFLL NKEMYLKLRSDVLLPLTQYNRYLALYNKYKYFSGA MDTTSYREAACCHLAKALNDFSNSGSDVLYQPPQT SITSAVLQSGFRKMAFPSGKVEGCMVQVTCGTTTL NGLWLDDVVYCPRHVICTSEDMLNPNYEDLLIRKS NHNFLVQAGNVQLRVIGHSMQNCVLKLKVDTANPK TPKYKFVRIQPGQTFSVLACYNGSPSGVYQCAMRP NFTIKGSFLNGSCGSVGFNIDYDCVSFCYMHHMEL PTGVHAGTDLEGNFYGPFVDRQTAQAAGTDTTITV NVLAWLYAAVINGDRWFLNRFTTTLNDFNLVAMKY NYEPLTQDHVDILGPLSAQTGIAVLDMCASLKELL QNGMNGRTILGSALLEDEFTPFDVVRQCSGVTFQS AVKRTIKGTHHWLLLTILTSLLVLVQSTQWSLFFF LYENAFLPFAMGIIAMSAFAMMFVKHKHAFLCLFL LPSLATVAYFNMVYMPASWVMRIMTWLDMVDTSLS GFKLKDCVMYASAVVLLILMTARTVYDDGARRVWT LMNVLTLVYKVYYGNALDQAISMWALIISVTSNYS GVVTTVMFLARGIVFMCVEYCPIFFITGNTLQCIM LVYCFLGYFCTCYFGLFCLLNRYFRLTLGVYDYLV STQEFRYMNSQGLLPPKNSIDAFKLNIKLLGVGGK

TABLE 1-continued

Sequences		
Sequence Description	SEQ ID NO.	Sequence
		PCIKVATVQSKMSDVKCTSVVLLSVLQQLRVESSS KLWAQCVQLHNDILLAKDTTEAFEKMVSLLSVLLS MQGAVDINKLCEEMLDNRATLQAIASEFSSLPSYA AFATAQEAYEQAVANGDSEVVLKKLKKSLNVAKSE FDRDAAMQRKLEKMADQAMTQMYKQARSEDKRAKV TSAMQTMLFTMLRKLDNDALNNIINNARDGCVPLN IIPLTTAAKLMVVIPDYNTYKNTCDGTTFTYASAL WEIQQVVDADSKIVQLSEISMDNSPNLAWPLIVTA LRANSAVKLQNNELSPVALRQMSCAAGTTQTACTD DNALAYYNTTKGGRFVLALLSDLQDLKWARFPKSD GTGTIYTELEPPCRFVTDTPKGPKVKYLYFIKGLN NLNRGMVLGSLAATVRLQAGNATEVPANSTVLSFC AFAVDAAKAYKDYLASGGQPITNCVKMLCTHTGTG QAITVTPEANMDQESFGGASCCLYCRCHIDHPNPK GFCDLKGKYVQIPTTCANDPVGFTLKNTVCTVCGM WKGYGCSCDQLREPMLQSADAQSFLNRVCGVSAAR LTPCGTGTSTDVVYRAFDIYNDKVAGFAKFLKTNC CRFQEKDEDDNLIDSYFVVKRHTFSNYQHEETIYN LLKDCPAVAKHDFFKFRIDGDMVPHISRQRLTKYT MADLVYALRHFDEGNCDTLKEILVTYNCCDDDYFN KKDWYDFVENPDILRVYANLGERVRQALLKTVQFC DAMRNAGIVGVLTLDNQDLNGNWYDFGDFIQTTPG SGVPVVDSYYSLLMPILTLTRALTAESHVDTDLTK PYIKWDLLKYDFTEERLKLFDRYFKYWDQTYHPNC VNCLDDRCILHCANFNVLFSTVFPPTSFGPLVRKI FVDGVPFVVSTGYHFRELGVVHNQDVNLHSSRLSF KELLVYAADPAMHAASGNLLLDKRTTCFSVAALTN NVAFQTVKPGNFNKDFYDFAVSKGFFKEGSSVELK HFFFAQDGNAAISDYDYYRYNLPTMCDIRQLLFVV EVVDKYFDCYDGGCINANQVIVNNLDKSAGFPFNK WGKARLYYDSMSYEDQDALFAYTKRNVIPTITQMN LKYAISAKNRARTVAGVSICSTMTNRQFHQKLLKS IAATRGATVVIGTSKFYGGWHNMLKTVYSDVENPH LMGWDYPKCDRAMPNMLRIMASLVLARKHTTCCSL SHRFYRLANECAQVLSEMVMCGGSLYVKPGGTSSG DATTAYANSVFNICQAVTANVNALLSTDGNKIADK YVRNLQHRLYECLYRNRDVDTDFVNEFYAYLRKHF SMMILSDDAVVCFNSTYASQGLVASIKNFKSVLYY QNNVFMSEAKCWTETDLTKGPHEFCSQHTMLVKQG DDYVYLPYPDPSRILGAGCFVDDIVKTDGTLMIER FVSLAIDAYPLTKHPNQEYADVFHLYLQYIRKLHD ELTGHMLDMYSVMLTNDNTSRYWEPEFYEAMYTPH TVLQAVGACVLCNSQTSLRCGACIRRPFLCCKCCY DHVISTSHKLVLSVNPYVCNAPGCDVTDVTQLYLG GMSYYCKSHKPPISFPLCANGQVFGLYKNTCVGSD NVTDFNAIATCDWTNAGDYILANTCTERLKLFAAE TLKATEETFKLSYGIATVREVLSDRELHLSWEVGK PRPPLNRNYVFTGYRVTKNSKVQIGEYTFEKGDYG DAVVYRGTTTYKLNVGDYFVLTSHTVMPLSAPTLV PQEHYVRITGLYPTLNISDEFSSNVANYQKVGMQK YSTLQGPPGTGKSHFAIGLALYYPSARIVYTACSH AAVDALCEKALKYLPIDKCSRIIPARARVECFDKF KVNSTLEQYVFCTVNALPETTADIVVFDEISMATN YDLSVVNARLRAKHYVYIGDPAQLPAPRTLLTKGT LEPEYFNSVCRLMKTIGPDMFLGTCRRCPAEIVDT VSALVYDNKLKAHKDKSAQCFKMFYKGVITHDVSS AINRPQIGVVREFLTRNPAWRKAVFISPYNSQNAV ASKILGLPTQTVDSSQGSEYDYVIFTQTTETAHSC NVNRFNVAITRAKVGILCIMSDRDLYDKLQFTSLE IPRRNVATLQAENVTGLFKDCSKVITGLHPTQAPT HLSVDTKFKTEGLCVDIPGIPKDMTYRRLISMMGF KMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCH ATREAVGTNLPLQLGFSTGVNLVAVPTGYVDTPNN TDFSRVSAKPPPGDQFKHLIPLMYKGLPWNVVRIK IVQMLSDTLKNLSDRVVFVLWAHGFELTSMKYFVK IGPERTCCLCDRRATCFSTASDTYACWHHSIGFDY VYNPFMIDVQQWGFTGNLQSNHDLYCQVHGNAHVA SCDAIMTRCLAVHECFVKRVDWTIEYPIIGDELKI NAACRKVQHMVVKAALLADKFPVLHDIGNPKAIKC VPQADVEWKFYDAQPCSDKAYKIEELFYSYATHSD KFTDGVCLFWNCNVDRYPANSIVCRFDTRVLSNLN LPGCDGGSLYVNKHAFHTPAFDKSAFVNLKQLPFF

TABLE 1-continued

Sequences		
Sequence Description	SEQ ID NO.	Sequence
		YYSDSPCESHGKQVVSDIDYVPLKSATCITRONLG GAVCRHHANEYRLYLDAYNMMISAGFSLWVYKQFD TYNLWNTFTRLQSLENVAFNVVNKGHFDGQQGEVP VSIINNTVYTKVDGVDVELFENKTTLPVNVAFELW AKRNIKPVPEVKILNNLGVDIAANTVIWDYKRDAP AHISTIGVCSMTDIAKKPTETICAPLTVFFDGRVD GQVDLFRNARNGVLITEGSVKGLQPSVGPKQASLN GVTLIGEAVKTQFNYYKKVDGVVQQLPETYFTQSR NLQEFKPRSQMEIDFLELAMDEFIERYKLEGYAFE HIVYGDFSHSQLGGLHLLIGLAKRFKESPFELEDF IPMDSTVKNYFITDAQTGSSKCVCSVIDLLLDDFV EIIKSQDLSVVSKVVKVTIDYTEISFMLWCKDGHV ETFYPKLQSSQAWQPGVAMPNLYKMQRMLLEKCDL QNYGDSATLPKGIMMNVAKYTQLCQYLNTLTLAVP YNMRVIHFGAGSDKGVAPGTAVLRQWLPTGTLLVD SDLNDFVSDADSTLIGDCATVHTANKWDLIISDMY DPKTKNVTKENDSKEGFFTYICGFIQQKLALGGSV AIKITEHSWNADLYKLMGHFAWWTAFVTNVNASSS EAFLIGCNYLGKPREQIDGYVMHANYIFWRNTNPI QLSSYSLFDMSKFPLKLRGTAVMSLKEGQINDMIL SLLSKGRLIIRENNRVVISSDVLVNN
surface glycoprotein [Wuhan seafood market pneumonia virus]; GenBank: QHD43416.1; Jan. 23, 2020	371	mfvflvllpl vssqcvnltt rtqlppaytn sftrgvyypd kvfrssvlhs tqdlflpffs 61 nvtwfhaihv sgtngtkrfd npvlpfndgv yfasteksni irgwifgttl dsktqslliv 121 nnatnvvikv cefqfcndpf lgvyyhknnk swmesefrvy ssannctfey vsqpflmdle 181 gkqgnfknlr efvfknidgy fkiyskhtpi nlvrdlpqgf saleplvdlp iginitrfqt 241 llalhrsylt pgdsssgwta gaaayyvgyl qprtfllkyn engtitdavd caldplsetk 301 ctlksftvek giyqtsnfrv qptesivrfp nitnlcpfge vfnatrfasv yawnrkrisn 361 cvadysvlyn sasfstfkcy gvsptklndl cftnvyadsf virgdevrqi apgqtgkiad 421 ynyklpddft gcviawnsnn ldskvggnyn ylyrlfrksn lkpferdist eiyqagstpc 481 ngvegfncyf plqsygfqpt ngvgyqpyrv vvlsfellha patvcgpkks tnlvknkcvn 541 fnfngltgtg vltesnkkfl pfqqfgrdia dttdavrdpq tleilditpc sfggvsvitp 601 gtntsnqvav lyqdvnctev pvaihadqlt ptwrvystgs nvfqtragcl igaehvnnsy 661 ecdipigagi casyqtqtns prrarsvasq siiaytmslg aensvaysnn siaiptnfti 721 svtteilpvs mtktsvdctm yicgdstecs nlllqygsfc tqlnraltgi aveqdkntqe 781 vfaqvkqiyk tppikdfggf nfsqilpdps kpskrsfied llfnkvtlad agfikqygdc 841 lgdiaardli caqkfngltv lpplltdemi aqytsallag titsgwtfga gaalqipfam 901 qmayrfngig vtqnvlyenq klianqfnsa igkiqdslss tasalgklqd vvnqnaqaln 961 tlvkqlssnf gaissvlndi lsrldkveae vqidrlitgr lqslqtyvtq qliraaeira 1021 sanlaatkms ecvlgqskrv dfcgkgyhlm sfpqsaphgv vflhvtyvpa qeknfttapa 1081 ichdgkahfp regvfvsngt hwfvtqrnfy epqiittdnt fvsgncdvvi givnntvydp 1141 lqpeldsfke eldkyfknht spdvdlgdis ginasvvniq keidrlneva knlneslidl 1201 qelgkyeqyi kwpwyiwlgf iagliaivmv timlccmtsc csclkgccsc gscckfdedd 1261 sepvlkgvkl hyt
nCoV-10 mAb VH (nt-CO)	372	CAAGTGCAACTCGTGGAGTCCGGCGGCGGCG TCGTCCAGCCAGGTCGGTCTCTAAGGCTGTCG TGCGCTGCAAGTGGGTTTACATTCTCTAATTA TGGTATGCATTGGGTGAGGCAGGCTCCCGGC AAGGGGCTGGAATGGCTCGCTGTGATTTCAA GCGATGGTCGAATTAAATTTTATGCTGACTCT GTTAAAGGCAGATTTACTATGAGTAGAGACT CATCAAAAAACACTCTGTACCTGCAAATGAA TAGCCTGCGCGCCGAGGATACGGCTGTCTAC TACTGCGCCAAAGACCGGTTCCAATTCGCAA GATCATGGTATGGAGACTACTTCGATTATTGG GGGCAAGGTACTCAGGTGACTGTCTCCTCA
nCoV-10 mAb VH-v3 (nt-CO)	373	CAGGTGCAACTTGTGGAAAGTGGCGGAGGCG TGGTGCAGCCGGGGCGATCCTTGCGCCTCTCC TGTGCCGCCAGCGGGTTTACATTTTCCAATTA TGGCATGCACTGGGTGCGTCAGGCCCCCGGG AAGGGCCTGGAATGGCTTGCCGTGATCAGCA GTGACGGACGCATTAAATTCTACGCCGATTCT GTCAAGGGTCGGTTCACCATGAGTAGAGACT CCTCAAAGAACACTCTGTACCTGCAGATGAA TAGCCTGCGGGCCGAAGACACCGCTGTGTAC TACTGTGCTAAGGACCGGTTTCAATTTGCTAG ATCATTCTACGGGGACTACTTCGACTATTGGG GCCAAGGCACGCAGGTGACAGTCAGCTCA

TABLE 1-continued

Sequences		
Sequence Description	SEQ ID NO.	Sequence
nCoV-10 mAb VH-v3 (aa)	374	QVQLVESGGGVVQPGRSLRLSCAAS**GFTFSNY** **G**MHWVRQAPGKGLEWLAV**ISSDGRIK**FYADS VKGRFTMSRDSSKNTLYLQMNSLRAEDTAVYY C**AKDRFQFARSFYGDYFDY**WGQGTQVTVSS
nCoV-10 mAb VH-v3 CDRH3 (aa)	375	**AKDRFQFARSFYGDYFDY**
nCoV-10 mAb VH-v4 (nt-CO)	376	CAAGTCCAGCTTGTCGAGTCTGGAGGGGGCG TAGTGCAGCCCGGGCGCAGTTTGAGATTAAG CTGCGCCGCCTCTGGTTTCACGTTCTCCAATT ACGGTATGCACTGGGTGCGACAGGCACCCGG CAAGGGGCTGGAATGGCTGGCCGTCATTAGT TCAGACGGGCGGATCAAATTTTACGCTGACA GTGTGAAGGGTAGGTTTACCATGTCAAGAGA CTCCAGCAAAAACACATTATACCTGCAGATG AACAGCCTGCGCGCCGAGGACACCGCCGTAT ATTATTGCGCTAAGGACCGCTTTCAGTTCGCT AGGTCTGCCTACGGTGACTATTTTGATTATTG GGGACAGGGAACTCAGGTAACGGTCAGCTCA
nCoV-10 mAb VH-v4 (aa)	377	QVQLVESGGGVVQPGRSLRLSCAAS**GFTFSNY** **G**MHWVRQAPGKGLEWLAV**ISSDGRIK**FYADS VKGRFTMSRDSSKNTLYLQMNSLRAEDTAVYY C**AKDRFQFARSAYGDYFDY**WGQGTQVTVSS
nCoV-10 mAb VH-v4 CDRH3 (aa)	378	AKDRFQFARSAYGDYFDY
nCoV-10 mAb VL (Vk) (nt-CO)	379	GCGGTTGCAATGACTCAGTCCCCACTCTCCTT GCCCGTGACACTCGGGCAACCGGCCTCCATC TCTTGCCGGAGCAATCAGTCCCTTGTTTATAG CGACGGGAATATCTATCTGAATTGGTTCCAGC AGAGGCCCGGGCAGTCACCAATGCGCCTCAT CTATCGGGTGTCCAACCGGGATTCAGGTGTG CCCGACCGGTTTTCTGGCAGCGGATCAGGAA CGGACTTTACACTCAAAATTTCCCGCGTGGAG GCTGAGGATGTCGGAATCTATTATTGCATGCA GGGCACGCACTGGCCTCCAACCTTCGGCGGA GGAACCAAGGTGGAGATCAAG
nCoV-10 mAb VL-v3 (Vk) (aa)	380	DVVMTQSPLSLPVTLGQPASISCRSQ**QSLVYSD** **GNIY**LNWFQQRPGQSPMRLIY**RVS**NRDSGVPD RFSGSGSGTDFTLKISRVEAEDVGIYYC**MQGTH** **WPPT**FGGGTKVEIK
nCoV-10 mAb VL-v3 (Vk) (nt-CO)	381	GATGTGGTAATGACCCAAAGCCCCCTGTCATT GCCAGTGACACTGGGCCAGCCGGCCTCAATT AGTTGCAGGTCTCAGCAGTCACTGGTGTACTC CGATGGCAATATCTACCTAAACTGGTTCCAGC AGCGGCCTGGGCAATCTCCTATGCGACTTATA TATAGAGTGAGTAACCGGGACAGTGGGGTCC CTGATAGATTTTCAGGTAGCGGCAGTGGCAC AGATTTCACCCTGAAGATATCTCGGGTAGAA GCAGAGGACGTGGGGATATATTATTGCATGC AGGGAACGCACTGGCCCCCTACCTTCGGCGG CGGAACAAAAGTGGAAATAAAA
surface glycoprotein RBD [Wuhan seafood market pneumonia virus]; GenBank: QHD43416.1; Jan. 23, 2020	382	nitnlcpfgevfnatrfasvyawnrkrisncvadysvlynsasfstfkcyg vsptklndlcftnvyadsfvirgdevrqiapgqtgkiadynyklpddftg cviawnsnnldskvggnynylyrlfrksnlkpferdisteiyqagstpcn gvegfncyfplqsygfqptngvgyqpyrvvvlsfellhapatvcgpkks tnlvknkcvnfnfngltgtg

TABLE 1-continued

Sequences		
Sequence Description	SEQ ID NO.	Sequence
nCoV-10 mAb VL-v4 (Vk) (aa)	383	DVVMTQSPLSLPVTLGQPASISCRSS**QSLVYSD** **GNIY**LNWFQQRPGQSPMRLIY**RVS**NRDSGVPD RFSGSGSGTDFTLKISRVEAEDVGIYYC**MQGTH** **WPPT**FGGGTKVEIK
nCoV-10 mAb VL-v4 (Vk) (nt-CO)	384	GACGTGGTGATGACACAGAGCCCACTATCCC TTCCGGTCACCTTGGGCCAGCCAGCAAGCATT TCCTGTCGGTCGAGCCAGTCTCTGGTCTATAG TGACGGAAACATTTATTTGAATTGGTTTCAAC AGAGGCCCGGACAGTCACCAATGCGCCTCAT CTACCGCGTCTCTAACAGAGACTCTGGAGTCC CCGATCGCTTTTCCGGTAGCGGGTCTGGGACC GATTTTACATTGAAGATCTCCAGGGTGGAAG CCGAGGACGTTGGTATCTACTACTGCATGCA GGGTACCCATTGGCCACCGACCTTCGGCGGG GGCACCAAAGTGGAGATCAAA
nCoV-10 mAb VL-v5 (Vk) (aa)	385	DVVMTQSPLSLPVTLGQPASISCRSS**QSLVYSD** **GNIY**LNWFQQRPGQSPMRLIY**RVS**NRDSGVPD RFSGSGSGTDFTLKISRVEAEDVGIYYC**MQGTH** **FPPT**FGGGTKVEIK
nCoV-10 mAb VL-v5 (Vk) CDRL3 (aa)	386	**MQGTHFPPT**
nCoV-10 mAb VL-v5 (Vk) (nt-CO)	387	GATGTCGTGATGACACAGTCGCCACTGAGTC TACCGGTGACACTGGGGCAGCCGGCCTCCAT TTCATGTAGGAGCAGTCAGTCGTTAGTGTACT CTGACGGTAACATCTATCTTAATTGGTTCCAG CAAAGACCTGGCCAGTCACCTATGCGGCTGA TATATAGAGTTTCCAACAGAGACTCCGGGGT GCCAGACAGGTTCTCTGGAAGTGGCTCTGGA ACTGACTTTACACTGAAGATCAGCAGGGTGG AGGCAGAGGACGTGGGTATCTATTACTGTAT GCAAGGGACTCATTTCCCTCCAACATTCGGA GGAGGGACAAAAGTGGAGATAAAA
nCoV-10 mAb VL-v6 (Vk) (aa)	388	DVVMTQSPLSLPVTLGQPASISCRSQQSLVYSD GNIYLNWFQQRPGQSPMRLIYRVSNRDSGVPD RFSGSGSGTDFTLKISRVEAEDVGIYYCMQGTH FPPTFGGGTKVEIK
nCoV-10 mAb VL-v6 (Vk) (nt-CO)	389	GACGTGGTGATGACTCAATCACCCCTCTCCCT ACCGGTCACACTGGGCCAGCCAGCAAGCATT TCATGCCGTTCGCAGCAGTCCCTCGTCTATTC GGACGGCAATATTTACCTCAACTGGTTTCAGC AGCGACCCGGGCAGTCACCCATGCGACTTAT CTACAGGGTGAGCAACAGAGATTCCGGGGTC CCCGATCGCTTCTCAGGCAGTGGCAGCGGCA CCGATTTCACCCTAAAAATTAGCCGCGTGGA AGCGGAAGATGTGGGTATCTACTACTGCATG CAGGGAACTCACTTTCCACCCACTTTTGGAGG GGGGACCAAAGTTGAAATCAAG
Receptor Binding Motif (RBM) in surface glycoprotein RBD [Wuhan seafood market pneumonia virus]; GenBank: QHD43416.1; Jan. 23, 2020	390	nsnnldskvggnynylyrlfrksnlkpferdistei yqagstpcngvegfncyfplqsygfqptngvgyqpy
nCoV10 mAb CL (Ck),	391	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDST

TABLE 1-continued

Sequences		
Sequence Description	SEQ ID NO.	Sequence
k1m3, IGKC*01		YSLSSTLTLSKADYEKHKVYACEVTHQGLSSPV TKSFNRGEC
nCoV-10 mAb VL-v7 (Vk) (aa)	392	DVVMTQSPLSLPVTLGQPASISCRSS**QSLVYSD** **GNIY**LNWFQQRPGQSPMRLIY**RVS**NRDSGVPD RFSGSGSGTDFTLKISRVEAEDVGIYYC**MQGTH** **YPPT**FGGGTKVEIK
nCoV-10 mAb VL-v8 (Vk) (aa)	393	DVVMTQSPLSLPVTLGQPASISCRSS**QSLVYSE** **GNIY**LNWFQQRPGQSPMRLIY**RVS**NRDSGVPD RFSGSGSGTDFTLKISRVEAEDVGIYYC**MQGTH** **YPPT**FGGGTKVEIK
nCoV-10 mAb VL-v7/8 (Vk) CDRL3 (aa)	394	**MQGTHYPPT**
nCov10 CH1-CH3 G1m17; IgHG1*01_M LNS	395	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVLHEALHSHYTQKSLSLSP GK
nCoV-10 mAb VH-v5 (aa)	396	QVQLVESGGGVVQPGRSLRLSCAAS**GFTFSNY** **G**MHWVRQAPGKGLEWLAV**ISSDGRIK**FYADS VKGRFTMSRDSSKNTLYLQMNSLRAEDTAVYY C**AKDRFQFARSYYGDYFDY**WGQGTQVTVSS
nCoV-10 mAb VH-v5 CDRH3 (aa)	397	**AKDRFQFARSYYGDYFDY**
nCoV-10 mAb VL-v8 (Vk) CDRL1 (aa)	398	**QSLVYSEGNIY**
nCoV-10 mAb VL-v9 (Vk) CDRL1 (aa)	399	**QALVYSDGNIY**
nCoV-10 mAb VL-v9 (Vk) (aa)	400	AVAMTQSPLSLPVTLGQPASISCRSN**QALVY** **SDGNIY**LNWFQQRPGQSPMRLIY**RVS**NRDS GVPDRFSGSGSGTDFTLKISRVEAEDVGIYYC **MQGTHWPPT**FGGGTKVEIK
nCoV-10 mAb VL-v10 (Vk) CDRL1 (aa)	401	**QGLVYSDGNIY**
nCoV-10 mAb VL-v10 (Vk) (aa)	402	AVAMTQSPLSLPVTLGQPASISCRSN**QGLVY** **SDGNIY**LNWFQQRPGQSPMRLIY**RVS**NRDS GVPDRFSGSGSGTDFTLKISRVEAEDVGIYY**C** **MQGTHWPPT**FGGGTKVEIK
nCoV-10 mAb VL-v11 (Vk) CDRL1 (aa)	403	**QVLVYSDGNIY**
nCoV-10 mAb VL-v11 (Vk) (aa)	404	AVAMTQSPLSLPVTLGQPASISCRSN**QVLVY** **SDGNIY**LNWFQQRPGQSPMRLIY**RVS**NRDS GVPDRFSGSGSGTDFTLKISRVEAEDVGIYY**C** **MQGTHWPPT**FGGGTKVEIK

TABLE 1-continued

Sequences		
Sequence Description	SEQ ID NO.	Sequence
nCoV-10 mAb VL-v12 (Vk) CDRL1 (aa)	405	**PSLVYSDGNIY**
nCoV-10 mAb VL-v12 (Vk) (aa)	406	AVAMTQSPLSLPVTLGQPASISCRSN**PSLVYS** **DGNIY**LNWFQQRPGQSPMRLIY**RVS**NRDSG VPDRFSGSGSGTDFTLKISRVEAEDVGIYYC **MQGTHWPPT**FGGGTKVEIK
nCoV-10 mAb VL-v13 (Vk) (aa)	407	AVAMTQSPLSLPVTLGQPASISCRSD**QSLVY** **SDGNIY**LNWFQQRPGQSPMRLIY**RVS**NRDS GVPDRFSGSGSGTDFTLKISRVEAEDVGIYYC **MQGTHWPPT**FGGGTKVEIK
nCoV-10 mAb VL-v14 (Vk) (aa)	408	AVAMTQSPLSLPVTLGQPASISCRSE**QSLVYS** **DGNIY**LNWFQQRPGQSPMRLIY**RVS**NRDSG VPDRFSGSGSGTDFTLKISRVEAEDVGIYYC **MQGTHWPPT**FGGGTKVEIK
nCoV-10 mAb VL-v15 (Vk) (aa)	409	DVVMTQSPLSLPVTLGQPASISCRSN**QALVY** **SDGNIY**LNWFQQRPGQSPMRLIY**RVS**NRDS GVPDRFSGSGSGTDFTLKISRVEAEDVGIYYC **MQGTHWPPT**FGGGTKVEIK
nCoV-10 mAb VL-v16 (Vk) (aa)	410	DVVMTQSPLSLPVTLGQPASISCRSN**QGLVY** **SDGNIY**LNWFQQRPGQSPMRLIY**RVS**NRDS GVPDRFSGSGSGTDFTLKISRVEAEDVGIYYC **MQGTHWPPT**FGGGTKVEIK
nCoV-10mAb VL-v17 (Vk) (aa)	411	DVVMTQSPLSLPVTLGQPASISCRSN**QVLVY** **SDGNIY**LNWFQQRPGQSPMRLIY**RVS**NRDS GVPDRFSGSGSGTDFTLKISRVEAEDVGIYYC **MQGTHWPPT**FGGGTKVEIK
nCoV-10 mAb VL-v18 (Vk) (aa)	412	DVVMTQSPLSLPVTLGQPASISCRSN**PSLVYS** **DGNIY**LNWFQQRPGQSPMRLIY**RVS**NRDSG VPDRFSGSGSGTDFTLKISRVEAEDVGIYYC **MQGTHWPPT**FGGGTKVEIK
nCoV-10 mAb VL-v19 (Vk) (aa)	413	DVVMTQSPLSLPVTLGQPASISCRSD**QSLVY** **SDGNIY**LNWFQQRPGQSPMRLIY**RVS**NRDS GVPDRFSGSGSGTDFTLKISRVEAEDVGIYYC **MQGTHWPPT**FGGGTKVEIK
nCoV-10 mAb VL-v20 (Vk) (aa)	414	DVVMTQSPLSLPVTLGQPASISCRSE**QSLVYS** **DGNIY**LNWFQQRPGQSPMRLIY**RVS**NRDSG VPDRFSGSGSGTDFTLKISRVEAEDVGIYYC **MQGTHWPPT**FGGGTKVEIK
nCoV-10 mAb VH-v21 (aa)	415	QVQLVESGGGVVQPGRSLRLSCAAS**GFTFS** **NY**GMHWVRQAPGKGLEWLAV**ISFDGRIK**F YADSVKGRFTMSRDSSKNTLYLQMNSLRAE DTAVYYC**AKDRFQFARSWYGDYFDY**WGQ GTQVTVSS
nCoV-10 mAb VH-v21 CDRH2 (aa)	416	**ISFDGRIK**
nCoV-10 mAb VH-v21 (nt)	417	GCCAGTGTCAGGTGCAGCTGGTGGAGTCT GGGGGAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCCTCTGGATT CACCTTCAGTAACTATGGCATGCACTGGGT CCGCCAGGCTCCAGGCAAGGGGCTGGAGT GGCTGGCAGTTATATCATTTGATGGAAGAA TTAAGTTCTATGCAGACTCCGTGAAGGGCC GATTCACCATGTCCAGAGACAGTTCCAAG AACACGCTGTATCTGCAAATGAACAGCCT GAGAGCTGAGGACACGGCTGTGTATTACT

TABLE 1-continued

Sequences		
Sequence Description	SEQ ID NO.	Sequence
		GTGCGAAAGATCGGTTCCAGTTTGCCAGA AGCTGGTACGGTGACTACTTTGACTACTGG GGCCAGGGAACCCAGGTCACCGTCTCCTC AGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACC

EXAMPLES

Example 1

Cross-Reactivity of Human Monoclonal Antibodies Against the Spike Protein of SARS-CoV-2

[0174] A panel of twenty human SARS-CoV-neutralizing monoclonal antibodies recognizing SARS-CoV RBD were initially tested for binding to SARS-CoV Spike protein by ELISA (FIGS. **1**A-**1**D). All antibodies were confirmed to bind to SARS-CoV Spike protein. The antibodies comprise the VH and VL sequences as shown in Table 2.

[0175] To test the ability of the twenty anti-SARS-CoV antibodies to cross-react with the spike (S) protein of SARS-CoV-2, a flow cytometry-based assay was utilized. ExpiCHO cells were transfected with S protein of SARS-CoV-2, SARS-CoV and MERS-CoV, or with an empty plasmid as a negative control. The twenty monoclonal antibodies were then tested by flow cytometry at 10 μg/ml for their ability to stain ExpiCHO cells expressing the S protein of SARS-CoV-2, SARS-CoV, MERS-CoV or Mock cell transfectants. As expected, all twenty antibodies recognized SARS-CoV Spike protein on cells, and none recognized MERS-CoV or Mock transfectants (FIGS. **2**A and **2**B). Two antibodies, nCoV-6 and nCoV-10, recognized SARS-CoV-2 Spike protein on well over 30% (nCoV-6, approximately 40%; nCov-10, approximately 60%) of the cells using this assay.

[0176] The binding of nCoV-6 and nCoV-10 to SARS-CoV-2, SARS-CoV and MERS-CoV S proteins on cells was further investigated by testing multiple concentrations of each antibody. As shown in FIGS. **3**A and **3**B, antibody nCoV-10 recognizes SARS-CoV-2 S protein displayed 24 hours after transfection with higher avidity and similarly to its binding to SARS-CoV. As shown in FIGS. **4**A and **4**B, antibody nCoV-6 binds to SARS-CoV-2 S with lower avidity than it binds to SARS-CoV S.

[0177] The same experiment was repeated on cells 24 hours after transfection, and similar results were obtained (FIG. **4**C).

[0178] Variants of antibody nCoV-10 and antibody nCoV-2 were constructed. The variant antibodies comprise the VH and VL sequences shown in Table 3. Certain of the nCoV-10 variants comprise a variant VH which may be combined with nCoV-10 wild type VL or any nCoV-10 variant VL, and others comprise a variant VL which may be combined with nCoV-10 wild type VH or any nCoV-10 variant VH.

TABLE 2

	SEQ ID NO.	
Antibody	VH	VL
nCoV-3	5	13
nCoV-10	21	29
nCoV-17	53	61
nCoV-6	69	77
nCoV-16	85	93
nCoV-20	101	109
nCoV-4	117	125
nCoV-15	165	173
nCoV-12	181	189
nCoV-5	197	205
nCoV-14	213	221
nCoV-9	229	237
nCoV-18	245	253
nCoV-8	261	269
nCoV-7	277	285
nCoV-2	293	301
nCoV-19	309	317
nCoV-1	325	333
nCoV-11	341	349
nCoV-13	357	365

TABLE 3

	SEQ ID NO.	
Antibody	VH	VL
nCoV-4-v2	133	141
nCoV-4-v3	149	157
nCoV-10-v2	37	45
nCoV-10 VH-v3	374	
nCoV-10 VH-v4	377	
nCoV-10 VL-v3		380
nCoV-10 VL-v4		383
nCoV-10 VL-v5		385
nCoV-10 VL-v6		388
nCoV-10 VL-v7		392
nCoV-10 VL-v8		393
nCoV-10 VL-v9		400
nCoV-10 VL-v10		402
nCoV-10 VL-v11		404
nCoV-10 VL-v12		406
nCoV-10 VL-v13		407
nCoV-10 VL-v14		408
nCoV-10 VL-v15		409
nCoV-10 VL-v16		410
nCoV-10 VL-v17		411
nCoV-10 VL-v18		412
nCoV-10 VL-v19		413
nCoV-10 VL-v20		414
nCoV-10 VH-v21	415	

Example 2

Epitope Study of NcoV-1 Monoclonal Antibody

[0179] Epitope analysis of monoclonal antibody nCoV-1 for SARS-CoV RBD was performed using low resolution cryo-EM and SARS CoV S glycoprotein (crystal structure 6NB7). Based on these studies, the SARS CoV S glycoprotein epitope residues of nCoV1 comprise Thr402, Gly403, Val404, Asp407, Tyr408, Tyr442, Arg444, His445, Gly446, Lys447, Ser461, Pro462, Asp463, Gly464, Cys467, Leu472, Asn473, Cys474, Tyr475, Leu478, and Asn479.

Example 3

Cross-Competition Analysis of Binding of Antibodies NCoV-6 and NCoV-10 to SARS-CoV RBD

[0180] To test whether two antibodies nCoV-6 and nCoV-10 bind distinct epitopes, competition experiments were conducted using the receptor binding domain (RBD) of SARS-CoV. The Octet binding profile demonstrated that nCoV-10 does not compete with nCoV-6, which indicates that the two antibodies bind to different sites on the RBD. As a control, homologous competition of the antibodies was conducted. Based on the observation that nCoV-10, but not nCoV-4, bound to 2019-nCoV, competition of the Fab fragment of nCoV-4 with nCoV-10 or nCoV-6 was also conducted. nCoV-10 competes with nCoV-4, but not with nCoV-6. This experiment was repeated using monoclonal antibody nCoV-1 for which the epitope was defined using low resolution cryo-EM and SARS CoV S glycoprotein, and found to map in the receptor binding motif (corresponding to the footprint of human ACE2 receptor on SARS-CoV S protein). In this experiment, SARS-CoV S1 domain (that comprises RBD) was used.

[0181] The results confirmed that nCoV-10 does not compete with nCoV-6, and also showed that nCoV-10 competes with nCoV-1 (FIGS. **5**A-**5**F). This finding further suggests that nCoV-10 recognizes an epitope on the S glycoprotein of SARS-CoV and SARS-CoV-2 that is located in the receptor binding motif.

[0182] Of note, the SARS-CoV RBD and the SARS-CoV-2 RBD have differences at certain amino acid sequence positions. Consistent with the induction of the same SARS-CoV escape mutant (i.e. P462H), nCoV-10 and nCoV4 recognize overlapping epitopes in SARS-CoV RBD. Of note, the SARS-CoV RBD L443, F460 and P462 residues found to be critical for nCoV-10 neutralization (based on the lack of neutralization of SARS-CoV escape mutants L443R, F460C and P462H) are not conserved in SARS-CoV-2. The SARS-CoV escape mutant L443R was selected using nCoV-1. In particular, residue 443 (455 according to SARS-CoV-2 numbering) is phenylalanine instead of leucine, residue 460 (473 according to SARS-CoV-2 numbering) is tyrosine instead of phenylalanine, and the residue 462 (475 according to SARS-CoV-2 numbering) is alanine instead of proline (FIGS. **6**A and **6**B). These three critical residues (443, 460 and 462) are all in the interface with ACE2 and therefore are part of the receptor binding motif (FIG. **6**A, **6**B, and **7**). These data, combined with the competition data between nCoV-10 and nCoV-1 (for which antibody the epitope is defined at the structural level), provide further evidence that nCoV-10 recognizes an epitope in the receptor binding motif of SARS-CoV-2 (FIG. **8**).

[0183] The overall sequence similarity between SARS-CoV-2 S and SARS-CoV S is around 75%-77% for the RBD, and only approximately 50% for the RBM (FIG. **6**A). Taken together, these findings indicate that nCoV-10 is uniquely able to cross-react to epitopes in the receptor binding motif (i.e. at the interface between RBD and ACE2) of both SARS-CoV and SARS-CoV-2. The SARS-CoV neutralizing antibody nCoV-6 might recognize a distinct epitope outside the RBM and due to the lack of competition with nCoV-10 could be combined (as a mix or in multi-specific formats) with it to increase barrier to resistance as well as to provide potential additive or synergistic effects on SARS-CoV-2 neutralization.

Example 4

Blocking Binding of RBD to the Human ACE2 Receptor

[0184] To test whether nCoV-10 and nCoV-6 can inhibit binding of the RBD to the human ACE2 receptor, Octet experiments were conducted in which SARS-CoV RBD was incubated with nCoV-6 or nCoV-10 antibodies and the formed complexes were then evaluated for binding to solid-phase hACE2 (i.e. on Octet pins). By this analysis, nCOV-10, but not nCoV-6, could clearly block the binding of SARS-CoV RBD to hACE2 (FIG. **9**). This inhibitory activity of nCoV-10 is expected to correlate with the neutralizing activity of the antibody against SARS-CoV (for which hACE2 is the principal receptor for viral entry) and possibly also against SARS-CoV-2 (for which hACE2 is currently also described to be the principal receptor for viral entry).

Example 5

Conservation of RBD in SARS-CoV-2 Sequences

[0185] Analysis of all publicly available full genome sequences of SARS-CoV-2 as to Feb. 7, 2020 (n=71) revealed that SARS-CoV-2 RBD is highly conserved. The only exception is the appearance of mutations V367F (V354 numbering in SARS-CoV RBD) in two isolates from France (BetaCoV/France/IDF0372/2020 and BetaCoV/France/IDF0373/2020) and D364Y (V351 numbering in SARS-CoV RBD) (FIG. **7**) in other isolates recently published. The residue V367 (V354 in SARS-CoV) was analysed on the structure of SARS-CoV RBD (pdb, 2AJF). Both residues D364 and V367 were found to be positioned outside of the receptor binding motif and opposite in the RBD to the residues L443, F460 and P462 (475 in SARS-CoV-2) (FIG. **10**).

Example 6

SARS-CoV-2 Neutralization Assay

[0186] Replication-incompetent viruses pseudotyped with the SARS-CoV-2 S gene (isolate BetaCoV/Wuhan-Hu-1/2019; accession number MN908947) were produced using methods as previously described (Temperton NJ, et al. (2005) Longitudinally profiling neutralizing antibody response to SARS coronavirus with pseudotypes. *Emerg Infect Dis* 11(3):411-416.). Briefly, HEK293T/17 was

cotransfected with a SARS-CoV-2 S-expressing plasmid (phCMV1, Genlantis) and with a complementing viral-genome reporter gene vector, pNL4-3. Luc+.E-R+. A single-cycle infectivity assay was used to measure the neutralization of luciferase-encoding virions pseudotyped with the SARS-CoV-2 S protein, as previously described (Temperton NJ, et al. (2007). *A sensitive retroviral pseudotype assay for influenza H5N1-neutralizing antibodies*. Influenza Other Respi Viruses 1(3):105-112.). Briefly, appropriate dilutions of the virion-containing culture supernatants were preincubated at 37° C. for 1 h with antibodies at various concentrations and the virus-mAb mixtures was then added to Vero E6 cells that were seeded the day before infection. The cells were then lysed with Steady-Glo reagent (Promega, E2520), and the relative luminescence units (RLU) in the cell lysates was determined on a luminometer microplate reader (Synergy H1 Hybrid Multi-Mode Reader; Biotek). The reduction of infectivity was determined by comparing the RLU in the presence and absence of antibody and expressed as percentage of neutralization.

Example 7

Inhibition of SARS-S1 Association with ACE2

[0187] The ability of monoclonal antibodies nCoV-1 and nCoV-10 to inhibit association of SARS-S1 protein with ACE2 was assayed by Octet (BLI). SARS-CoV S1 was incubated with nCoV-1 or nCoV-10 antibodies and the formed complexes were then evaluated for binding to solid-phase hACE2 (i.e. on Octet pins). Results are shown in FIGS. **11**A and **11**B and in Table 4. FIG. **11**A shows % inhibition on the y-axis. FIG. **11**B shows response on the y-axis. In these experiments, the IC50 for nCoV-1 was calculated to be 1129 ng/ml. The IC50 for nCoV-10 was calculated to be 2688 ng/ml.

TABLE 4

Antibody	Concentration (ng/ml)	Response (60 sec)	% Inhibition (60 sec)
nCoV-1	60000	−0.0174	100
	20000	−0.0181	100.2115443
	6666.7	−0.0181	100.2115443
	2222.2	0.0086	92.14264128
	740.74	0.2353	23.63251738
	246.91	0.2758	11.39317014
	82.30	0.3091	1.32970686
	No mAb	0.3165	−0.906618314
nCoV-10	60000	0.0037	93.62345119
	20000	−0.0081	97.18948323
	6666.7	−0.0014	95.16470233
	2222.2	0.2141	30.03928679
	740.74	0.2898	7.162284678
	246.91	0.3037	2.961619825
	82.30	0.3328	−5.832577818
	No mAb	0.3105	0.906618314

Example 8

Materials and Methods

Transient Expression of Recombinant SARS-CoV-2 Protein

[0188] The full-length S gene of SARS-CoV-2 strain (SARS-CoV-2-S) isolate BetaCoV/Wuhan-Hu-1/2019 (accession number MN908947) was codon optimized for human cell expression and cloned into the phCMV1 expression vector (Genlantis). Expi-CHO cells were transiently transfected with phCMV1-2019-nCoV-S, phCMV1-MERS-CoV-S (Londonl/2012), pl.18-SARS-CoV-S (Urbani strain) or the empty phCMV1 (Mock) using Expifectamine CHO Enhancer. One and two days after transfection, cells were collected, fixed, or fixed and permeabilized with saponin for immunostaining with a panel of 21 monoclonal antibodies reactive to SARS-CoV Receptor Binding Domain (RBD). An Alexa647-labelled secondary antibody anti-human IgG Fc was used for detection. Binding of antibodies to transfected cells was analyzed by flow-cytometry using a ZE5 Cell Analyzer (Biorad) and FlowJo software (TreeStar). Positive binding was defined by differential staining of CoV-S-transfectants versus mock-transfectants.

Competition Experiments Using Octet (BLI, Biolayer Interferometry)

[0189] Anti-His sensors (BIOSENSOR ANTI-PENTA-HIS (HIS1K)) were used to immobilize the S1 subunit protein of SARS-CoV (Sino Biological Europe GmbH). Sensors were hydrated for 10 min with Kinetics Buffer (KB; 0.01% endotoxin-free BSA, 0.002^ Tween-20, 0.005% NaN3 in PBS). SARS-CoV S1 subunit protein was then loaded for 8 min at a concentration of 10 μg/ml in KB. Antibodies were associated for 6 min at 15 μg/ml for full length mAbs nCoV-10 and nCov-6 mAbs or 5 μg/ml for Fab nCoV-4, and in a subsequent experiment comprising nCoV-1 all at 10 μg/ml. Competing antibodies were then associated at the same concentration for additional 6 minutes.

Competition Experiments Using Octet (BLI, Biolayer Interferometry)

[0190] Anti-His sensors (BIOSENSOR ANTI-PENTA-HIS (HIS1K)) were used to immobilize human ACE2 (at 5 μg/ml; R&D). Sensors were hydrated for 10 min with Kinetics Buffer (KB; 0.01% endotoxin-free BSA, 0.002^ Tween-20, 0.005% NaN3 in PBS). Human ACE2 was then loaded for 30 min at a concentration of 5 μg/ml in KB. Antibodies (2 μg/ml) were mixed with SARS-CoV RBD-Fc (Sino Biological Europe GmbH, 2 μg/ml) and exposed to human ACE2 loaded sensors for an association time of 15 min, followed by a dissociation step of 6 minutes.

ELISA Binding

[0191] The reactivities of mAbs with SARS-CoV Spike S1 Subunit Protein (strain WH20) protein were determined by enzyme-linked immunosorbent assays (ELISA). Briefly, 96-well plates were coated with 3 μg/ml of recombinant SARS-CoV Spike S1 Subunit Protein (Sino. Biological). Wells were washed and blocked with PBS+1% BSA for 1 h at room temperature and were then incubated with serially diluted mAbs for 1 h at room temperature. Bound mAbs were detected by incubating alkaline phosphatase-conjugated goat anti-human IgG (Southern Biotechnology: 2040-04) for 1 h at room temperature and were developed by 1 mg/ml p-nitrophenylphosphate substrate in 0.1 M glycine buffer (pH 10.4) for 30 min at room temperature. The optical density (OD) values were measured at a wavelength of 405 nm in an ELISA reader (Powerwave 340/96 spectrophotometer, BioTek).

Example 9

Additional Experiments

[0192] SARS-CoV-2 RBDs (two variants) are synthesized with C-terminal peptide tags (Strep-Tag II; His-Tag) for purification and labelling. A full-length spike protein from SARS-CoV-2 is synthesized to produce SARS-CoV-2 pseudoviruses, and the pseudoviruses are used in neutralization assays and membrane expression studies.

[0193] The various embodiments described above can be combined to provide further embodiments. All of the U.S. patents, U.S. patent application publications, U.S. patent applications, foreign patents, foreign patent applications and non-patent publications referred to in this specification and/or listed in the Application Data Sheet, including U.S. Patent Application No. 62/969,592, filed Feb. 3, 2020, U.S. Patent Application No. 62/970,062, filed Feb. 4, 2020, U.S. Patent Application No. 62/971,552, filed Feb. 7, 2020, U.S. Patent Application No. 62/977,941, filed Feb. 18, 2020, U.S. Patent Application No. 63/016,228, filed Apr. 27, 2020, and U.S. Patent Application No. 63/023,858, filed May 12, 2020, are incorporated herein by reference, in their entirety. Aspects of the embodiments can be modified, if necessary to employ concepts of the various patents, applications and publications to provide yet further embodiments.

[0194] These and other changes can be made to the embodiments in light of the above-detailed description. In general, in the following claims, the terms used should not be construed to limit the claims to the specific embodiments disclosed in the specification and the claims, but should be construed to include all possible embodiments along with the full scope of equivalents to which such claims are entitled. Accordingly, the claims are not limited by the disclosure.

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ccaggcaagg ggctggagtg ggtctcaact attagtggtg gtggtggtga cacatactcc     180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagag cacgctgtat     240

ttgcaaatga acagcctgag agccgcggac acggccctat attactgtgc gagattggaa     300

agcgcgacgc agcccctcgg ctactatttc tacggtatgg acgtctgggg ccaagggact     360

acggtcaccg tctcctcag                                                  379


<210> SEQ ID NO 2
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-3 mAb CDRH1

<400> SEQUENCE: 2

ggattcacct ttgccagcta tgcc                                             24


<210> SEQ ID NO 3
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-3 mAb CDRH2

<400> SEQUENCE: 3

attagtggtg gtggtggtga caca                                             24


<210> SEQ ID NO 4
<211> LENGTH: 57
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-3 mAb CDRH3

<400> SEQUENCE: 4

gcgagattgg aaagcgcgac gcagcccctc ggctactatt tctacggtat ggacgtc 57

<210> SEQ ID NO 5
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-3 mAb VH

<400> SEQUENCE: 5

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

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Ala Ser Tyr
20 25 30

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

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

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

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

Ala Arg Leu Glu Ser Ala Thr Gln Pro Leu Gly Tyr Tyr Phe Tyr Gly
100 105 110

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

<210> SEQ ID NO 6
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-3 mAb CDRH1

<400> SEQUENCE: 6

Gly Phe Thr Phe Ala Ser Tyr Ala
1 5

<210> SEQ ID NO 7
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-3 mAb CDRH2

<400> SEQUENCE: 7

Ile Ser Gly Gly Gly Gly Asp Thr
1 5

<210> SEQ ID NO 8
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-3 mAb CDRH3

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<400> SEQUENCE: 8

Ala Arg Leu Glu Ser Ala Thr Gln Pro Leu Gly Tyr Tyr Phe Tyr Gly
1 5 10 15

Met Asp Val

<210> SEQ ID NO 9
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-3 mAb VL

<400> SEQUENCE: 9

tcctatgagc tgacacagcc accctcggtg tcagtgtccc caggacagac ggccaggatc 60

acctgctctg gagatgcatt gccaaagcaa tatgcttttt ggtaccagca gaggccaggc 120

caggcccctg tgttggtgat atctaaagac agtgagaggc cctcagggat ccctgagcga 180

ttctctggct ccagctcagg gacaacagtc acgttgacca tcagtggagt ccaggcagaa 240

gacgaggctg actattactg tcattcagca gacatcagtg ctacttcttg ggttttcggc 300

ggagggacca agctgaccgt cgtt 324

<210> SEQ ID NO 10
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-3 mAb CDRL1

<400> SEQUENCE: 10

gcattgccaa agcaatat 18

<210> SEQ ID NO 11
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-3 mAb CDRL2

<400> SEQUENCE: 11

aaagacagt 9

<210> SEQ ID NO 12
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-3 mAb CDRL3

<400> SEQUENCE: 12

cattcagcag acatcagtgc tacttcttgg gtt 33

<210> SEQ ID NO 13
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-3 mAb VL

<400> SEQUENCE: 13

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

Thr Ala Arg Ile Thr Cys Ser Gly Asp Ala Leu Pro Lys Gln Tyr Ala
            20                  25                  30

Phe Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Val Leu Val Ile Ser
        35                  40                  45

Lys Asp Ser Glu Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60

Ser Ser Gly Thr Thr Val Thr Leu Thr Ile Ser Gly Val Gln Ala Glu
65                  70                  75                  80

Asp Glu Ala Asp Tyr Tyr Cys His Ser Ala Asp Ile Ser Ala Thr Ser
                85                  90                  95

Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Val
            100                 105


<210> SEQ ID NO 14
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-3 mAb CDRL1

<400> SEQUENCE: 14

Ala Leu Pro Lys Gln Tyr
1               5


<210> SEQ ID NO 15
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-3 mAb CDRL2

<400> SEQUENCE: 15

Lys Asp Ser
1


<210> SEQ ID NO 16
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-3 mAb CDRL3

<400> SEQUENCE: 16

His Ser Ala Asp Ile Ser Ala Thr Ser Trp Val
1               5                   10


<210> SEQ ID NO 17
<211> LENGTH: 376
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VH

<400> SEQUENCE: 17

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc      60

tcctgtgcag cctctggatt caccttcagt aactatggca tgcactgggt ccgccaggct     120

ccaggcaagg ggctggagtg gctggcagtt atatcatctg atggaagaat taagttctat     180
```

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gcagactccg tgaagggccg attcaccatg tccagagaca gttccaagaa cacgctgtat    240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gaaagatcgg    300

ttccagtttg ccagaagctg gtacggtgac tactttgact actggggcca gggaacccag    360

gtcaccgtct cctcag                                                    376


<210> SEQ ID NO 18
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb CDRH1

<400> SEQUENCE: 18

ggattcacct tcagtaacta tggc                                            24


<210> SEQ ID NO 19
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb CDRH2

<400> SEQUENCE: 19

atatcatctg atggaagaat taag                                            24


<210> SEQ ID NO 20
<211> LENGTH: 54
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb CDRH3

<400> SEQUENCE: 20

gcgaaagatc ggttccagtt tgccagaagc tggtacggtg actactttga ctac           54


<210> SEQ ID NO 21
<211> LENGTH: 125
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VH

<400> SEQUENCE: 21

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 Asn Tyr
            20                  25                  30

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

Ala Val Ile Ser Ser Asp Gly Arg Ile Lys Phe Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Met Ser Arg Asp Ser 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 Lys Asp Arg Phe Gln Phe Ala Arg Ser Trp Tyr Gly Asp Tyr Phe
            100                 105                 110

Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
```

-continued

115 120 125

<210> SEQ ID NO 22
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb CDRH1

<400> SEQUENCE: 22

Gly Phe Thr Phe Ser Asn Tyr Gly
1 5

<210> SEQ ID NO 23
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb CDRH2

<400> SEQUENCE: 23

Ile Ser Ser Asp Gly Arg Ile Lys
1 5

<210> SEQ ID NO 24
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb CDRH3

<400> SEQUENCE: 24

Ala Lys Asp Arg Phe Gln Phe Ala Arg Ser Trp Tyr Gly Asp Tyr Phe
1 5 10 15

Asp Tyr

<210> SEQ ID NO 25
<211> LENGTH: 337
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VL (Vk)

<400> SEQUENCE: 25

gctgttgcga tgactcagtc tccactctcc ctgcccgtca cccttggaca gccggcctcc 60

atctcctgca ggtctaatca aagcctcgta tacagtgatg gaaacatcta cttgaattgg 120

tttcaacaga ggccaggcca atctccaatg cgcctaattt atagggtttc taaccgggac 180

tctggggtcc cagacagatt cagcggcagt gggtcaggca ctgatttcac actgaaaatc 240

agcagggtgg aggctgaaga tgttgggatt tattactgca tgcaagggac acactggcct 300

ccgactttcg gcggagggac caaggtggag atcaaac 337

<210> SEQ ID NO 26
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb CDRL1

<400> SEQUENCE: 26

caaagcctcg tatacagtga tggaaacatc tac 33

-continued

<210> SEQ ID NO 27
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb CDRL2

<400> SEQUENCE: 27

agggtttct 9

<210> SEQ ID NO 28
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb CDRL3

<400> SEQUENCE: 28

atgcaaggga cacactggcc tccgact 27

<210> SEQ ID NO 29
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VL (Vk)

<400> SEQUENCE: 29

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Asn Gln Ser Leu Val Tyr Ser
20 25 30

Asp Gly Asn Ile Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Met Arg Leu Ile Tyr Arg Val Ser Asn Arg Asp 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 Ile Tyr Tyr Cys Met Gln Gly
85 90 95

Thr His Trp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> SEQ ID NO 30
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb CDRL1

<400> SEQUENCE: 30

Gln Ser Leu Val Tyr Ser Asp Gly Asn Ile Tyr
1 5 10

<210> SEQ ID NO 31
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb CDRL2

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<400> SEQUENCE: 31

Arg Val Ser
1

<210> SEQ ID NO 32
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb CDRL3

<400> SEQUENCE: 32

Met Gln Gly Thr His Trp Pro Pro Thr
1 5

<210> SEQ ID NO 33
<211> LENGTH: 376
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10-v2 mAb VH

<400> SEQUENCE: 33

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt aactatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg gctggcagtt atatcatctg atggaagaat taagttctat 180

gcagactccg tgaagggccg attcaccatg tccagagaca gttccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gaaagatcgg 300

ttccagtttg ccagaagctg gtacggtgac tactttgact actggggcca gggaacccag 360

gtcaccgtct cctcag 376

<210> SEQ ID NO 34
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10-v2 mAb CDRH1

<400> SEQUENCE: 34

ggattcacct tcagtaacta tggc 24

<210> SEQ ID NO 35
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10-v2 mAb CDRH2

<400> SEQUENCE: 35

atatcatctg atggaagaat taag 24

<210> SEQ ID NO 36
<211> LENGTH: 54
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10-v2 mAb CDRH3

<400> SEQUENCE: 36

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gcgaaagatc ggttccagtt tgccagaagc tggtacggtg actactttga ctac          54


<210> SEQ ID NO 37
<211> LENGTH: 125
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10-v2 mAb VH

<400> SEQUENCE: 37

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 Asn Tyr
            20                  25                  30

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

Ala Val Ile Ser Ser Asp Gly Arg Ile Lys Phe Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Met Ser Arg Asp Ser 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 Lys Asp Arg Phe Gln Phe Ala Arg Ser Trp Tyr Gly Asp Tyr Phe
            100                 105                 110

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


<210> SEQ ID NO 38
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10-v2 mAb CDRH1

<400> SEQUENCE: 38

Gly Phe Thr Phe Ser Asn Tyr Gly
1               5


<210> SEQ ID NO 39
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10-v2 mAb CDRH2

<400> SEQUENCE: 39

Ile Ser Ser Asp Gly Arg Ile Lys
1               5


<210> SEQ ID NO 40
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10-v2 mAb CDRH3

<400> SEQUENCE: 40

Ala Lys Asp Arg Phe Gln Phe Ala Arg Ser Trp Tyr Gly Asp Tyr Phe
1               5                   10                  15
```

-continued

Asp Tyr

<210> SEQ ID NO 41
<211> LENGTH: 337
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10-v2 (N to S) mAb VL
(Vk)

<400> SEQUENCE: 41

gctgttgcga tgactcagtc tccactctcc ctgcccgtca cccttggaca gccggcctcc 60

atctcctgca ggtctagtca aagcctcgta tacagtgatg gaaacatcta cttgaattgg 120

tttcaacaga ggccaggcca atctccaatg cgcctaattt atagggtttc taaccgggac 180

tctggggtcc cagacagatt cagcggcagt gggtcaggca ctgatttcac actgaaaatc 240

agcagggtgg aggctgaaga tgttgggatt tattactgca tgcaagggac acactggcct 300

ccgactttcg gcggagggac caaggtggag atcaaac 337

<210> SEQ ID NO 42
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10-v2 mAb CDRL1

<400> SEQUENCE: 42

caaagcctcg tatacagtga tggaaacatc tac 33

<210> SEQ ID NO 43
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10-v2 mAb CDRL2

<400> SEQUENCE: 43

agggtttct 9

<210> SEQ ID NO 44
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10-v2 mAb CDRL3

<400> SEQUENCE: 44

atgcaaggga cacactggcc tccgact 27

<210> SEQ ID NO 45
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10-v2 (N to S) mAb VL
(Vk)

<400> SEQUENCE: 45

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Ser

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            20                  25                  30

Asp Gly Asn Ile Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
        35                  40                  45

Pro Met Arg Leu Ile Tyr Arg Val Ser Asn Arg Asp 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 Ile Tyr Tyr Cys Met Gln Gly
                85                  90                  95

Thr His Trp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> SEQ ID NO 46
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10-v2 mAb CDRL1

<400> SEQUENCE: 46

Gln Ser Leu Val Tyr Ser Asp Gly Asn Ile Tyr
1               5                   10


<210> SEQ ID NO 47
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10-v2 mAb CDRL2

<400> SEQUENCE: 47

Arg Val Ser
1


<210> SEQ ID NO 48
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10-v2 mAb CDRL3

<400> SEQUENCE: 48

Met Gln Gly Thr His Trp Pro Pro Thr
1               5


<210> SEQ ID NO 49
<211> LENGTH: 370
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-17 mAb VH

<400> SEQUENCE: 49

caggtgcagc tggtggagtc ggggggaggc gtggtccagc ctgggaggtc cctgagactc      60

tcctgtgcag cctctggatt cactttcagt tcctatgcta tacactgggt ccgccaggct     120

ccaggcaagg gtctggagtg gctggcagtt atatcatttg atggaagaca taaatactac     180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacggtgtat     240

ctgcaaatga acagcctgag agttgaggac acggctgtct attcctgtgc gagagatatt     300
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cgtcatttga tagtagtggt ttccgatatg gacgtctggg gccaagggac cacggtcacc    360

gtctcctcag                                                           370


<210> SEQ ID NO 50
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-17 mAb CDRH1

<400> SEQUENCE: 50

ggattcactt tcagttccta tgct                                            24


<210> SEQ ID NO 51
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-17 mAb CDRH2

<400> SEQUENCE: 51

atatcatttg atggaagaca taaa                                            24


<210> SEQ ID NO 52
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-17 mAb CDRH3

<400> SEQUENCE: 52

gcgagagata ttcgtcattt gatagtagtg gtttccgata tggacgtc                  48


<210> SEQ ID NO 53
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-17 mAb VH

<400> SEQUENCE: 53

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

Ala Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45

Ala Val Ile Ser Phe Asp Gly Arg His Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

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

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

Ala Arg Asp Ile Arg His Leu Ile Val Val Val Ser Asp Met Asp Val
            100                 105                 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> SEQ ID NO 54
```

-continued

<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-17 mAb CDRH1

<400> SEQUENCE: 54

Gly Phe Thr Phe Ser Ser Tyr Ala
1 5

<210> SEQ ID NO 55
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-17 mAb CDRH2

<400> SEQUENCE: 55

Ile Ser Phe Asp Gly Arg His Lys
1 5

<210> SEQ ID NO 56
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-17 mAb CDRH3

<400> SEQUENCE: 56

Ala Arg Asp Ile Arg His Leu Ile Val Val Val Ser Asp Met Asp Val
1 5 10 15

<210> SEQ ID NO 57
<211> LENGTH: 337
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-17 mAb VL (Vk)

<400> SEQUENCE: 57

gatgttgtga tgactcagtc tccactctcc ctgcccgtca cccttggaca gccggcctcc 60

atctcctgca ggtctagtca aagcctcgta aacagtgatg gagacacctc cttgaattgg 120

tttcagcaga ggccaggcca atctccaagg cgcctgattt ataaggtttc taaccgggac 180

tctggggtcc cagacagaat cagcggcagt gggtcaggca ctgatttcac actgaaaatc 240

agcagggtgg aggctgagga tgttggggtt tattactgca tgcaaggtac acactggcct 300

ccgacttttg gccaggggac caagctggag atcaaac 337

<210> SEQ ID NO 58
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-17 mAb CDRL1

<400> SEQUENCE: 58

caaagcctcg taaacagtga tggagacacc tcc 33

<210> SEQ ID NO 59
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-17 mAb CDRL2

<400> SEQUENCE: 59

caaagcctcg taaacagtga tggagacacc tcc 33

<210> SEQ ID NO 60
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-17 mAb CDRL3

<400> SEQUENCE: 60

atgcaaggta cacactggcc tccgact 27

<210> SEQ ID NO 61
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-17 mAb VL (Vk)

<400> SEQUENCE: 61

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Asn Ser
20 25 30

Asp Gly Asp Thr Ser Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Arg Asp Ser Gly Val Pro
50 55 60

Asp Arg Ile 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 Gly
85 90 95

Thr His Trp Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> SEQ ID NO 62
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-17 mAb CDRL1

<400> SEQUENCE: 62

Gln Ser Leu Val Asn Ser Asp Gly Asp Thr Ser
1 5 10

<210> SEQ ID NO 63
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-17 mAb CDRL2

<400> SEQUENCE: 63

Lys Val Ser
1

-continued

<210> SEQ ID NO 64
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-17 mAb CDRL3

<400> SEQUENCE: 64

Met Gln Gly Thr His Trp Pro Pro Thr
1 5

<210> SEQ ID NO 65
<211> LENGTH: 376
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-6 mAb VH

<400> SEQUENCE: 65

caggtcacct tgaaggagtc tggtcctgtg ctggtgaaac ccacagagac cctcacgctg 60

acctgcaccg tctctgtgtt ctcactcagc aatgctagaa tgggtgtgag ctggatccgt 120

cagcccccag ggaaggccct ggagtggctt gcacacattt tttcgagtga ccaaaaatcc 180

tacagcacat ctctgaagag caggctcacc atctccaagg acacctccaa aagccaggtg 240

gtccttacca tgaccaacat ggaccctgag gacacaggca catattactg tgcacgaata 300

aacacggcgg cgtatgatta tgatagtacc acctttgata tctggggcca agggacaatg 360

gtcaccgtct cttcag 376

<210> SEQ ID NO 66
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-6 mAb CDRH1

<400> SEQUENCE: 66

gtgttctcac tcagcaatgc tagaatgggt 30

<210> SEQ ID NO 67
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-6 mAb CDRH2

<400> SEQUENCE: 67

attttttcga gtgaccaaaa a 21

<210> SEQ ID NO 68
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-6 mAb CDRH3

<400> SEQUENCE: 68

gcacgaataa acacggcggc gtatgattat gatagtacca cctttgatat c 51

<210> SEQ ID NO 69
<211> LENGTH: 125

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-6 mAb VH

<400> SEQUENCE: 69

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

Thr Leu Thr Leu Thr Cys Thr Val Ser Val Phe Ser Leu Ser Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Ser Asp Gln Lys Ser Tyr Ser Thr Ser
50 55 60

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

Val Leu Thr Met Thr Asn Met Asp Pro Glu Asp Thr Gly Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Asn Thr Ala Ala Tyr Asp Tyr Asp Ser Thr Thr Phe
100 105 110

Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120 125

<210> SEQ ID NO 70
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-6 mAb CDRH1

<400> SEQUENCE: 70

Val Phe Ser Leu Ser Asn Ala Arg Met Gly
1 5 10

<210> SEQ ID NO 71
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-6 mAb CDRH2

<400> SEQUENCE: 71

Ile Phe Ser Ser Asp Gln Lys
1 5

<210> SEQ ID NO 72
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-6 mAb CDRH3

<400> SEQUENCE: 72

Ala Arg Ile Asn Thr Ala Ala Tyr Asp Tyr Asp Ser Thr Thr Phe Asp
1 5 10 15

Ile

<210> SEQ ID NO 73
<211> LENGTH: 322
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-6 mAb VL (Vk)

<400> SEQUENCE: 73

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gaccattagc aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gctctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaactt 240

gaagattttg caacttacta ctgtcaacag agttacagta cccctcccac tttcggcgga 300

gggaccaagg tggagatcaa ac 322

<210> SEQ ID NO 74
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-6 mAb CDRL1

<400> SEQUENCE: 74

cagaccatta gcaactat 18

<210> SEQ ID NO 75
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-6 mAb CDRL2

<400> SEQUENCE: 75

gctgcatcc 9

<210> SEQ ID NO 76
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-6 mAb CDRL3

<400> SEQUENCE: 76

caacagagtt acagtacccc tcccact 27

<210> SEQ ID NO 77
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-6 mAb VL (Vk)

<400> SEQUENCE: 77

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 Thr Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Leu
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Leu
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105


<210> SEQ ID NO 78
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-6 mAb CDRL1

<400> SEQUENCE: 78

Gln Thr Ile Ser Asn Tyr
1               5


<210> SEQ ID NO 79
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-6 mAb CDRL2

<400> SEQUENCE: 79

Ala Ala Ser
1


<210> SEQ ID NO 80
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-6 mAb CDRL3

<400> SEQUENCE: 80

Gln Gln Ser Tyr Ser Thr Pro Pro Thr
1               5


<210> SEQ ID NO 81
<211> LENGTH: 376
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-16 mAb VH

<400> SEQUENCE: 81

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc      60

tcctgtgcag cctctggatt caccttcagt agctatggca tgcactgggt ccgccaggct     120

ccaggcaagg ggctggagtg ggtggcattt atatcatatg atggaagtaa tatacagtat     180

gcagactccg tgcagggccg attcaccatc tccagagaca attccaagac cacgttgtat     240

ctgcaaatga acagcctgag agttgaggac acggctatgt actactgtgc gaaagatctt     300

ttcggatatt gtaggagtac cagctgcgag tctcttgacg actggggcca gggagccctg     360

gtcaccgtct cctcag                                                     376


<210> SEQ ID NO 82
<211> LENGTH: 24
<212> TYPE: DNA
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-16 mAb CDRH1

<400> SEQUENCE: 82

ggattcacct tcagtagcta tggc 24

<210> SEQ ID NO 83
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-16 mAb CDRH2

<400> SEQUENCE: 83

atatcatatg atggaagtaa tata 24

<210> SEQ ID NO 84
<211> LENGTH: 54
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-16 mAb CDRH3

<400> SEQUENCE: 84

gcgaaagatc ttttcggata ttgtaggagt accagctgcg agtctcttga cgac 54

<210> SEQ ID NO 85
<211> LENGTH: 125
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-16 mAb VH

<400> SEQUENCE: 85

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 His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Phe Ile Ser Tyr Asp Gly Ser Asn Ile Gln Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Asp Leu Phe Gly Tyr Cys Arg Ser Thr Ser Cys Glu Ser Leu
100 105 110

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

<210> SEQ ID NO 86
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-16 mAb CDRH1

<400> SEQUENCE: 86

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Gly Phe Thr Phe Ser Ser Tyr Gly
1 5

<210> SEQ ID NO 87
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-16 mAb CDRH2

<400> SEQUENCE: 87

Ile Ser Tyr Asp Gly Ser Asn Ile
1 5

<210> SEQ ID NO 88
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-16 mAb CDRH3

<400> SEQUENCE: 88

Ala Lys Asp Leu Phe Gly Tyr Cys Arg Ser Thr Ser Cys Glu Ser Leu
1 5 10 15

Asp Asp

<210> SEQ ID NO 89
<211> LENGTH: 322
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-16 mAb VL (Vk)

<400> SEQUENCE: 89

gacatccagt tgacccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggccagtca gggcattagc agttatttag cctggtatca gcaaaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccactt tgcaaagtgg ggtcccatca 180

aggttcagcg gcactggata tgggacagaa ttcactctca caatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtcaacag cttaataatt accctctcac tttcggcgga 300

gggaccaagg tggagatcaa ac 322

<210> SEQ ID NO 90
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-16 mAb CDRL1

<400> SEQUENCE: 90

cagggcatta gcagttat 18

<210> SEQ ID NO 91
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-16 mAb CDRL2

<400> SEQUENCE: 91

gctgcatcc 9

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<210> SEQ ID NO 92
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-16 mAb CDRL3

<400> SEQUENCE: 92

caacagctta ataattaccc tctcact 27

<210> SEQ ID NO 93
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-16 mAb VL (Vk)

<400> SEQUENCE: 93

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

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Thr Gly Tyr 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 Asn Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> SEQ ID NO 94
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-16 mAb CDRL1

<400> SEQUENCE: 94

Gln Gly Ile Ser Ser Tyr
1 5

<210> SEQ ID NO 95
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-16 mAb CDRL2

<400> SEQUENCE: 95

Ala Ala Ser
1

<210> SEQ ID NO 96
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic sequence nCoV-16 mAb CDRL3

<400> SEQUENCE: 96

Gln Gln Leu Asn Asn Tyr Pro Leu Thr
1 5

<210> SEQ ID NO 97
<211> LENGTH: 373
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-20 mAb VH

<400> SEQUENCE: 97

caggtcacct tgcgggagtc tggtcctgcg ctggtgaaac ccacacagac cctcacactg 60

acctgcacct tctctgggtt ctcactcacc actactgaaa tgtgtgtggg ctggatccgt 120

cagcccccag ggaaggccct ggagtggctt gcactcattg attgggatga tgataaatac 180

tacagcacat ctctgaggac caggctcacc atctccaagg acacctccaa aaaccaggtg 240

gtccttacca tgaccaacat ggaccctgtg gacacagcca catattactg tgcacggatg 300

ttcgggcgaa agcgtctggc accaactggg ttcgacccct ggggccaggg aaccctggtc 360

accgtctcct cag 373

<210> SEQ ID NO 98
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-20mAb CDRH1

<400> SEQUENCE: 98

gggttctcac tcaccactac tgaaatgtgt 30

<210> SEQ ID NO 99
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-20 mAb CDRH2

<400> SEQUENCE: 99

attgattggg atgatgataa a 21

<210> SEQ ID NO 100
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-20 mAb CDRH3

<400> SEQUENCE: 100

gcacggatgt tcgggcgaaa gcgtctggca ccaactgggt tcgacccc 48

<210> SEQ ID NO 101
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-20 mAb VH

<400> SEQUENCE: 101

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Thr Thr Thr
            20                  25                  30

Glu Met Cys Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45

Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
    50                  55                  60

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

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95

Cys Ala Arg Met Phe Gly Arg Lys Arg Leu Ala Pro Thr Gly Phe Asp
            100                 105                 110

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


<210> SEQ ID NO 102
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-20 mAb CDRH1

<400> SEQUENCE: 102

Gly Phe Ser Leu Thr Thr Thr Glu Met Cys
1               5                   10


<210> SEQ ID NO 103
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-20mAb CDRH2

<400> SEQUENCE: 103

Ile Asp Trp Asp Asp Asp Lys
1               5


<210> SEQ ID NO 104
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-20 mAb CDRH3

<400> SEQUENCE: 104

Ala Arg Met Phe Gly Arg Lys Arg Leu Ala Pro Thr Gly Phe Asp Pro
1               5                   10                  15


<210> SEQ ID NO 105
<211> LENGTH: 337
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-20 mAb VL (Vk)

<400> SEQUENCE: 105

gatattgtga tgactcagtc tccactctcc ctgcccgtca cccctggaga gccggcctcc     60
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atctcctgca ggtctagtca gagcctcctg catagtaatg gaaagaacta tttggattgg    120

tacctgcaga agccagggca gtctccacag ctcctgatct gtttgggttc ttatcgggcc    180

tccggggtcc ctgacaggtt cagtggcagt ggatcaggca cagattttac actgaaaatc    240

agcagagtgg aggctgaaga tgttggggtt tattactgca tgcaagctct acaaactccc    300

tggacgttcg gccaagggac caaggtggaa atcaaac                             337


<210> SEQ ID NO 106
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-20 mAb CDRL1

<400> SEQUENCE: 106

cagagcctcc tgcatagtaa tggaaagaac tat                                  33


<210> SEQ ID NO 107
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-20 mAb CDRL2

<400> SEQUENCE: 107

ttgggttct                                                              9


<210> SEQ ID NO 108
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-20 mAb CDRL3

<400> SEQUENCE: 108

atgcaagctc tacaaactcc ctggacg                                         27


<210> SEQ ID NO 109
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-20 mAb VL (Vk)

<400> SEQUENCE: 109

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 Lys Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35                  40                  45

Pro Gln Leu Leu Ile Cys Leu Gly Ser Tyr 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 Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105                 110
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<210> SEQ ID NO 110
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-20 mAb CDRL1

<400> SEQUENCE: 110

Gln Ser Leu Leu His Ser Asn Gly Lys Asn Tyr
1 5 10

<210> SEQ ID NO 111
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-20 mAb CDRL2

<400> SEQUENCE: 111

Leu Gly Ser
1

<210> SEQ ID NO 112
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-20 mAb CDRL3

<400> SEQUENCE: 112

Met Gln Ala Leu Gln Thr Pro Trp Thr
1 5

<210> SEQ ID NO 113
<211> LENGTH: 370
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4 mAb VH

<400> SEQUENCE: 113

caggtgcaac tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgaag cctctggatt caccctcaga accagtagtc tccactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atatcaaatg atggagccac taaattctac 180

gcagacgccg tgaagggccg attcaccatc tccagagaca actccaacaa caaaatatat 240

ctgcaactga acggcctgaa acctgaggac acggctgtct attactgtgc gagagaaaca 300

cgtcattaca gccatggttt gaactggttc gacccctggg gccagggaac cctggtcaac 360

gtctcctcag 370

<210> SEQ ID NO 114
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4 mAb CDRH1

<400> SEQUENCE: 114

ggattcaccc tcagaaccag tagt 24

-continued

<210> SEQ ID NO 115
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4 mAb CDRH2

<400> SEQUENCE: 115

atatcaaatg atggagccac taaa 24

<210> SEQ ID NO 116
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4 mAb CDRH3

<400> SEQUENCE: 116

gcgagagaaa cacgtcatta cagccatggt ttgaactggt tcgacccc 48

<210> SEQ ID NO 117
<211> LENGTH: 98
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4 mAb VH

<400> SEQUENCE: 117

Gly Phe Thr Leu Arg Thr Ser Ser Leu His Trp Val Arg Gln Ala Pro
1 5 10 15

Gly Lys Gly Leu Glu Trp Val Ala Val Ile Ser Asn Asp Gly Ala Thr
20 25 30

Lys Phe Tyr Ala Asp Ala Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
35 40 45

Asn Ser Asn Asn Lys Ile Tyr Leu Gln Leu Asn Gly Leu Lys Pro Glu
50 55 60

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Thr Arg His Tyr Ser His
65 70 75 80

Gly Leu Asn Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Asn Val
85 90 95

Ser Ser

<210> SEQ ID NO 118
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4 mAb CDRH1

<400> SEQUENCE: 118

Gly Phe Thr Leu Arg Thr Ser Ser
1 5

<210> SEQ ID NO 119
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4 mAb CDRH2

<400> SEQUENCE: 119

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Ile Ser Asn Asp Gly Ala Thr Lys
1 5

<210> SEQ ID NO 120
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4 mAb CDRH3

<400> SEQUENCE: 120

Ala Arg Glu Thr Arg His Tyr Ser His Gly Leu Asn Trp Phe Asp Pro
1 5 10 15

<210> SEQ ID NO 121
<211> LENGTH: 322
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4 mAb VL (Vk)

<400> SEQUENCE: 121

gaaagagtga tgacgcagtc tccagtcacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcgacttag cctggtacca gcagaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240

gaagattttg cagtttatta ctgtcagcag tataataact ggccgaccac cttcggccaa 300

gggacacgac tggacattaa ac 322

<210> SEQ ID NO 122
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4 mAb CDRL1

<400> SEQUENCE: 122

cagagtgtta gcagcgac 18

<210> SEQ ID NO 123
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4 mAb CDRL2

<400> SEQUENCE: 123

ggtgcatcc 9

<210> SEQ ID NO 124
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4 mAb CDRL3

<400> SEQUENCE: 124

cagcagtata ataactggcc gaccacc 27

-continued

<210> SEQ ID NO 125
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4 mAb VL (Vk)

<400> SEQUENCE: 125

Glu Arg Val Met Thr Gln Ser Pro Val 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 Asp
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 Thr
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Asp Ile Lys
100 105

<210> SEQ ID NO 126
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4 mAb CDRL1

<400> SEQUENCE: 126

Gln Ser Val Ser Ser Asp
1 5

<210> SEQ ID NO 127
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4 mAb CDRL2

<400> SEQUENCE: 127

Gly Ala Ser
1

<210> SEQ ID NO 128
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4 mAb CDRL3

<400> SEQUENCE: 128

Gln Gln Tyr Asn Asn Trp Pro Thr Thr
1 5

<210> SEQ ID NO 129
<211> LENGTH: 370
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4-v2(N to T) mAb VH

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<400> SEQUENCE: 129

caggtgcaac tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgaag cctctggatt caccctcaga accagtagtc tccactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atatcaaatg atggagccac taaattctac 180

gcagacgccg tgaagggccg attcaccatc tccagagaca actccaacaa caaaatatat 240

ctgcaactga acggcctgaa acctgaggac acggctgtct attactgtgc gagagaaaca 300

cgtcattaca gccatggttt gaactggttc gacccctggg gccagggaac cctggtcacc 360

gtctcctcag 370

<210> SEQ ID NO 130
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4-v2 mAb CDRH1

<400> SEQUENCE: 130

ggattcaccc tcagaaccag tagt 24

<210> SEQ ID NO 131
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4-v2 mAb CDRH2

<400> SEQUENCE: 131

atatcaaatg atggagccac taaa 24

<210> SEQ ID NO 132
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4-v2 mAb CDRH3

<400> SEQUENCE: 132

gcgagagaaa cacgtcatta cagccatggt ttgaactggt tcgacccc 48

<210> SEQ ID NO 133
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4-v2 (NVS to TVS) mAb
VH

<400> SEQUENCE: 133

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 Glu Ala Ser Gly Phe Thr Leu Arg Thr Ser
20 25 30

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

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

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

Leu Gln Leu Asn Gly Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Thr Arg His Tyr Ser His Gly Leu Asn Trp Phe Asp Pro
            100                 105                 110

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


<210> SEQ ID NO 134
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4-v2 mAb CDRH1

<400> SEQUENCE: 134

Gly Phe Thr Leu Arg Thr Ser Ser
1               5


<210> SEQ ID NO 135
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4-v2 mAb CDRH2

<400> SEQUENCE: 135

Ile Ser Asn Asp Gly Ala Thr Lys
1               5


<210> SEQ ID NO 136
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4-v2 mAb CDRH3

<400> SEQUENCE: 136

Ala Arg Glu Thr Arg His Tyr Ser His Gly Leu Asn Trp Phe Asp Pro
1               5                   10                  15


<210> SEQ ID NO 137
<211> LENGTH: 322
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4-v2 mAb VL (Vk)

<400> SEQUENCE: 137

gaaagagtga tgacgcagtc tccagtcacc ctgtctgtgt ctccagggga aagagccacc      60

ctctcctgca gggccagtca gagtgttagc agcgacttag cctggtacca gcagaaacct     120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc     180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct     240

gaagattttg cagtttatta ctgtcagcag tataataact ggccgaccac cttcggccaa     300

gggacacgac tggacattaa ac                                              322


<210> SEQ ID NO 138
<211> LENGTH: 18
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4-v2 mAb CDRL1

<400> SEQUENCE: 138

cagagtgtta gcagcgac 18

<210> SEQ ID NO 139
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV4-v2 mAb CDRL2

<400> SEQUENCE: 139

ggtgcatcc 9

<210> SEQ ID NO 140
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4-v2 mAb CDRL3

<400> SEQUENCE: 140

cagcagtata ataactggcc gaccacc 27

<210> SEQ ID NO 141
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4-v2 mAb VL (Vk)

<400> SEQUENCE: 141

Glu Arg Val Met Thr Gln Ser Pro Val 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 Asp
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 Thr
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Asp Ile Lys
100 105

<210> SEQ ID NO 142
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4-v2 mAb CDRL1

<400> SEQUENCE: 142

Gln Ser Val Ser Ser Asp
1 5

-continued

<210> SEQ ID NO 143
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4-v2 mAb CDRL2

<400> SEQUENCE: 143

Gly Ala Ser
1

<210> SEQ ID NO 144
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4-v2 mAb CDRL3

<400> SEQUENCE: 144

Gln Gln Tyr Asn Asn Trp Pro Thr Thr
1 5

<210> SEQ ID NO 145
<211> LENGTH: 370
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4-v3(N to T) mAb VH

<400> SEQUENCE: 145

caggtgcaac tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgaag cctctggatt caccctcaga accagtagtc tccactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atatcaaatg atggagccac taaattctac 180

gcagacgccg tgaagggccg attcaccatc tccagagaca actccaacaa caaaatatat 240

ctgcaactga acggcctgaa acctgaggac acggctgtct attactgtgc gagagaaaca 300

cgtcattaca gccatggttt gaactggttc gacccctggg gccagggaac cctggtcacc 360

gtctcctcag 370

<210> SEQ ID NO 146
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4-v3 mAb CDRH1

<400> SEQUENCE: 146

ggattcaccc tcagaaccag tagt 24

<210> SEQ ID NO 147
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4-v3 mAb CDRH2

<400> SEQUENCE: 147

atatcaaatg atggagccac taaa 24

-continued

<210> SEQ ID NO 148
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4-v3 mAb CDRH3

<400> SEQUENCE: 148

gcgagagaaa cacgtcatta cagccatggt ttgaactggt tcgacccc 48

<210> SEQ ID NO 149
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4-v3(N to T) mAb VH

<400> SEQUENCE: 149

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 Glu Ala Ser Gly Phe Thr Leu Arg Thr Ser
20 25 30

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

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

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

Leu Gln Leu Asn Gly Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Thr Arg His Tyr Ser His Gly Leu Asn Trp Phe Asp Pro
100 105 110

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

<210> SEQ ID NO 150
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4-v3 mAb CDRH1

<400> SEQUENCE: 150

Gly Phe Thr Leu Arg Thr Ser Ser
1 5

<210> SEQ ID NO 151
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4-v3 mAb CDRH2

<400> SEQUENCE: 151

Ile Ser Asn Asp Gly Ala Thr Lys
1 5

<210> SEQ ID NO 152
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

-continued

<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4-v3 mAb CDRH3

<400> SEQUENCE: 152

Ala Arg Glu Thr Arg His Tyr Ser His Gly Leu Asn Trp Phe Asp Pro
1 5 10 15

<210> SEQ ID NO 153
<211> LENGTH: 322
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4-v3 (W to F) mAb VL
(Vk)

<400> SEQUENCE: 153

gaaagagtga tgacgcagtc tccagtcacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcgacttag cctggtacca gcagaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240

gaagattttg cagtttatta ctgtcagcag tataataact tcccgaccac cttcggccaa 300

gggacacgac tggacattaa ac 322

<210> SEQ ID NO 154
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4-v3 mAb CDRL1

<400> SEQUENCE: 154

cagagtgtta gcagcgac 18

<210> SEQ ID NO 155
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4-v3 mAb CDRL2

<400> SEQUENCE: 155

ggtgcatcc 9

<210> SEQ ID NO 156
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4-v3 mAb CDRL3

<400> SEQUENCE: 156

cagcagtata ataacttccc gaccacc 27

<210> SEQ ID NO 157
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4-v3 (W to F) mAb VL
(Vk)

-continued

<400> SEQUENCE: 157

Glu Arg Val Met Thr Gln Ser Pro Val 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 Asp
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 Phe Pro Thr
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Asp Ile Lys
100 105

<210> SEQ ID NO 158
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4-v3 mAb CDRL1

<400> SEQUENCE: 158

Gln Ser Val Ser Ser Asp
1 5

<210> SEQ ID NO 159
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4-v3 mAb CDRL2

<400> SEQUENCE: 159

Gly Ala Ser
1

<210> SEQ ID NO 160
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-4-v3 mAb CDRL3

<400> SEQUENCE: 160

Gln Gln Tyr Asn Asn Phe Pro Thr Thr
1 5

<210> SEQ ID NO 161
<211> LENGTH: 352
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-15 mAb VH

<400> SEQUENCE: 161

gaggtgcagc tggtggagtc tgggggaggc ttggtaacgc cagggcggtc cctgagactc 60

tcctgtacag cttctggatt cacgtttggt gattatgctc tgagctggtt ccgccaggct 120

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ccagggaagg ggctggagtg ggtagctttc attagaagca aagcttatgg tgggacaaca    180

gaatacgccg cgtctgtgaa aggcagattc accatctcaa gagatgattc gcaaatcatt    240

gtctatctgc aaatggacag cctgaaaacc gaagacacag ccgtatatta ttgtagttgg    300

atacaccgga tagtctcctg gggccaggga accctggtca ccgtctcctc ag            352


<210> SEQ ID NO 162
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-15 mAb CDRH1

<400> SEQUENCE: 162

ggattcacgt ttggtgatta tgct                                            24


<210> SEQ ID NO 163
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-15 mAb CDRH2

<400> SEQUENCE: 163

attagaagca aagcttatgg tgggacaaca                                      30


<210> SEQ ID NO 164
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-15 mAb CDRH3

<400> SEQUENCE: 164

agttggatac accggatagt ctcc                                            24


<210> SEQ ID NO 165
<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-15 mAb VH

<400> SEQUENCE: 165

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

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Gly Asp Tyr
            20                  25                  30

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

Ala Phe Ile Arg Ser Lys Ala Tyr Gly Gly Thr Thr Glu Tyr Ala Ala
    50                  55                  60

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

Val Tyr Leu Gln Met Asp Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Tyr Cys Ser Trp Ile His Arg Ile Val Ser Trp Gly Gln Gly Thr Leu
            100                 105                 110

Val Thr Val Ser Ser
```

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115

<210> SEQ ID NO 166
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-15 mAb CDRH1

<400> SEQUENCE: 166

Gly Phe Thr Phe Gly Asp Tyr Ala
1 5

<210> SEQ ID NO 167
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-15 mAb CDRH2

<400> SEQUENCE: 167

Ile Arg Ser Lys Ala Tyr Gly Gly Thr Thr
1 5 10

<210> SEQ ID NO 168
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-15 mAb CDRH3

<400> SEQUENCE: 168

Ser Trp Ile His Arg Ile Val Ser
1 5

<210> SEQ ID NO 169
<211> LENGTH: 322
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-15 mAb VL (Vk)

<400> SEQUENCE: 169

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgaaggaga cagagtcacc 60

atcacttgcc aggcgagtca ggacattagc atctatttaa attggtttca gcagaaacca 120

gggaaagccc ctaagctcct gatctacgag gcatccaatt tgaaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct 240

gaagatattg caacatatta ctgtcaacag tatgataatc tcccctacac ttttggccag 300

gggaccaagc tggagatcaa ac 322

<210> SEQ ID NO 170
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-15 mAb CDRL1

<400> SEQUENCE: 170

caggacatta gcatctat 18

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<210> SEQ ID NO 171
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-15 mAb CDRL2

<400> SEQUENCE: 171

gaggcatcc 9

<210> SEQ ID NO 172
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-15 mAb CDRL3

<400> SEQUENCE: 172

caacagtatg ataatctccc ctacact 27

<210> SEQ ID NO 173
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-15 mAb VL (Vk)

<400> SEQUENCE: 173

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Glu Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Ile Tyr
20 25 30

Leu Asn Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Glu Ala Ser Asn Leu Lys Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> SEQ ID NO 174
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-15 mAb CDRL1

<400> SEQUENCE: 174

Gln Asp Ile Ser Ile Tyr
1 5

<210> SEQ ID NO 175
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-15 mAb CDRL2

<400> SEQUENCE: 175

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Glu Ala Ser
1

<210> SEQ ID NO 176
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-15 mAb CDRL3

<400> SEQUENCE: 176

Gln Gln Tyr Asp Asn Leu Pro Tyr Thr
1 5

<210> SEQ ID NO 177
<211> LENGTH: 370
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-12 mAb VH

<400> SEQUENCE: 177

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag gctctggatt caccttcagt agctttggtt tgcactgggt ccgccaggcg 120

ccaggcaagg gactggagtg gttggcactt atttcagatg agggacgcat taaatactac 180

gcaaactccg tgaagggccg attctttatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag aggtgaggac acggctgtat attactgtgc gagagatgtc 300

aaaggacata ttgtggtgat gacttctctt gactactggg gccagggagc cctggtcacc 360

gtctcctcag 370

<210> SEQ ID NO 178
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-12 mAb CDRH1

<400> SEQUENCE: 178

ggattcacct tcagtagctt tggt 24

<210> SEQ ID NO 179
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-12 mAb CDRH2

<400> SEQUENCE: 179

atttcagatg agggacgcat taaa 24

<210> SEQ ID NO 180
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-12 mAb CDRH3

<400> SEQUENCE: 180

gcgagagatg tcaaaggaca tattgtggtg atgacttctc ttgactac 48

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<210> SEQ ID NO 181
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-12 mAb VH

<400> SEQUENCE: 181

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 Gly Ser Gly Phe Thr Phe Ser Ser Phe
20 25 30

Gly Leu His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Ala Leu Ile Ser Asp Glu Gly Arg Ile Lys Tyr Tyr Ala Asn Ser Val
50 55 60

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

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

Ala Arg Asp Val Lys Gly His Ile Val Val Met Thr Ser Leu Asp Tyr
100 105 110

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

<210> SEQ ID NO 182
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-12 mAb CDRH1

<400> SEQUENCE: 182

Gly Phe Thr Phe Ser Ser Phe Gly
1 5

<210> SEQ ID NO 183
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-12 mAb CDRH2

<400> SEQUENCE: 183

Ile Ser Asp Glu Gly Arg Ile Lys
1 5

<210> SEQ ID NO 184
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-12 mAb CDRH3

<400> SEQUENCE: 184

Ala Arg Asp Val Lys Gly His Ile Val Val Met Thr Ser Leu Asp Tyr
1 5 10 15

<210> SEQ ID NO 185

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<211> LENGTH: 337
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-12 mAb VL (Vk)

<400> SEQUENCE: 185

gatgttgtga tgactcagtc tccactctcc ctgcccgtca cccttggaca gccggcctcc 60

atctcctgta ggtctagtca aagcctcgtc tccagtgatg gagacacctc cttgagttgg 120

tttcagcaga ggccaggcca atctccaagg cgcctaattt atgaggtttc taaccgggac 180

tctggggtcc cagacagatt cagcggcagt gggtcaggca ctgatttcac actgaaaatc 240

agcagggtgg aggctgagga tgttggggtt tattactgca tgcaaggtac acactggcct 300

ccgacgttcg gccaagggac caaggtggaa atcaaac 337

<210> SEQ ID NO 186
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-12 mAb CDRL1

<400> SEQUENCE: 186

caaagcctcg tctccagtga tggagacacc tcc 33

<210> SEQ ID NO 187
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-12 mAb CDRL2

<400> SEQUENCE: 187

gaggtttct 9

<210> SEQ ID NO 188
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-12 mAb CDRL3

<400> SEQUENCE: 188

atgcaaggta cacactggcc tccgacg 27

<210> SEQ ID NO 189
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-12 mAb VL (Vk)

<400> SEQUENCE: 189

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Ser Ser
20 25 30

Asp Gly Asp Thr Ser Leu Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Glu Val Ser Asn Arg Asp Ser Gly Val Pro

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    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 Gly
                85                  90                  95

Thr His Trp Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> SEQ ID NO 190
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-12 mAb CDRL1

<400> SEQUENCE: 190

Gln Ser Leu Val Ser Ser Asp Gly Asp Thr Ser
1               5                   10


<210> SEQ ID NO 191
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-12 mAb CDRL2

<400> SEQUENCE: 191

Glu Val Ser
1


<210> SEQ ID NO 192
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-12 mAb CDRL3

<400> SEQUENCE: 192

Met Gln Gly Thr His Trp Pro Pro Thr
1               5


<210> SEQ ID NO 193
<211> LENGTH: 376
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-5 mAb VH

<400> SEQUENCE: 193

caaatgcagc tggtgcagtc tgggcctgag atgaagaagc ctgggacctc agtgaaggtc     60

tcctgcaagg cctctggatt cacttttagt aaaactacct tgcagtgggt acgtcaggct    120

cgtggacaac gccctgagtg gataggatgg atcgtccttg gcagcggtaa cacaaactac    180

gcacattact tccaggcaag agtcaccatt accagggaca tgtccacgag cacagcctac    240

atggaactga gcagcctgag ttccgaggac acggccgtct attactgtgc ggcagagatg    300

gctacaattc agaattacta ttactactat ggtatggacg tctggggcca agggaccacg    360

gtcaccgtct cctcag                                                    376


<210> SEQ ID NO 194
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<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-5 mAb CDRH1

<400> SEQUENCE: 194

ggattcactt ttagtaaaac tacc 24

<210> SEQ ID NO 195
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-5 mAb CDRH2

<400> SEQUENCE: 195

atcgtccttg gcagcggtaa caca 24

<210> SEQ ID NO 196
<211> LENGTH: 54
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-5 mAb CDRH3

<400> SEQUENCE: 196

gcggcagaga tggctacaat tcagaattac tattactact atggtatgga cgtc 54

<210> SEQ ID NO 197
<211> LENGTH: 125
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-5 mAb VH

<400> SEQUENCE: 197

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

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

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

Gly Trp Ile Val Leu Gly Ser Gly Asn Thr Asn Tyr Ala His Tyr Phe
50 55 60

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

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

Ala Ala Glu Met Ala Thr Ile Gln Asn Tyr Tyr Tyr Tyr Tyr Gly Met
100 105 110

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

<210> SEQ ID NO 198
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-5 mAb CDRH1

-continued

<400> SEQUENCE: 198

Gly Phe Thr Phe Ser Lys Thr Thr
1 5

<210> SEQ ID NO 199
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-5 mAb CDRH2

<400> SEQUENCE: 199

Ile Val Leu Gly Ser Gly Asn Thr
1 5

<210> SEQ ID NO 200
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-5 mAb CDRH3

<400> SEQUENCE: 200

Ala Ala Glu Met Ala Thr Ile Gln Asn Tyr Tyr Tyr Tyr Tyr Gly Met
1 5 10 15

Asp Val

<210> SEQ ID NO 201
<211> LENGTH: 322
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-5 mAb VL (Vk)

<400> SEQUENCE: 201

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtcgggga cagagtcacc 60

atcacttgcc gggcaagtca gagcattaac tactatttaa attggtatca gcagaaacct 120

gggaaagccc ctaacctcct gatctatgct gcatccagtt tgcctggtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcaccag tctgcaacct 240

gaggattttg caacttactt ctgtcaacag agttacagta cccctccgac ttttggccag 300

gggaccaagc tggagatcaa ac 322

<210> SEQ ID NO 202
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-5 mAb CDRL1

<400> SEQUENCE: 202

cagagcatta actactat 18

<210> SEQ ID NO 203
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-5 mAb CDRL2

<400> SEQUENCE: 203

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gctgcatcc 9

<210> SEQ ID NO 204
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-5 mAb CDRL3

<400> SEQUENCE: 204

caacagagtt acagtacccc tccgact 27

<210> SEQ ID NO 205
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-5 mAb VL (Vk)

<400> SEQUENCE: 205

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 Asn Tyr Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Pro Gly Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Ser Tyr Ser Thr Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> SEQ ID NO 206
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-5 mAb CDRL1

<400> SEQUENCE: 206

Gln Ser Ile Asn Tyr Tyr
1 5

<210> SEQ ID NO 207
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-5 mAb CDRL2

<400> SEQUENCE: 207

Ala Ala Ser
1

<210> SEQ ID NO 208
<211> LENGTH: 9
<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-5 mAb CDRL3

<400> SEQUENCE: 208

Gln Gln Ser Tyr Ser Thr Pro Pro Thr
1 5

<210> SEQ ID NO 209
<211> LENGTH: 367
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-14 mAb VH

<400> SEQUENCE: 209

caggtgcagc tggtgcactc tggggctgag gtgaagaagc ctggggcctc agtgagggtc 60

tcctgcaagg cctctggata cacctacacc gcctactata tacactggct gcggcaggcc 120

cctggacaag ggcttgagtg gatgggatgg atcaacgctg acaatggtga cacacactct 180

gtgcagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcaa tacagcctac 240

ctggaggtga gcaggctgaa gtctgacgac acggccgtct attattgtgc gagaggagac 300

gttccagttg gtactggctg ggtctttgac ttctggggcc agggaaccct ggtcaccgtc 360

tcctcag 367

<210> SEQ ID NO 210
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-14 mAb CDRH1

<400> SEQUENCE: 210

ggatacacct acaccgccta ctat 24

<210> SEQ ID NO 211
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-14 mAb CDRH2

<400> SEQUENCE: 211

atcaacgctg acaatggtga caca 24

<210> SEQ ID NO 212
<211> LENGTH: 45
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-14 mAb CDRH3

<400> SEQUENCE: 212

gcgagaggag acgttccagt tggtactggc tgggtctttg acttc 45

<210> SEQ ID NO 213
<211> LENGTH: 122
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-14 mAb VH

-continued

<400> SEQUENCE: 213

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

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

Tyr Ile His Trp Leu Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Ala Asp Asn Gly Asp Thr His Ser Val Gln Lys Phe
50 55 60

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

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

Ala Arg Gly Asp Val Pro Val Gly Thr Gly Trp Val Phe Asp Phe Trp
100 105 110

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

<210> SEQ ID NO 214
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-14 mAb CDRH1

<400> SEQUENCE: 214

Gly Tyr Thr Tyr Thr Ala Tyr Tyr
1 5

<210> SEQ ID NO 215
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-14 mAb CDRH2

<400> SEQUENCE: 215

Ile Asn Ala Asp Asn Gly Asp Thr
1 5

<210> SEQ ID NO 216
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-14 mAb CDRH3

<400> SEQUENCE: 216

Ala Arg Gly Asp Val Pro Val Gly Thr Gly Trp Val Phe Asp Phe
1 5 10 15

<210> SEQ ID NO 217
<211> LENGTH: 319
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-14 mAb VL (Vk)

<400> SEQUENCE: 217

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gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtgggaga cagcgtcacc     60

atcagttgcc gggcaagtca gaccattaac aactttttaa attggtacca gcagaagcca    120

gggaaagccc ctaacctcct gatctatggt gcatacaatt tgcaaagtgg ggtcccatca    180

aggttcagtg gcagtggatc cgggacagat ttcactctca ccatcagcag cctgcaacct    240

gaggatgttg caatttacta ttgtcaacag agtctcagta tggtcacctt cggccaaggg    300

acacgactgg acattaaac                                                 319


<210> SEQ ID NO 218
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-14 mAb CDRL1

<400> SEQUENCE: 218

cagaccatta acaacttt                                                   18


<210> SEQ ID NO 219
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-14 mAb CDRL2

<400> SEQUENCE: 219

ggtgcatac                                                              9


<210> SEQ ID NO 220
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-14 mAb CDRL3

<400> SEQUENCE: 220

caacagagtc tcagtatggt cacc                                            24


<210> SEQ ID NO 221
<211> LENGTH: 106
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-14 mAb VL (Vk)

<400> SEQUENCE: 221

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Ser Val Thr Ile Ser Cys Arg Ala Ser Gln Thr Ile Asn Asn Phe
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
        35                  40                  45

Tyr Gly Ala Tyr Asn 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 Ile Tyr Tyr Cys Gln Gln Ser Leu Ser Met Val Thr
                85                  90                  95
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Phe Gly Gln Gly Thr Arg Leu Asp Ile Lys
100 105

<210> SEQ ID NO 222
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-14 mAb CDRL1

<400> SEQUENCE: 222

Gln Thr Ile Asn Asn Phe
1 5

<210> SEQ ID NO 223
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-14 mAb CDRL2

<400> SEQUENCE: 223

Gly Ala Tyr
1

<210> SEQ ID NO 224
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-14 mAb CDRL3

<400> SEQUENCE: 224

Gln Gln Ser Leu Ser Met Val Thr
1 5

<210> SEQ ID NO 225
<211> LENGTH: 379
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-9 mAb VH

<400> SEQUENCE: 225

caggtgcttc tggtggagtc tgggggaggc gtggtccagc ctgggatgtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt tcctatgcta tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atctcatatg atggaagcac taaattctac 180

gcagactccg tgaggggccg attccccatc tccagagaca attccaagaa cacggtgtat 240

ctgcaaatga acagcctgag acctgaggac acggcagtct attactgtgc gacagttagt 300

gtcgaggggt ataccagtgg ctggtatttg ggaacccttg acttctgggg ccagggaacc 360

ccggtcaccg tctcctcag 379

<210> SEQ ID NO 226
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-9 mAb CDRH1

<400> SEQUENCE: 226

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```
ggattcacct tcagttccta tgct                                          24


<210> SEQ ID NO 227
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-9 mAb CDRH2

<400> SEQUENCE: 227

atctcatatg atggaagcac taaa                                          24


<210> SEQ ID NO 228
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-9 mAb CDRH3

<400> SEQUENCE: 228

gcgacagtta gtgtcgaggg gtataccagt ggctggtatt tgggaaccct tgacttc        57


<210> SEQ ID NO 229
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-9 mAb VH

<400> SEQUENCE: 229

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

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

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

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

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

Ala Thr Val Ser Val Glu Gly Tyr Thr Ser Gly Trp Tyr Leu Gly Thr
            100                 105                 110

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


<210> SEQ ID NO 230
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-9 mAb CDRH1

<400> SEQUENCE: 230

Gly Phe Thr Phe Ser Ser Tyr Ala
1               5


<210> SEQ ID NO 231
<211> LENGTH: 8
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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-9 mAb CDRH2

<400> SEQUENCE: 231

Ile Ser Tyr Asp Gly Ser Thr Lys
1 5

<210> SEQ ID NO 232
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-9 mAb CDRH3

<400> SEQUENCE: 232

Cys Ala Thr Val Ser Val Glu Gly Tyr Thr Ser Gly Trp Tyr Leu Gly
1 5 10 15

Thr Leu Asp Phe
20

<210> SEQ ID NO 233
<211> LENGTH: 322
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-9 mAb VL (Vk)

<400> SEQUENCE: 233

gaaagagtga tgacgcagtt tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagt agcaacttag cctggtacca gcagaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccattgg tgtcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240

gaagattttg cagtttatta ctgtcagcag tataataact ggccgggaac ttttggccag 300

gggaccaagc tggagatcaa ac 322

<210> SEQ ID NO 234
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-9 mAb CDRL1

<400> SEQUENCE: 234

cagagtgtta gtagcaac 18

<210> SEQ ID NO 235
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-9 mAb CDRL2

<400> SEQUENCE: 235

ggtgcatcc 9

<210> SEQ ID NO 236
<211> LENGTH: 27
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-9 mAb CDRL3

<400> SEQUENCE: 236

cagcagtata ataactggcc gggaact 27

<210> SEQ ID NO 237
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-9 mAb VL (Vk)

<400> SEQUENCE: 237

Glu Arg Val Met Thr Gln Phe 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 Ile 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 Tyr Cys Gln Gln Tyr Asn Asn Trp Pro Gly
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> SEQ ID NO 238
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-9 mAb CDRL1

<400> SEQUENCE: 238

Gln Ser Val Ser Ser Asn
1 5

<210> SEQ ID NO 239
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-9 mAb CDRL2

<400> SEQUENCE: 239

Gly Ala Ser
1

<210> SEQ ID NO 240
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-9 mAb CDRL3

<400> SEQUENCE: 240

Gln Gln Tyr Asn Asn Trp Pro Gly Thr

-continued

1 5

<210> SEQ ID NO 241
<211> LENGTH: 367
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-18 mAb VH

<400> SEQUENCE: 241

caggttcagc tggtgcagtc tggagctgag gtgaggcagc ctgggacctc agtgaaggtc 60

tcctgcaagg cttctggtta cacctttatg aataatgata tcacctgggt gcgacaggcc 120

cctggacagg tgcttcagtg gatggggtgg atcaggcctt ccaatggaaa cacaaactac 180

gcacagaagt tccagggcag agtcaccctg accacagaca catccacgaa cacagcccac 240

atggaactga ggagcctgaa atctgacgac acggccgtgt attattgtgc gagacaatct 300

cattcgacgc ggggtggctg gcacttcagc ccctggggcc agggaaccct ggtcaccgtc 360

tcctcag 367

<210> SEQ ID NO 242
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-18 mAb CDRH1

<400> SEQUENCE: 242

ggttacacct ttatgaataa tgat 24

<210> SEQ ID NO 243
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-18 mAb CDRH2

<400> SEQUENCE: 243

atcaggcctt ccaatggaaa caca 24

<210> SEQ ID NO 244
<211> LENGTH: 45
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-18 mAb CDRH3

<400> SEQUENCE: 244

gcgagacaat ctcattcgac gcggggtggc tggcacttca gcccc 45

<210> SEQ ID NO 245
<211> LENGTH: 122
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-18 mAb VH

<400> SEQUENCE: 245

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Met Asn Asn

-continued

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            20                  25                  30

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

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

Gln Gly Arg Val Thr Leu Thr Thr Asp Thr Ser Thr Asn Thr Ala His
65                  70                  75                  80

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

Ala Arg Gln Ser His Ser Thr Arg Gly Gly Trp His Phe Ser Pro Trp
            100                 105                 110

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


<210> SEQ ID NO 246
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-18 mAb CDRH1

<400> SEQUENCE: 246

Gly Tyr Thr Phe Met Asn Asn Asp
1               5


<210> SEQ ID NO 247
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-18 mAb CDRH2

<400> SEQUENCE: 247

Ile Arg Pro Ser Asn Gly Asn Thr
1               5


<210> SEQ ID NO 248
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-18 mAb CDRH3

<400> SEQUENCE: 248

Ala Arg Gln Ser His Ser Thr Arg Gly Gly Trp His Phe Ser Pro
1               5                   10                  15


<210> SEQ ID NO 249
<211> LENGTH: 322
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-18 mAb VL (Vk)

<400> SEQUENCE: 249

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc      60

atcacttgcc ggccaagtca acccattagc tactttttaa attggtatca gcagacacca     120

gggaaagccc ctaagctcct catctatgct gcatccagtt tgcaaagtgg ggtcccatca     180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct     240
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gaagattctg caacttacta ctgtcaacag agttatagtg tcccgtacac ttttggccag 300

gggaccaagc tggagatcaa ac 322

<210> SEQ ID NO 250
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-18 mAb CDRL1

<400> SEQUENCE: 250

caacccatta gctacttt 18

<210> SEQ ID NO 251
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-18 mAb CDRL2

<400> SEQUENCE: 251

gctgcatcc 9

<210> SEQ ID NO 252
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-18 mAb CDRL3

<400> SEQUENCE: 252

caacagagtt atagtgtccc gtacact 27

<210> SEQ ID NO 253
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-18 mAb VL (Vk)

<400> SEQUENCE: 253

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 Pro Ser Gln Pro Ile Ser Tyr Phe
20 25 30

Leu Asn Trp Tyr Gln Gln Thr Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser 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 Ser Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Val Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> SEQ ID NO 254
<211> LENGTH: 6
<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-18 mAb CDRL1

<400> SEQUENCE: 254

Gln Pro Ile Ser Tyr Phe
1 5

<210> SEQ ID NO 255
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-18 mAb CDRL2

<400> SEQUENCE: 255

Ala Ala Ser
1

<210> SEQ ID NO 256
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-18 mAb CDRL3

<400> SEQUENCE: 256

Gln Gln Ser Tyr Ser Val Pro Tyr Thr
1 5

<210> SEQ ID NO 257
<211> LENGTH: 382
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-8 mAb VH

<400> SEQUENCE: 257

gaagtgctcc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgtag tctctggatt cacctttgat tattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attagttgga atagtgataa cacagactat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgaa aactgaggac acggccttgt attactgtgc aaaagatatt 300

agtctagttt tttggagtgt taaccctccc cgtaacggaa tggacgtctg gggccaaggg 360

accacggtca ccgtctcctc ag 382

<210> SEQ ID NO 258
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-8 mAb CDRH1

<400> SEQUENCE: 258

ggattcacct ttgattatta tgcc 24

<210> SEQ ID NO 259
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-8 mAb CDRH2

<400> SEQUENCE: 259

attagttgga atagtgataa caca 24

<210> SEQ ID NO 260
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-8 mAb CDRH3

<400> SEQUENCE: 260

gcaaaagata ttagtctagt tttttggagt gttaaccctc cccgtaacgg aatggacgtc 60

<210> SEQ ID NO 261
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-8 mAb VH

<400> SEQUENCE: 261

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

Ser Leu Arg Leu Ser Cys Val Val Ser Gly Phe Thr Phe Asp Tyr Tyr
20 25 30

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

Ser Gly Ile Ser Trp Asn Ser Asp Asn Thr Asp Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Asp Ile Ser Leu Val Phe Trp Ser Val Asn Pro Pro Arg Asn
100 105 110

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

<210> SEQ ID NO 262
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-8 mAb CDRH1

<400> SEQUENCE: 262

Gly Phe Thr Phe Asp Tyr Tyr Ala Met
1 5

<210> SEQ ID NO 263
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-8 mAb CDRH2

<400> SEQUENCE: 263

-continued

Ile Ser Trp Asn Ser Asp Asn Thr
1 5

<210> SEQ ID NO 264
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-8 mAb CDRH3

<400> SEQUENCE: 264

Ala Lys Asp Ile Ser Leu Val Phe Trp Ser Val Asn Pro Pro Arg Asn
1 5 10 15

Gly Met Asp Val
20

<210> SEQ ID NO 265
<211> LENGTH: 322
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-8 mAb VL (Vk)

<400> SEQUENCE: 265

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattcgc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaacctcct gatctatact gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg cgacttacta ctgtcaacag agttacagtt cccctctcac tttcggcgga 300

gggaccaagg tggagatcaa ac 322

<210> SEQ ID NO 266
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-8 mAb CDRL1

<400> SEQUENCE: 266

cagagcattc gcagctat 18

<210> SEQ ID NO 267
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-8 mAb CDRL2

<400> SEQUENCE: 267

actgcatcc 9

<210> SEQ ID NO 268
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-8 mAb CDRL3

<400> SEQUENCE: 268

caacagagtt acagttcccc tctcact 27

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<210> SEQ ID NO 269
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-8 mAb VL (Vk)

<400> SEQUENCE: 269

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 Arg Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
35 40 45

Tyr Thr Ala Ser Ser 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 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ser Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> SEQ ID NO 270
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-8 mAb CDRL1

<400> SEQUENCE: 270

Gln Ser Ile Arg Ser Tyr
1 5

<210> SEQ ID NO 271
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-8 mAb CDRL2

<400> SEQUENCE: 271

Thr Ala Ser
1

<210> SEQ ID NO 272
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-8 mAb CDRL3

<400> SEQUENCE: 272

Gln Gln Ser Tyr Ser Ser Pro Leu Thr
1 5

<210> SEQ ID NO 273
<211> LENGTH: 367
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-7 mAb VH

<400> SEQUENCE: 273

caggagcagg tggtggagtc tgggggaggc gtggtccagc ctgggaagtc cctgagactc 60

tcctgtgcag cctctggatt cagcttgaat gactttgcta tccactgggt ccgccaggct 120

ccaggcaaga ggctggagtg ggtggcaatc atatcatacg atggaagggt taaattttac 180

gcagactcag tgaagggccg attcaccatc tcccgagact cttccgtgca tctgcaaatg 240

gacagcctga gacctgagga cacgggtctg tattactgtg cgagagactc ttcgtggcag 300

agcactgggt ggcctataaa ctggttcgac cgctggggcc ggggaaccct ggtcaccgtc 360

tcctcag 367

<210> SEQ ID NO 274
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-7 mAb CDRH1

<400> SEQUENCE: 274

ggattcagct tgaatgactt tgct 24

<210> SEQ ID NO 275
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-7 mAb CDRH2

<400> SEQUENCE: 275

atatcatacg atggaagggt taaa 24

<210> SEQ ID NO 276
<211> LENGTH: 54
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-7 mAb CDRH3

<400> SEQUENCE: 276

gcgagagact cttcgtggca gagcactggg tggcctataa actggttcga ccgc 54

<210> SEQ ID NO 277
<211> LENGTH: 122
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-7 mAb VH

<400> SEQUENCE: 277

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu Asn Asp Phe
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Lys Arg Leu Glu Trp Val
35 40 45

Ala Ile Ile Ser Tyr Asp Gly Arg Val Lys Phe Tyr Ala Asp Ser Val
50 55 60

-continued

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Lys Gly Arg Phe Thr Ile Ser Arg Asp Ser Ser Val His Leu Gln Met
65                  70                  75                  80

Asp Ser Leu Arg Pro Glu Asp Thr Gly Leu Tyr Tyr Cys Ala Arg Asp
                85                  90                  95

Ser Ser Trp Gln Ser Thr Gly Trp Pro Ile Asn Trp Phe Asp Arg Trp
            100                 105                 110

Gly Arg Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> SEQ ID NO 278
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-7 mAb CDRH1

<400> SEQUENCE: 278

Gly Phe Ser Leu Asn Asp Phe Ala
1               5


<210> SEQ ID NO 279
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-7 mAb CDRH2

<400> SEQUENCE: 279

Ile Ser Tyr Asp Gly Arg Val Lys
1               5


<210> SEQ ID NO 280
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-7 mAb CDRH3

<400> SEQUENCE: 280

Ala Arg Asp Ser Ser Trp Gln Ser Thr Gly Trp Pro Ile Asn Trp Phe
1               5                   10                  15

Asp Arg


<210> SEQ ID NO 281
<211> LENGTH: 322
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-7 mAb VL (Vk)

<400> SEQUENCE: 281

gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggca aagagccacc      60

ctctcctgca gggccagtca gagtgttctc agctccttag cctggtacca gcacaaacct     120

ggccaggctc ccaggctcct catctatgat gcatccagca gggccactgg cgtcccagcc     180

aggttcagtg gcagtgggtc tgagacagac ttcactctca ccatcagcag cctagagcct     240

gaagattttg cagtttatta ctgtcagcag cgtagcaact ggcctccgac gttcggccaa     300

gggaccaagg tggaaatcaa ac                                              322
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<210> SEQ ID NO 282
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-7 mAb CDRL1

<400> SEQUENCE: 282

cagagtgttc tcagctcc 18

<210> SEQ ID NO 283
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-7 mAb CDRL2

<400> SEQUENCE: 283

gatgcatcc 9

<210> SEQ ID NO 284
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-7 mAb CDRL3

<400> SEQUENCE: 284

cagcagcgta gcaactggcc tccgacg 27

<210> SEQ ID NO 285
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-7 mAb VL (Vk)

<400> SEQUENCE: 285

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

Gln Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Leu Ser Ser
20 25 30

Leu Ala Trp Tyr Gln His Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Glu Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> SEQ ID NO 286
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-7 mAb CDRL1

<400> SEQUENCE: 286

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Gln Ser Val Leu Ser Ser
1 5

<210> SEQ ID NO 287
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-7 mAb CDRL2

<400> SEQUENCE: 287

Asp Ala Ser
1

<210> SEQ ID NO 288
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-7 mAb CDRL3

<400> SEQUENCE: 288

Gln Gln Arg Ser Asn Trp Pro Pro Thr
1 5

<210> SEQ ID NO 289
<211> LENGTH: 358
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-2 mAb VH

<400> SEQUENCE: 289

gacgtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cagctttagc agctatgcca tgacctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaact atgagtgcta gtggggatag cacaaacgac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgttt 240

ctgcaaatga acagcctcag acccgaggac acggccgtat attactgtgc gtcccccctt 300

cggaattatg gtgacttgct ctactggggc cagggaaccc tggtcaccgt ctcctccg 358

<210> SEQ ID NO 290
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-2 mAb CDRH1

<400> SEQUENCE: 290

ggattcagct ttagcagcta tgcc 24

<210> SEQ ID NO 291
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-2 mAb CDRH2

<400> SEQUENCE: 291

atgagtgcta gtggggatag caca 24

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<210> SEQ ID NO 292
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-2 mAb CDRH3

<400> SEQUENCE: 292

gcgtcccccc ttcggaatta tggtgacttg ctctac 36

<210> SEQ ID NO 293
<211> LENGTH: 119
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-2 mAb VH

<400> SEQUENCE: 293

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
20 25 30

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

Ala Thr Met Ser Ala Ser Gly Asp Ser Thr Asn Asp Ala Asp Ser Val
50 55 60

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

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

Ala Ser Pro Leu Arg Asn Tyr Gly Asp Leu Leu Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> SEQ ID NO 294
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequencenCoV-2 mAb CDRH1

<400> SEQUENCE: 294

Gly Phe Ser Phe Ser Ser Tyr Ala
1 5

<210> SEQ ID NO 295
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-2 mAb CDRH2

<400> SEQUENCE: 295

Met Ser Ala Ser Gly Asp Ser Thr
1 5

<210> SEQ ID NO 296
<211> LENGTH: 12
<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-2 mAb CDRH3

<400> SEQUENCE: 296

Ala Ser Pro Leu Arg Asn Tyr Gly Asp Leu Leu Tyr
1 5 10

<210> SEQ ID NO 297
<211> LENGTH: 322
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-2 mAb VL (Vk)

<400> SEQUENCE: 297

gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggccagtca gaatattcat cgtttttttgg cctggtatca gcagaaacca 120

gggaaagccc ctaaactcct gatctatacg gcgtctagtt tagaaagtgg ggtcccatca 180

aggttcagcg gcagtggatt tgggacagaa ttcactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaacaa tataatagtt actcgtggac gttcggccaa 300

gggaccaagg tggaaatcaa ac 322

<210> SEQ ID NO 298
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-2 mAb CDRL1

<400> SEQUENCE: 298

cagaatattc atcgtttt 18

<210> SEQ ID NO 299
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-2 mAb CDRL2

<400> SEQUENCE: 299

acggcgtct 9

<210> SEQ ID NO 300
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-2 mAb CDRL3

<400> SEQUENCE: 300

caacaatata atagttactc gtggacg 27

<210> SEQ ID NO 301
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-2 mAb VL (Vk)

<400> SEQUENCE: 301

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Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile His Arg Phe
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Thr Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Phe Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ser Trp
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105


<210> SEQ ID NO 302
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-2 mAb CDRL1

<400> SEQUENCE: 302

Gln Asn Ile His Arg Phe
1               5


<210> SEQ ID NO 303
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-2 mAb CDRL2

<400> SEQUENCE: 303

Thr Ala Ser
1


<210> SEQ ID NO 304
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-2 mAb CDRL3

<400> SEQUENCE: 304

Gln Gln Tyr Asn Ser Tyr Ser Trp Thr
1               5


<210> SEQ ID NO 305
<211> LENGTH: 370
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-19 mAb VH

<400> SEQUENCE: 305

caggtgaagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc      60

tcctgtgcag cctctggatt caccttcagt agcaatgcta tgcactgggt ccgccagact     120

ccaggcaagg ggctggagtg ggtggcactt atatcatatg atgaaaggaa taaatactac     180
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gcagagtccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat    240

ctgcaaatga acagcctgag acatgaggac acggctgtgt attactgtgc gagagatctg    300

caaatgagag tagtggttgt ttcaaacttt gactactggg gccagggaac cctggtcacc    360

gtctcctcag                                                           370


<210> SEQ ID NO 306
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-19 mAb CDRH1

<400> SEQUENCE: 306

ggattcacct tcagtagcaa tgct                                            24


<210> SEQ ID NO 307
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-19 mAb CDRH2

<400> SEQUENCE: 307

atatcatatg atgaaaggaa taaa                                            24


<210> SEQ ID NO 308
<211> LENGTH: 49
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-19 mAb CDRH3

<400> SEQUENCE: 308

gcgagagatc tgcaaatgag agtagtggtt gtttcaaact ttgactact                 49


<210> SEQ ID NO 309
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-19 mAb VH

<400> SEQUENCE: 309

Gln Val Lys 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 Asn
            20                  25                  30

Ala Met His Trp Val Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Leu Ile Ser Tyr Asp Glu Arg Asn Lys Tyr Tyr Ala Glu 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 His Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Leu Gln Met Arg Val Val Val Val Ser Asn Phe Asp Tyr
            100                 105                 110
```

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


<210> SEQ ID NO 310
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-19 mAb CDRH1

<400> SEQUENCE: 310

Gly Phe Thr Phe Ser Ser Asn Ala
1               5


<210> SEQ ID NO 311
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-19 mAb CDRH2

<400> SEQUENCE: 311

Ile Ser Tyr Asp Glu Arg Asn Lys
1               5


<210> SEQ ID NO 312
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-19 mAb CDRH3

<400> SEQUENCE: 312

Ala Arg Asp Leu Gln Met Arg Val Val Val Val Ser Asn Phe Asp Tyr
1               5                   10                  15


<210> SEQ ID NO 313
<211> LENGTH: 337
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-19 mAb VL (Vk)

<400> SEQUENCE: 313

gatgttgtga tgactcagtc tccactctcc ctgcccgtca cccttggaca gccggcctcc     60

atctcctgca ggtctagtca aagcctcgta tacagtgatg gaaacaccta cttgaattgg    120

tttcagcaga ggccaggcca atctccaagg cgcctaattt atgaggtttc taactgggac    180

tctggggtcc cagacagatt cagcggcagt gggtcaggca ctgatttcac actgaaaatc    240

agcagggtgg aggctgagga tgttggggtt tattactgca tgcaagctac acactggcct    300

cccacttttg gccaggggac caagctggag atcaaac                             337


<210> SEQ ID NO 314
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-19 mAb CDRL1

<400> SEQUENCE: 314

caaagcctcg tatacagtga tggaaacacc tac                                  33
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<210> SEQ ID NO 315
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-19 mAb CDRL2

<400> SEQUENCE: 315

gaggtttct 9

<210> SEQ ID NO 316
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-19 mAb CDRL3

<400> SEQUENCE: 316

atgcaagcta cacactggcc tcccact 27

<210> SEQ ID NO 317
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-19 mAb VL (Vk)

<400> SEQUENCE: 317

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Ser
20 25 30

Asp Gly Asn Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Glu Val Ser Asn Trp Asp 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

Thr His Trp Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> SEQ ID NO 318
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-19 mAb CDRL1

<400> SEQUENCE: 318

Gln Ser Leu Val Tyr Ser Asp Gly Asn Thr Tyr
1 5 10

<210> SEQ ID NO 319
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-19 mAb CDRL2

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<400> SEQUENCE: 319

Glu Val Ser
1

<210> SEQ ID NO 320
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-19 mAb CDRL3

<400> SEQUENCE: 320

Met Gln Ala Thr His Trp Pro Pro Thr
1 5

<210> SEQ ID NO 321
<211> LENGTH: 382
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-1 mAb VH

<400> SEQUENCE: 321

caggcgcaac tggtggagtc tgggggagcc ttggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagg aattatgcta tgcactgggt ccgccaggct 120

ccagccacgg ggctgcagtg gctggcagtc ataacatctg atggaaggaa taaattctat 180

gcagactccg tgaagggccg attcaccatc tccagagagg attccaagaa cacgctgtat 240

ctgcaaatgg atagcctgag aggagaggac acggctgtct actactgcgt gacacagcgt 300

gataatagtc gcgattactt cccccactac ttccacgaca tggacgtctg gggccaaggg 360

accacggtcg ccgtctcctc ag 382

<210> SEQ ID NO 322
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-1 mAb CDRH1

<400> SEQUENCE: 322

ggattcacct tcaggaatta tgct 24

<210> SEQ ID NO 323
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-1 mAb CDRH2

<400> SEQUENCE: 323

ataacatctg atggaaggaa taaa 24

<210> SEQ ID NO 324
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-1 mAb CDRH3

<400> SEQUENCE: 324

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gtgacacagc gtgataatag tcgcgattac ttcccccact acttccacga catggacgtc 60

<210> SEQ ID NO 325
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-1 mAb VH

<400> SEQUENCE: 325

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asn Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Ala Thr Gly Leu Gln Trp Leu
35 40 45

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

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

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

Val Thr Gln Arg Asp Asn Ser Arg Asp Tyr Phe Pro His Tyr Phe His
100 105 110

Asp Met Asp Val Trp Gly Gln Gly Thr Thr Val Ala Val Ser Ser
115 120 125

<210> SEQ ID NO 326
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-1 mAb CDRH1

<400> SEQUENCE: 326

Gly Phe Thr Phe Arg Asn Tyr Ala
1 5

<210> SEQ ID NO 327
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-1 mAb CDRH2

<400> SEQUENCE: 327

Ile Thr Ser Asp Gly Arg Asn Lys
1 5

<210> SEQ ID NO 328
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-1 mAb CDRH3

<400> SEQUENCE: 328

Val Thr Gln Arg Asp Asn Ser Arg Asp Tyr Phe Pro His Tyr Phe His
1 5 10 15

Asp Met Asp Val

-continued

20

<210> SEQ ID NO 329
<211> LENGTH: 337
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-1 mAb VL (Vk)

<400> SEQUENCE: 329

gatgttgtgc tgactcagtc tccactctcc ctgcccgtca cccttggaca gccggcctcc 60

atctcctgca ggtctagtca aagcctcgtt tacagtgatg gagacaccta cttgaattgg 120

tttcagcaga ggccaggcca atctccaagg cgcctaattt atcaggtttc taatcgggac 180

tctggggtcc cagacagatt tagcggcagt gggtcaggca ctgatttcac actgaaaatc 240

agcagggtgg aggctgagga tgttggggtt tattactgca tgcaaggttc acactggcct 300

ccgacgttcg gccaagggac caaggtggaa atcaaac 337

<210> SEQ ID NO 330
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-1 mAb CDRL1

<400> SEQUENCE: 330

caaagcctcg tttacagtga tggagacacc tac 33

<210> SEQ ID NO 331
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-1 mAb CDRL2

<400> SEQUENCE: 331

caggtttct 9

<210> SEQ ID NO 332
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-1 mAb CDRL3

<400> SEQUENCE: 332

atgcaaggtt cacactggcc tccgacg 27

<210> SEQ ID NO 333
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-1 mAb VL (Vk)

<400> SEQUENCE: 333

Asp Val Val Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Ser
20 25 30

-continued

```
Asp Gly Asp Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
        35                  40                  45

Pro Arg Arg Leu Ile Tyr Gln Val Ser Asn Arg Asp 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 Gly
                85                  90                  95

Ser His Trp Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> SEQ ID NO 334
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-1 mAb CDRL1

<400> SEQUENCE: 334

Gln Ser Leu Val Tyr Ser Asp Gly Asp Thr Tyr
1               5                   10


<210> SEQ ID NO 335
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-1 mAb CDRL2

<400> SEQUENCE: 335

Gln Val Ser
1


<210> SEQ ID NO 336
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-1 mAb CDRL3

<400> SEQUENCE: 336

Met Gln Gly Ser His Trp Pro Pro Thr
1               5


<210> SEQ ID NO 337
<211> LENGTH: 373
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-11 mAb VH

<400> SEQUENCE: 337

ctggtgcaac tggtagagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc      60

tcctgtgcag gctctggatt cacctttagc agctatggca tgcactgggt ccgccagact     120

ccaggcaagg ggctggagtg ggtggcagtt atatcgtttg atggaaggaa caaattctac     180

gcagaccccg tgaagggtcg attcaccatc tccagagaca attccaagaa cacggtgttc     240

ttggaattgg atagcctgac aactgaggac acggcttttt attactgtgc gagagacgac     300

aacttggaca gacactggcc ccttcgactc gggggttact ggggccaggg aaccctggtc     360
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accgtctcct cag                                                        373


<210> SEQ ID NO 338
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-11 mAb CDRH1

<400> SEQUENCE: 338

ggattcacct ttagcagcta tggc                                             24


<210> SEQ ID NO 339
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-11 mAb CDRH2

<400> SEQUENCE: 339

atatcgtttg atggaaggaa caaa                                             24


<210> SEQ ID NO 340
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-11 mAb CDRH3

<400> SEQUENCE: 340

gcgagagacg acaacttgga cagacactgg ccccttcgac tcgggggtta c               51


<210> SEQ ID NO 341
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-11 mAb VH

<400> SEQUENCE: 341

Leu 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 Gly Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Gly Met His Trp Val Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Val Ile Ser Phe Asp Gly Arg Asn Lys Phe Tyr Ala Asp Pro Val
    50                  55                  60

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

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

Ala Arg Asp Asp Asn Leu Asp Arg His Trp Pro Leu Arg Leu Gly Gly
            100                 105                 110

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


<210> SEQ ID NO 342
<211> LENGTH: 8
<212> TYPE: PRT
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-11 mAb CDRH1

<400> SEQUENCE: 342

Gly Phe Thr Phe Ser Ser Tyr Gly
1 5

<210> SEQ ID NO 343
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-11 mAb CDRH2

<400> SEQUENCE: 343

Ile Ser Phe Asp Gly Arg Asn Lys
1 5

<210> SEQ ID NO 344
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-11 mAb CDRH3

<400> SEQUENCE: 344

Ala Arg Asp Asp Asn Leu Asp Arg His Trp Pro Leu Arg Leu Gly Gly
1 5 10 15

Tyr

<210> SEQ ID NO 345
<211> LENGTH: 337
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-11 mAb VL (Vk)

<400> SEQUENCE: 345

gaaattgtga tgactcagtc tccactctcc ctgcccgtca cccttggaca gccggcctcc 60

atctcctgca ggtctagtca agacctccta tacaatgatg gaggcaccga cttgaactgg 120

tttcagcaga ggccaggcca atctccaagg cgcctaattt acagggtttc taaccgggac 180

tctggggtcc cagacagatt cagcggcagt gggtcaggca gtgatttcac actgaaaatc 240

agcagggtgg aggctgagga tgttggaatt tattactgca tgcaaggtgc acactggcct 300

ccgactttcg gccctgggac caaagtggag atcaaac 337

<210> SEQ ID NO 346
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-11 mAb CDRL1

<400> SEQUENCE: 346

caagacctcc tatacaatga tggaggcacc gac 33

<210> SEQ ID NO 347
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-11 mAb CDRL2

<400> SEQUENCE: 347

agggtttct 9

<210> SEQ ID NO 348
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-11 mAb CDRL3

<400> SEQUENCE: 348

atgcaaggtg cacactggcc tccgact 27

<210> SEQ ID NO 349
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-11 mAb VL (Vk)

<400> SEQUENCE: 349

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Asp Leu Leu Tyr Asn
20 25 30

Asp Gly Gly Thr Asp Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Arg Val Ser Asn Arg Asp Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Ile Tyr Tyr Cys Met Gln Gly
85 90 95

Ala His Trp Pro Pro Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> SEQ ID NO 350
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-11 mAb CDRL1

<400> SEQUENCE: 350

Gln Asp Leu Leu Tyr Asn Asp Gly Gly Thr Asp
1 5 10

<210> SEQ ID NO 351
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-11 mAb CDRL2

<400> SEQUENCE: 351

Arg Val Ser
1

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<210> SEQ ID NO 352
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-11 mAb CDRL3

<400> SEQUENCE: 352

Met Gln Gly Ala His Trp Pro Pro Thr
1 5

<210> SEQ ID NO 353
<211> LENGTH: 355
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-13 mAb VH

<400> SEQUENCE: 353

gaggtgcagc tggtggagtc tgggggaggc ctggtcaagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt aactataaca tgaactgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcatcc attggtagta gtagcactta catatactcc 180

gcagactcag tgaagggccg attcaccatc tccagagaca acgccatgaa ctcgctgttt 240

ctgcaaatga agagcctgag agccgaggac acggctgtgt attactgtgc gagaggtttc 300

gagaggtact actttgactc ctggggccag ggaaccctgg tcaccgtctc ctcag 355

<210> SEQ ID NO 354
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-13 mAb CDRH1

<400> SEQUENCE: 354

ggattcacct tcagtaacta taac 24

<210> SEQ ID NO 355
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-13 mAb CDRH2

<400> SEQUENCE: 355

attggtagta gtagcactta cata 24

<210> SEQ ID NO 356
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-13 mAb CDRH3

<400> SEQUENCE: 356

gcgagaggtt tcgagaggta ctactttgac tcc 33

<210> SEQ ID NO 357
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-13 mAb VH

<400> SEQUENCE: 357

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 Tyr
20 25 30

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

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

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

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

Ala Arg Gly Phe Glu Arg Tyr Tyr Phe Asp Ser Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> SEQ ID NO 358
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-13 mAb CDRH1

<400> SEQUENCE: 358

Gly Phe Thr Phe Ser Asn Tyr Asn
1 5

<210> SEQ ID NO 359
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-13 mAb CDRH2

<400> SEQUENCE: 359

Ile Gly Ser Ser Ser Thr Tyr Ile
1 5

<210> SEQ ID NO 360
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-13 mAb CDRH3

<400> SEQUENCE: 360

Ala Arg Gly Phe Glu Arg Tyr Tyr Phe Asp Ser
1 5 10

<210> SEQ ID NO 361
<211> LENGTH: 331
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-13 mAb VL

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<400> SEQUENCE: 361

cagtctgtgc tgactcagcc accctcagcg tctgggaccc ccgggcagag ggtcaccatc 60

tcttgttctg gaagcacctc caacatcgga actaatgttg taaactggta ccagcagctc 120

ccaggaacgg cccccaaact cctcatctat agtaataatc agcggccctc ttgggtccct 180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag 240

tctgaggatg aggctgatta ttactgtgtg gcatgggatg acatcctgaa tgctgtggtc 300

ttcgccggag ggaccaagct gaccgtccta g 331

<210> SEQ ID NO 362
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-13 mAb CDRL1

<400> SEQUENCE: 362

acctccaaca tcggaactaa tgtt 24

<210> SEQ ID NO 363
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-13 mAb CDRL2

<400> SEQUENCE: 363

agtaataat 9

<210> SEQ ID NO 364
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-13 mAb CDRL3

<400> SEQUENCE: 364

gtggcatggg atgacatcct gaatgctgtg gtc 33

<210> SEQ ID NO 365
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-13 mAb VL

<400> SEQUENCE: 365

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

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

Val Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Ser Asn Asn Gln Arg Pro Ser Trp Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Val Ala Trp Asp Asp Ile Leu

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                85                  90                  95

Asn Ala Val Val Phe Ala Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110


<210> SEQ ID NO 366
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-13 mAb CDRL1

<400> SEQUENCE: 366

Thr Ser Asn Ile Gly Thr Asn Val
1               5


<210> SEQ ID NO 367
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-13 mAb CDRL2

<400> SEQUENCE: 367

Ser Asn Asn
1


<210> SEQ ID NO 368
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-13 mAb CDRL3

<400> SEQUENCE: 368

Val Ala Trp Asp Asp Ile Leu Asn Ala Val Val
1               5                   10


<210> SEQ ID NO 369
<211> LENGTH: 29902
<212> TYPE: DNA
<213> ORGANISM: betacoronavirus SARS coronavirus 2

<400> SEQUENCE: 369

attaaaggtt tataccttcc caggtaacaa accaaccaac tttcgatctc ttgtagatct      60

gttctctaaa cgaactttaa aatctgtgtg gctgtcactc ggctgcatgc ttagtgcact     120

cacgcagtat aattaataac taattactgt cgttgacagg acacgagtaa ctcgtctatc     180

ttctgcaggc tgcttacggt ttcgtccgtg ttgcagccga tcatcagcac atctaggttt     240

cgtccgggtg tgaccgaaag gtaagatgga gagccttgtc cctggtttca acgagaaaac     300

acacgtccaa ctcagtttgc ctgttttaca ggttcgcgac gtgctcgtac gtggctttgg     360

agactccgtg gaggaggtct tatcagaggc cgtcaacatc ttaaagatgg cacttgtggc     420

ttagtagaag ttgaaaaagg cgttttgcct caacttgaac agccctatgt gttcatcaaa     480

cgttcggatg ctcgaactgc acctcatggt catgttatgg ttgagctggt agcagaactc     540

gaaggcattc agtacggtcg tagtggtgag acacttggtg tccttgtccc tcatgtgggc     600

gaaataccag tggcttaccg caaggttctt cttcgtaaga acggtaataa aggagctggt     660

ggccatagtt acggcgccga tctaaagtca tttgacttag gcgacgagct tggcactgat     720
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ccttatgaag attttcaaga aaactggaac actaaacata gcagtggtgt tacccgtgaa    780
ctcatgcgtg agcttaacgg aggggcatac actcgctatg tcgataacaa cttctgtggc    840
cctgatggct accctcttga gtgcattaaa gaccttctag cacgtgctgg taaagcttca    900
tgcactttgt ccgaacaact ggactttatt gacactaaga ggggtgtata ctgctgccgt    960
gaacatgagc atgaaattgc ttggtacacg gaacgttctg aaaagagcta tgaattgcag   1020
acaccttttg aaattaaatt ggcaaagaaa tttgacacct tcaatgggga atgtccaaat   1080
tttgtatttc ccttaaattc cataatcaag actattcaac caagggttga aaagaaaaag   1140
cttgatggct ttatgggtag aattcgatct gtctatccag ttgcgtcacc aaatgaatgc   1200
aaccaaatgt gcctttcaac tctcatgaag tgtgatcatt gtggtgaaac ttcatggcag   1260
acgggcgatt ttgttaaagc cacttgcgaa ttttgtggca ctgagaattt gactaaagaa   1320
ggtgccacta cttgtggtta cttaccccaa aatgctgttg ttaaaattta ttgtccagca   1380
tgtcacaatt cagaagtagg acctgagcat agtcttgccg aataccataa tgaatctggc   1440
ttgaaaacca ttcttcgtaa gggtggtcgc actattgcct ttggaggctg tgtgttctct   1500
tatgttggtt gccataacaa gtgtgcctat tgggttccac gtgctagcgc taacataggt   1560
tgtaaccata caggtgttgt tggagaaggt tccgaaggtc ttaatgacaa ccttcttgaa   1620
atactccaaa aagagaaagt caacatcaat attgttggtg actttaaact taatgaagag   1680
atcgccatta ttttggcatc tttttctgct tccacaagtg cttttgtgga aactgtgaaa   1740
ggtttggatt ataaagcatt caaacaaatt gttgaatcct gtggtaattt taaagttaca   1800
aaaggaaaag ctaaaaaagg tgcctggaat attggtgaac agaaatcaat actgagtcct   1860
ctttatgcat ttgcatcaga ggctgctcgt gttgtacgat caattttctc ccgcactctt   1920
gaaactgctc aaaattctgt gcgtgtttta cagaaggccg ctataacaat actagatgga   1980
atttcacagt attcactgag actcattgat gctatgatgt tcacatctga tttggctact   2040
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ctaactaaca tctttggcac tgtttatgaa aaactcaaac ccgtccttga ttggcttgaa   2160
gagaagttta aggaaggtgt agagtttctt agagacggtt gggaaattgt taaatttatc   2220
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gagagtgttc agacattctt taagcttgta aataaatttt tggctttgtg tgctgactct   2340
atcattattg gtggagctaa acttaaagcc ttgaatttag gtgaaacatt tgtcacgcac   2400
tcaaagggat tgtacagaaa gtgtgttaaa tccagagaag aaactggcct actcatgcct   2460
ctaaaagccc caaaagaaat tatcttctta gagggagaaa cacttcccac agaagtgtta   2520
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gctgttgaag ctccattggt tggtacacca gtttgtatta acgggcttat gttgctcgaa   2640
atcaaagaca cagaaaagta ctgtgccctt gcacctaata tgatggtaac aaacaatacc   2700
ttcacactca aaggcggtgc accaacaaag gttacttttg gtgatgacac tgtgatagaa   2760
gtgcaaggtt acaagagtgt gaatatcact tttgaacttg atgaaaggat tgataaagta   2820
cttaatgaga agtgctctgc ctatacagtt gaactcggta cagaagtaaa tgagttcgcc   2880
tgtgttgtgg cagatgctgt cataaaaact ttgcaaccag tatctgaatt acttacacca   2940
ctgggcattg atttagatga gtggagtatg gctacatact acttatttga tgagtctggt   3000
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gagtttaaat tggcttcaca tatgtattgt tctttctacc ctccagatga ggatgaagaa   3060
gaaggtgatt gtgaagaaga agagtttgag ccatcaactc aatatgagta tggtactgaa   3120
gatgattacc aaggtaaacc tttggaattt ggtgccactt ctgctgctct tcaacctgaa   3180
gaagagcaag aagaagattg gttagatgat gatagtcaac aaactgttgg tcaacaagac   3240
ggcagtgagg acaatcagac aactactatt caaacaattg ttgaggttca acctcaatta   3300
gagatggaac ttacaccagt tgttcagact attgaagtga atagttttag tggttattta   3360
aaacttactg acaatgtata cattaaaaat gcagacattg tggaagaagc taaaaaggta   3420
aaaccaacag tggttgttaa tgcagccaat gtttacctta aacatggagg aggtgttgca   3480
ggagccttaa ataaggctac taacaatgcc atgcaagttg aatctgatga ttacatagct   3540
actaatggac cacttaaagt gggtggtagt tgtgttttaa gcggacacaa tcttgctaaa   3600
cactgtcttc atgttgtcgg cccaaatgtt aacaaaggtg aagacattca acttcttaag   3660
agtgcttatg aaaattttaa tcagcacgaa gttctacttg caccattatt atcagctggt   3720
atttttggtg ctgaccctat acattcttta agagtttgtg tagatactgt tcgcacaaat   3780
gtctacttag ctgtctttga taaaaatctc tatgacaaac ttgtttcaag ctttttggaa   3840
atgaagagtg aaaagcaagt tgaacaaaag atcgctgaga ttcctaaaga ggaagttaag   3900
ccatttataa ctgaaagtaa accttcagtt gaacagagaa aacaagatga taagaaaatc   3960
aaagcttgtg ttgaagaagt tacaacaact ctggaagaaa ctaagttcct cacagaaaac   4020
ttgttacttt atattgacat taatggcaat cttcatccag attctgccac tcttgttagt   4080
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ctagcgaaag ctttgagaaa agtgccaaca gacaattata taaccactta cccgggtcag   4260
ggtttaaatg gttacactgt agaggaggca aagacagtgc ttaaaaagtg taaaagtgcc   4320
ttttacattc taccatctat tatctctaat gagaagcaag aaattcttgg aactgtttct   4380
tggaatttgc gagaaatgct tgcacatgca gaagaaacac gcaaattaat gcctgtctgt   4440
gtggaaacta aagccatagt ttcaactata cagcgtaaat ataagggtat taaaatacaa   4500
gagggtgtgg ttgattatgg tgctagattt tacttttaca ccagtaaaac aactgtagcg   4560
tcacttatca acacacttaa cgatctaaat gaaactcttg ttacaatgcc acttggctat   4620
gtaacacatg gcttaaattt ggaagaagct gctcggtata tgagatctct caaagtgcca   4680
gctacagttt ctgtttcttc acctgatgct gttacagcgt ataatggtta tcttacttct   4740
tcttctaaaa cacctgaaga acattttatt gaaaccatct cacttgctgg ttcctataaa   4800
gattggtcct attctggaca atctacacaa ctaggtatag aatttcttaa gagaggtgat   4860
aaaagtgtat attacactag taatcctacc acattccacc tagatggtga agttatcacc   4920
tttgacaatc ttaagacact tctttctttg agagaagtga ggactattaa ggtgtttaca   4980
acagtagaca acattaacct ccacacgcaa gttgtggaca tgtcaatgac atatggacaa   5040
cagtttggtc caacttattt ggatggagct gatgttacta aaataaaacc tcataattca   5100
catgaaggta aaacatttta tgttttacct aatgatgaca ctctacgtgt tgaggctttt   5160
gagtactacc acacaactga tcctagtttt ctgggtaggt acatgtcagc attaaatcac   5220
actaaaaagt ggaaataccc acaagttaat ggtttaactt ctattaaatg ggcagataac   5280
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aactgttatc ttgccactgc attgttaaca ctccaacaaa tagagttgaa gtttaatcca   5340
cctgctctac aagatgctta ttacagagca agggctggtg aagctgctaa cttttgtgca   5400
cttatcttag cctactgtaa taagacagta ggtgagttag gtgatgttag agaaacaatg   5460
agttacttgt ttcaacatgc caatttagat tcttgcaaaa gagtcttgaa cgtggtgtgt   5520
aaaacttgtg gacaacagca gacaaccctt aagggtgtag aagctgttat gtacatgggc   5580
acactttctt atgaacaatt taagaaaggt gttcagatac cttgtacgtg tggtaaacaa   5640
gctacaaaat atctagtaca acaggagtca ccttttgtta tgatgtcagc accacctgct   5700
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Glu Gln Pro Tyr Val Phe Ile Lys Arg Ser Asp Ala Arg Thr Ala Pro
65                  70                  75                  80

His Gly His Val Met Val Glu Leu Val Ala Glu Leu Glu Gly Ile Gln
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Tyr Gly Arg Ser Gly Glu Thr Leu Gly Val Leu Val Pro His Val Gly
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Glu Ile Pro Val Ala Tyr Arg Lys Val Leu Leu Arg Lys Asn Gly Asn
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Lys Gly Ala Gly Gly His Ser Tyr Gly Ala Asp Leu Lys Ser Phe Asp
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Leu Gly Asp Glu Leu Gly Thr Asp Pro Tyr Glu Asp Phe Gln Glu Asn
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Trp Asn Thr Lys His Ser Ser Gly Val Thr Arg Glu Leu Met Arg Glu
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Leu Asn Gly Gly Ala Tyr Thr Arg Tyr Val Asp Asn Asn Phe Cys Gly
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Pro Asp Gly Tyr Pro Leu Glu Cys Ile Lys Asp Leu Leu Ala Arg Ala
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Gly Lys Ala Ser Cys Thr Leu Ser Glu Gln Leu Asp Phe Ile Asp Thr
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Lys Arg Gly Val Tyr Cys Cys Arg Glu His Glu His Glu Ile Ala Trp
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Tyr Thr Glu Arg Ser Glu Lys Ser Tyr Glu Leu Gln Thr Pro Phe Glu
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Ile Lys Leu Ala Lys Lys Phe Asp Thr Phe Asn Gly Glu Cys Pro Asn
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Phe Val Phe Pro Leu Asn Ser Ile Ile Lys Thr Ile Gln Pro Arg Val
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Glu Lys Lys Lys Leu Asp Gly Phe Met Gly Arg Ile Arg Ser Val Tyr
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Pro Val Ala Ser Pro Asn Glu Cys Asn Gln Met Cys Leu Ser Thr Leu
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Met Lys Cys Asp His Cys Gly Glu Thr Ser Trp Gln Thr Gly Asp Phe
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Tyr Cys Pro Ala Cys His Asn Ser Glu Val Gly Pro Glu His Ser Leu
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Ala Glu Tyr His Asn Glu Ser Gly Leu Lys Thr Ile Leu Arg Lys Gly
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Gly Arg Thr Ile Ala Phe Gly Gly Cys Val Phe Ser Tyr Val Gly Cys
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Cys Glu Ile Val Gly Gly Gln Ile Val Thr Cys Ala Lys Glu Ile Lys
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Glu Ser Val Gln Thr Phe Phe Lys Leu Val Asn Lys Phe Leu Ala Leu
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705                 710                 715                 720

Val Lys Ser Arg Glu Glu Thr Gly Leu Leu Met Pro Leu Lys Ala Pro
                725                 730                 735

Lys Glu Ile Ile Phe Leu Glu Gly Glu Thr Leu Pro Thr Glu Val Leu
            740                 745                 750

Thr Glu Glu Val Val Leu Lys Thr Gly Asp Leu Gln Pro Leu Glu Gln
        755                 760                 765

Pro Thr Ser Glu Ala Val Glu Ala Pro Leu Val Gly Thr Pro Val Cys
    770                 775                 780

Ile Asn Gly Leu Met Leu Leu Glu Ile Lys Asp Thr Glu Lys Tyr Cys
785                 790                 795                 800

Ala Leu Ala Pro Asn Met Met Val Thr Asn Asn Thr Phe Thr Leu Lys
                805                 810                 815

Gly Gly Ala Pro Thr Lys Val Thr Phe Gly Asp Asp Thr Val Ile Glu
            820                 825                 830

Val Gln Gly Tyr Lys Ser Val Asn Ile Thr Phe Glu Leu Asp Glu Arg
        835                 840                 845
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Ile Asp Lys Val Leu Asn Glu Lys Cys Ser Ala Tyr Thr Val Glu Leu
    850                 855                 860

Gly Thr Glu Val Asn Glu Phe Ala Cys Val Val Ala Asp Ala Val Ile
865                 870                 875                 880

Lys Thr Leu Gln Pro Val Ser Glu Leu Leu Thr Pro Leu Gly Ile Asp
                885                 890                 895

Leu Asp Glu Trp Ser Met Ala Thr Tyr Tyr Leu Phe Asp Glu Ser Gly
            900                 905                 910

Glu Phe Lys Leu Ala Ser His Met Tyr Cys Ser Phe Tyr Pro Pro Asp
        915                 920                 925

Glu Asp Glu Glu Glu Gly Asp Cys Glu Glu Glu Glu Phe Glu Pro Ser
    930                 935                 940

Thr Gln Tyr Glu Tyr Gly Thr Glu Asp Asp Tyr Gln Gly Lys Pro Leu
945                 950                 955                 960

Glu Phe Gly Ala Thr Ser Ala Ala Leu Gln Pro Glu Glu Glu Gln Glu
                965                 970                 975

Glu Asp Trp Leu Asp Asp Asp Ser Gln Gln Thr Val Gly Gln Gln Asp
            980                 985                 990

Gly Ser Glu Asp Asn Gln Thr Thr  Thr Ile Gln Thr Ile  Val Glu Val
        995                 1000                1005

Gln Pro  Gln Leu Glu Met Glu  Leu Thr Pro Val Val  Gln Thr Ile
    1010                1015                1020

Glu Val  Asn Ser Phe Ser Gly  Tyr Leu Lys Leu Thr  Asp Asn Val
    1025                1030                1035

Tyr Ile  Lys Asn Ala Asp Ile  Val Glu Glu Ala Lys  Lys Val Lys
    1040                1045                1050

Pro Thr  Val Val Val Asn Ala  Ala Asn Val Tyr Leu  Lys His Gly
    1055                1060                1065

Gly Gly  Val Ala Gly Ala Leu  Asn Lys Ala Thr Asn  Asn Ala Met
    1070                1075                1080

Gln Val  Glu Ser Asp Asp Tyr  Ile Ala Thr Asn Gly  Pro Leu Lys
    1085                1090                1095

Val Gly  Gly Ser Cys Val Leu  Ser Gly His Asn Leu  Ala Lys His
    1100                1105                1110

Cys Leu  His Val Val Gly Pro  Asn Val Asn Lys Gly  Glu Asp Ile
    1115                1120                1125

Gln Leu  Leu Lys Ser Ala Tyr  Glu Asn Phe Asn Gln  His Glu Val
    1130                1135                1140

Leu Leu  Ala Pro Leu Leu Ser  Ala Gly Ile Phe Gly  Ala Asp Pro
    1145                1150                1155

Ile His  Ser Leu Arg Val Cys  Val Asp Thr Val Arg  Thr Asn Val
    1160                1165                1170

Tyr Leu  Ala Val Phe Asp Lys  Asn Leu Tyr Asp Lys  Leu Val Ser
    1175                1180                1185

Ser Phe  Leu Glu Met Lys Ser  Glu Lys Gln Val Glu  Gln Lys Ile
    1190                1195                1200

Ala Glu  Ile Pro Lys Glu Glu  Val Lys Pro Phe Ile  Thr Glu Ser
    1205                1210                1215

Lys Pro  Ser Val Glu Gln Arg  Lys Gln Asp Asp Lys  Lys Ile Lys
    1220                1225                1230
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Ala Cys  Val Glu Glu Val Thr  Thr Thr Leu Glu Glu  Thr Lys Phe
    1235                 1240                 1245

Leu Thr  Glu Asn Leu Leu Leu  Tyr Ile Asp Ile Asn  Gly Asn Leu
    1250                 1255                 1260

His Pro  Asp Ser Ala Thr Leu  Val Ser Asp Ile Asp  Ile Thr Phe
    1265                 1270                 1275

Leu Lys  Lys Asp Ala Pro Tyr  Ile Val Gly Asp Val  Val Gln Glu
    1280                 1285                 1290

Gly Val  Leu Thr Ala Val Val  Ile Pro Thr Lys Lys  Ala Gly Gly
    1295                 1300                 1305

Thr Thr  Glu Met Leu Ala Lys  Ala Leu Arg Lys Val  Pro Thr Asp
    1310                 1315                 1320

Asn Tyr  Ile Thr Thr Tyr Pro  Gly Gln Gly Leu Asn  Gly Tyr Thr
    1325                 1330                 1335

Val Glu  Glu Ala Lys Thr Val  Leu Lys Lys Cys Lys  Ser Ala Phe
    1340                 1345                 1350

Tyr Ile  Leu Pro Ser Ile Ile  Ser Asn Glu Lys Gln  Glu Ile Leu
    1355                 1360                 1365

Gly Thr  Val Ser Trp Asn Leu  Arg Glu Met Leu Ala  His Ala Glu
    1370                 1375                 1380

Glu Thr  Arg Lys Leu Met Pro  Val Cys Val Glu Thr  Lys Ala Ile
    1385                 1390                 1395

Val Ser  Thr Ile Gln Arg Lys  Tyr Lys Gly Ile Lys  Ile Gln Glu
    1400                 1405                 1410

Gly Val  Val Asp Tyr Gly Ala  Arg Phe Tyr Phe Tyr  Thr Ser Lys
    1415                 1420                 1425

Thr Thr  Val Ala Ser Leu Ile  Asn Thr Leu Asn Asp  Leu Asn Glu
    1430                 1435                 1440

Thr Leu  Val Thr Met Pro Leu  Gly Tyr Val Thr His  Gly Leu Asn
    1445                 1450                 1455

Leu Glu  Glu Ala Ala Arg Tyr  Met Arg Ser Leu Lys  Val Pro Ala
    1460                 1465                 1470

Thr Val  Ser Val Ser Ser Pro  Asp Ala Val Thr Ala  Tyr Asn Gly
    1475                 1480                 1485

Tyr Leu  Thr Ser Ser Ser Lys  Thr Pro Glu Glu His  Phe Ile Glu
    1490                 1495                 1500

Thr Ile  Ser Leu Ala Gly Ser  Tyr Lys Asp Trp Ser  Tyr Ser Gly
    1505                 1510                 1515

Gln Ser  Thr Gln Leu Gly Ile  Glu Phe Leu Lys Arg  Gly Asp Lys
    1520                 1525                 1530

Ser Val  Tyr Tyr Thr Ser Asn  Pro Thr Thr Phe His  Leu Asp Gly
    1535                 1540                 1545

Glu Val  Ile Thr Phe Asp Asn  Leu Lys Thr Leu Leu  Ser Leu Arg
    1550                 1555                 1560

Glu Val  Arg Thr Ile Lys Val  Phe Thr Thr Val Asp  Asn Ile Asn
    1565                 1570                 1575

Leu His  Thr Gln Val Val Asp  Met Ser Met Thr Tyr  Gly Gln Gln
    1580                 1585                 1590

Phe Gly  Pro Thr Tyr Leu Asp  Gly Ala Asp Val Thr  Lys Ile Lys
    1595                 1600                 1605

Pro His  Asn Ser His Glu Gly  Lys Thr Phe Tyr Val  Leu Pro Asn
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    1610                1615                1620

Asp Asp  Thr Leu Arg Val Glu  Ala Phe Glu Tyr Tyr  His Thr Thr
    1625                1630                1635

Asp Pro  Ser Phe Leu Gly Arg  Tyr Met Ser Ala Leu  Asn His Thr
    1640                1645                1650

Lys Lys  Trp Lys Tyr Pro Gln  Val Asn Gly Leu Thr  Ser Ile Lys
    1655                1660                1665

Trp Ala  Asp Asn Asn Cys Tyr  Leu Ala Thr Ala Leu  Leu Thr Leu
    1670                1675                1680

Gln Gln  Ile Glu Leu Lys Phe  Asn Pro Pro Ala Leu  Gln Asp Ala
    1685                1690                1695

Tyr Tyr  Arg Ala Arg Ala Gly  Glu Ala Ala Asn Phe  Cys Ala Leu
    1700                1705                1710

Ile Leu  Ala Tyr Cys Asn Lys  Thr Val Gly Glu Leu  Gly Asp Val
    1715                1720                1725

Arg Glu  Thr Met Ser Tyr Leu  Phe Gln His Ala Asn  Leu Asp Ser
    1730                1735                1740

Cys Lys  Arg Val Leu Asn Val  Val Cys Lys Thr Cys  Gly Gln Gln
    1745                1750                1755

Gln Thr  Thr Leu Lys Gly Val  Glu Ala Val Met Tyr  Met Gly Thr
    1760                1765                1770

Leu Ser  Tyr Glu Gln Phe Lys  Lys Gly Val Gln Ile  Pro Cys Thr
    1775                1780                1785

Cys Gly  Lys Gln Ala Thr Lys  Tyr Leu Val Gln Gln  Glu Ser Pro
    1790                1795                1800

Phe Val  Met Met Ser Ala Pro  Pro Ala Gln Tyr Glu  Leu Lys His
    1805                1810                1815

Gly Thr  Phe Thr Cys Ala Ser  Glu Tyr Thr Gly Asn  Tyr Gln Cys
    1820                1825                1830

Gly His  Tyr Lys His Ile Thr  Ser Lys Glu Thr Leu  Tyr Cys Ile
    1835                1840                1845

Asp Gly  Ala Leu Leu Thr Lys  Ser Ser Glu Tyr Lys  Gly Pro Ile
    1850                1855                1860

Thr Asp  Val Phe Tyr Lys Glu  Asn Ser Tyr Thr Thr  Thr Ile Lys
    1865                1870                1875

Pro Val  Thr Tyr Lys Leu Asp  Gly Val Val Cys Thr  Glu Ile Asp
    1880                1885                1890

Pro Lys  Leu Asp Asn Tyr Tyr  Lys Lys Asp Asn Ser  Tyr Phe Thr
    1895                1900                1905

Glu Gln  Pro Ile Asp Leu Val  Pro Asn Gln Pro Tyr  Pro Asn Ala
    1910                1915                1920

Ser Phe  Asp Asn Phe Lys Phe  Val Cys Asp Asn Ile  Lys Phe Ala
    1925                1930                1935

Asp Asp  Leu Asn Gln Leu Thr  Gly Tyr Lys Lys Pro  Ala Ser Arg
    1940                1945                1950

Glu Leu  Lys Val Thr Phe Phe  Pro Asp Leu Asn Gly  Asp Val Val
    1955                1960                1965

Ala Ile  Asp Tyr Lys His Tyr  Thr Pro Ser Phe Lys  Lys Gly Ala
    1970                1975                1980

Lys Leu  Leu His Lys Pro Ile  Val Trp His Val Asn  Asn Ala Thr
    1985                1990                1995
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Asn Lys  Ala Thr Tyr Lys Pro  Asn Thr Trp Cys Ile  Arg Cys Leu
    2000                 2005                 2010

Trp Ser  Thr Lys Pro Val Glu  Thr Ser Asn Ser Phe  Asp Val Leu
    2015                 2020                 2025

Lys Ser  Glu Asp Ala Gln Gly  Met Asp Asn Leu Ala  Cys Glu Asp
    2030                 2035                 2040

Leu Lys  Pro Val Ser Glu Glu  Val Val Glu Asn Pro  Thr Ile Gln
    2045                 2050                 2055

Lys Asp  Val Leu Glu Cys Asn  Val Lys Thr Thr Glu  Val Val Gly
    2060                 2065                 2070

Asp Ile  Ile Leu Lys Pro Ala  Asn Asn Ser Leu Lys  Ile Thr Glu
    2075                 2080                 2085

Glu Val  Gly His Thr Asp Leu  Met Ala Ala Tyr Val  Asp Asn Ser
    2090                 2095                 2100

Ser Leu  Thr Ile Lys Lys Pro  Asn Glu Leu Ser Arg  Val Leu Gly
    2105                 2110                 2115

Leu Lys  Thr Leu Ala Thr His  Gly Leu Ala Ala Val  Asn Ser Val
    2120                 2125                 2130

Pro Trp  Asp Thr Ile Ala Asn  Tyr Ala Lys Pro Phe  Leu Asn Lys
    2135                 2140                 2145

Val Val  Ser Thr Thr Thr Asn  Ile Val Thr Arg Cys  Leu Asn Arg
    2150                 2155                 2160

Val Cys  Thr Asn Tyr Met Pro  Tyr Phe Phe Thr Leu  Leu Leu Gln
    2165                 2170                 2175

Leu Cys  Thr Phe Thr Arg Ser  Thr Asn Ser Arg Ile  Lys Ala Ser
    2180                 2185                 2190

Met Pro  Thr Thr Ile Ala Lys  Asn Thr Val Lys Ser  Val Gly Lys
    2195                 2200                 2205

Phe Cys  Leu Glu Ala Ser Phe  Asn Tyr Leu Lys Ser  Pro Asn Phe
    2210                 2215                 2220

Ser Lys  Leu Ile Asn Ile Ile  Ile Trp Phe Leu Leu  Leu Ser Val
    2225                 2230                 2235

Cys Leu  Gly Ser Leu Ile Tyr  Ser Thr Ala Ala Leu  Gly Val Leu
    2240                 2245                 2250

Met Ser  Asn Leu Gly Met Pro  Ser Tyr Cys Thr Gly  Tyr Arg Glu
    2255                 2260                 2265

Gly Tyr  Leu Asn Ser Thr Asn  Val Thr Ile Ala Thr  Tyr Cys Thr
    2270                 2275                 2280

Gly Ser  Ile Pro Cys Ser Val  Cys Leu Ser Gly Leu  Asp Ser Leu
    2285                 2290                 2295

Asp Thr  Tyr Pro Ser Leu Glu  Thr Ile Gln Ile Thr  Ile Ser Ser
    2300                 2305                 2310

Phe Lys  Trp Asp Leu Thr Ala  Phe Gly Leu Val Ala  Glu Trp Phe
    2315                 2320                 2325

Leu Ala  Tyr Ile Leu Phe Thr  Arg Phe Phe Tyr Val  Leu Gly Leu
    2330                 2335                 2340

Ala Ala  Ile Met Gln Leu Phe  Phe Ser Tyr Phe Ala  Val His Phe
    2345                 2350                 2355

Ile Ser  Asn Ser Trp Leu Met  Trp Leu Ile Ile Asn  Leu Val Gln
    2360                 2365                 2370
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Met Ala  Pro Ile Ser Ala Met  Val Arg Met Tyr Ile  Phe Phe Ala
    2375                 2380                 2385

Ser Phe  Tyr Tyr Val Trp Lys  Ser Tyr Val His Val  Val Asp Gly
    2390                 2395                 2400

Cys Asn  Ser Ser Thr Cys Met  Met Cys Tyr Lys Arg  Asn Arg Ala
    2405                 2410                 2415

Thr Arg  Val Glu Cys Thr Thr  Ile Val Asn Gly Val  Arg Arg Ser
    2420                 2425                 2430

Phe Tyr  Val Tyr Ala Asn Gly  Gly Lys Gly Phe Cys  Lys Leu His
    2435                 2440                 2445

Asn Trp  Asn Cys Val Asn Cys  Asp Thr Phe Cys Ala  Gly Ser Thr
    2450                 2455                 2460

Phe Ile  Ser Asp Glu Val Ala  Arg Asp Leu Ser Leu  Gln Phe Lys
    2465                 2470                 2475

Arg Pro  Ile Asn Pro Thr Asp  Gln Ser Ser Tyr Ile  Val Asp Ser
    2480                 2485                 2490

Val Thr  Val Lys Asn Gly Ser  Ile His Leu Tyr Phe  Asp Lys Ala
    2495                 2500                 2505

Gly Gln  Lys Thr Tyr Glu Arg  His Ser Leu Ser His  Phe Val Asn
    2510                 2515                 2520

Leu Asp  Asn Leu Arg Ala Asn  Asn Thr Lys Gly Ser  Leu Pro Ile
    2525                 2530                 2535

Asn Val  Ile Val Phe Asp Gly  Lys Ser Lys Cys Glu  Glu Ser Ser
    2540                 2545                 2550

Ala Lys  Ser Ala Ser Val Tyr  Tyr Ser Gln Leu Met  Cys Gln Pro
    2555                 2560                 2565

Ile Leu  Leu Leu Asp Gln Ala  Leu Val Ser Asp Val  Gly Asp Ser
    2570                 2575                 2580

Ala Glu  Val Ala Val Lys Met  Phe Asp Ala Tyr Val  Asn Thr Phe
    2585                 2590                 2595

Ser Ser  Thr Phe Asn Val Pro  Met Glu Lys Leu Lys  Thr Leu Val
    2600                 2605                 2610

Ala Thr  Ala Glu Ala Glu Leu  Ala Lys Asn Val Ser  Leu Asp Asn
    2615                 2620                 2625

Val Leu  Ser Thr Phe Ile Ser  Ala Ala Arg Gln Gly  Phe Val Asp
    2630                 2635                 2640

Ser Asp  Val Glu Thr Lys Asp  Val Val Glu Cys Leu  Lys Leu Ser
    2645                 2650                 2655

His Gln  Ser Asp Ile Glu Val  Thr Gly Asp Ser Cys  Asn Asn Tyr
    2660                 2665                 2670

Met Leu  Thr Tyr Asn Lys Val  Glu Asn Met Thr Pro  Arg Asp Leu
    2675                 2680                 2685

Gly Ala  Cys Ile Asp Cys Ser  Ala Arg His Ile Asn  Ala Gln Val
    2690                 2695                 2700

Ala Lys  Ser His Asn Ile Ala  Leu Ile Trp Asn Val  Lys Asp Phe
    2705                 2710                 2715

Met Ser  Leu Ser Glu Gln Leu  Arg Lys Gln Ile Arg  Ser Ala Ala
    2720                 2725                 2730

Lys Lys  Asn Asn Leu Pro Phe  Lys Leu Thr Cys Ala  Thr Thr Arg
    2735                 2740                 2745

Gln Val  Val Asn Val Val Thr  Thr Lys Ile Ala Leu  Lys Gly Gly
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    2750                2755                2760

Lys Ile  Val Asn Asn Trp Leu  Lys Gln Leu Ile Lys  Val Thr Leu
    2765                2770                2775

Val Phe  Leu Phe Val Ala Ala  Ile Phe Tyr Leu Ile  Thr Pro Val
    2780                2785                2790

His Val  Met Ser Lys His Thr  Asp Phe Ser Ser Glu  Ile Ile Gly
    2795                2800                2805

Tyr Lys  Ala Ile Asp Gly Gly  Val Thr Arg Asp Ile  Ala Ser Thr
    2810                2815                2820

Asp Thr  Cys Phe Ala Asn Lys  His Ala Asp Phe Asp  Thr Trp Phe
    2825                2830                2835

Ser Gln  Arg Gly Gly Ser Tyr  Thr Asn Asp Lys Ala  Cys Pro Leu
    2840                2845                2850

Ile Ala  Ala Val Ile Thr Arg  Glu Val Gly Phe Val  Val Pro Gly
    2855                2860                2865

Leu Pro  Gly Thr Ile Leu Arg  Thr Thr Asn Gly Asp  Phe Leu His
    2870                2875                2880

Phe Leu  Pro Arg Val Phe Ser  Ala Val Gly Asn Ile  Cys Tyr Thr
    2885                2890                2895

Pro Ser  Lys Leu Ile Glu Tyr  Thr Asp Phe Ala Thr  Ser Ala Cys
    2900                2905                2910

Val Leu  Ala Ala Glu Cys Thr  Ile Phe Lys Asp Ala  Ser Gly Lys
    2915                2920                2925

Pro Val  Pro Tyr Cys Tyr Asp  Thr Asn Val Leu Glu  Gly Ser Val
    2930                2935                2940

Ala Tyr  Glu Ser Leu Arg Pro  Asp Thr Arg Tyr Val  Leu Met Asp
    2945                2950                2955

Gly Ser  Ile Ile Gln Phe Pro  Asn Thr Tyr Leu Glu  Gly Ser Val
    2960                2965                2970

Arg Val  Val Thr Thr Phe Asp  Ser Glu Tyr Cys Arg  His Gly Thr
    2975                2980                2985

Cys Glu  Arg Ser Glu Ala Gly  Val Cys Val Ser Thr  Ser Gly Arg
    2990                2995                3000

Trp Val  Leu Asn Asn Asp Tyr  Tyr Arg Ser Leu Pro  Gly Val Phe
    3005                3010                3015

Cys Gly  Val Asp Ala Val Asn  Leu Leu Thr Asn Met  Phe Thr Pro
    3020                3025                3030

Leu Ile  Gln Pro Ile Gly Ala  Leu Asp Ile Ser Ala  Ser Ile Val
    3035                3040                3045

Ala Gly  Gly Ile Val Ala Ile  Val Val Thr Cys Leu  Ala Tyr Tyr
    3050                3055                3060

Phe Met  Arg Phe Arg Arg Ala  Phe Gly Glu Tyr Ser  His Val Val
    3065                3070                3075

Ala Phe  Asn Thr Leu Leu Phe  Leu Met Ser Phe Thr  Val Leu Cys
    3080                3085                3090

Leu Thr  Pro Val Tyr Ser Phe  Leu Pro Gly Val Tyr  Ser Val Ile
    3095                3100                3105

Tyr Leu  Tyr Leu Thr Phe Tyr  Leu Thr Asn Asp Val  Ser Phe Leu
    3110                3115                3120

Ala His  Ile Gln Trp Met Val  Met Phe Thr Pro Leu  Val Pro Phe
    3125                3130                3135
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Trp Ile  Thr Ile Ala Tyr Ile  Ile Cys Ile Ser Thr  Lys His Phe
    3140                 3145                 3150

Tyr Trp  Phe Phe Ser Asn Tyr  Leu Lys Arg Arg Val  Val Phe Asn
    3155                 3160                 3165

Gly Val  Ser Phe Ser Thr Phe  Glu Glu Ala Ala Leu  Cys Thr Phe
    3170                 3175                 3180

Leu Leu  Asn Lys Glu Met Tyr  Leu Lys Leu Arg Ser  Asp Val Leu
    3185                 3190                 3195

Leu Pro  Leu Thr Gln Tyr Asn  Arg Tyr Leu Ala Leu  Tyr Asn Lys
    3200                 3205                 3210

Tyr Lys  Tyr Phe Ser Gly Ala  Met Asp Thr Thr Ser  Tyr Arg Glu
    3215                 3220                 3225

Ala Ala  Cys Cys His Leu Ala  Lys Ala Leu Asn Asp  Phe Ser Asn
    3230                 3235                 3240

Ser Gly  Ser Asp Val Leu Tyr  Gln Pro Pro Gln Thr  Ser Ile Thr
    3245                 3250                 3255

Ser Ala  Val Leu Gln Ser Gly  Phe Arg Lys Met Ala  Phe Pro Ser
    3260                 3265                 3270

Gly Lys  Val Glu Gly Cys Met  Val Gln Val Thr Cys  Gly Thr Thr
    3275                 3280                 3285

Thr Leu  Asn Gly Leu Trp Leu  Asp Asp Val Val Tyr  Cys Pro Arg
    3290                 3295                 3300

His Val  Ile Cys Thr Ser Glu  Asp Met Leu Asn Pro  Asn Tyr Glu
    3305                 3310                 3315

Asp Leu  Leu Ile Arg Lys Ser  Asn His Asn Phe Leu  Val Gln Ala
    3320                 3325                 3330

Gly Asn  Val Gln Leu Arg Val  Ile Gly His Ser Met  Gln Asn Cys
    3335                 3340                 3345

Val Leu  Lys Leu Lys Val Asp  Thr Ala Asn Pro Lys  Thr Pro Lys
    3350                 3355                 3360

Tyr Lys  Phe Val Arg Ile Gln  Pro Gly Gln Thr Phe  Ser Val Leu
    3365                 3370                 3375

Ala Cys  Tyr Asn Gly Ser Pro  Ser Gly Val Tyr Gln  Cys Ala Met
    3380                 3385                 3390

Arg Pro  Asn Phe Thr Ile Lys  Gly Ser Phe Leu Asn  Gly Ser Cys
    3395                 3400                 3405

Gly Ser  Val Gly Phe Asn Ile  Asp Tyr Asp Cys Val  Ser Phe Cys
    3410                 3415                 3420

Tyr Met  His His Met Glu Leu  Pro Thr Gly Val His  Ala Gly Thr
    3425                 3430                 3435

Asp Leu  Glu Gly Asn Phe Tyr  Gly Pro Phe Val Asp  Arg Gln Thr
    3440                 3445                 3450

Ala Gln  Ala Ala Gly Thr Asp  Thr Thr Ile Thr Val  Asn Val Leu
    3455                 3460                 3465

Ala Trp  Leu Tyr Ala Ala Val  Ile Asn Gly Asp Arg  Trp Phe Leu
    3470                 3475                 3480

Asn Arg  Phe Thr Thr Thr Leu  Asn Asp Phe Asn Leu  Val Ala Met
    3485                 3490                 3495

Lys Tyr  Asn Tyr Glu Pro Leu  Thr Gln Asp His Val  Asp Ile Leu
    3500                 3505                 3510
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Gly Pro  Leu Ser Ala Gln Thr  Gly Ile Ala Val Leu  Asp Met Cys
    3515                 3520                 3525

Ala Ser  Leu Lys Glu Leu Leu  Gln Asn Gly Met Asn  Gly Arg Thr
    3530                 3535                 3540

Ile Leu  Gly Ser Ala Leu Leu  Glu Asp Glu Phe Thr  Pro Phe Asp
    3545                 3550                 3555

Val Val  Arg Gln Cys Ser Gly  Val Thr Phe Gln Ser  Ala Val Lys
    3560                 3565                 3570

Arg Thr  Ile Lys Gly Thr His  His Trp Leu Leu Leu  Thr Ile Leu
    3575                 3580                 3585

Thr Ser  Leu Leu Val Leu Val  Gln Ser Thr Gln Trp  Ser Leu Phe
    3590                 3595                 3600

Phe Phe  Leu Tyr Glu Asn Ala  Phe Leu Pro Phe Ala  Met Gly Ile
    3605                 3610                 3615

Ile Ala  Met Ser Ala Phe Ala  Met Met Phe Val Lys  His Lys His
    3620                 3625                 3630

Ala Phe  Leu Cys Leu Phe Leu  Leu Pro Ser Leu Ala  Thr Val Ala
    3635                 3640                 3645

Tyr Phe  Asn Met Val Tyr Met  Pro Ala Ser Trp Val  Met Arg Ile
    3650                 3655                 3660

Met Thr  Trp Leu Asp Met Val  Asp Thr Ser Leu Ser  Gly Phe Lys
    3665                 3670                 3675

Leu Lys  Asp Cys Val Met Tyr  Ala Ser Ala Val Val  Leu Leu Ile
    3680                 3685                 3690

Leu Met  Thr Ala Arg Thr Val  Tyr Asp Asp Gly Ala  Arg Arg Val
    3695                 3700                 3705

Trp Thr  Leu Met Asn Val Leu  Thr Leu Val Tyr Lys  Val Tyr Tyr
    3710                 3715                 3720

Gly Asn  Ala Leu Asp Gln Ala  Ile Ser Met Trp Ala  Leu Ile Ile
    3725                 3730                 3735

Ser Val  Thr Ser Asn Tyr Ser  Gly Val Val Thr Thr  Val Met Phe
    3740                 3745                 3750

Leu Ala  Arg Gly Ile Val Phe  Met Cys Val Glu Tyr  Cys Pro Ile
    3755                 3760                 3765

Phe Phe  Ile Thr Gly Asn Thr  Leu Gln Cys Ile Met  Leu Val Tyr
    3770                 3775                 3780

Cys Phe  Leu Gly Tyr Phe Cys  Thr Cys Tyr Phe Gly  Leu Phe Cys
    3785                 3790                 3795

Leu Leu  Asn Arg Tyr Phe Arg  Leu Thr Leu Gly Val  Tyr Asp Tyr
    3800                 3805                 3810

Leu Val  Ser Thr Gln Glu Phe  Arg Tyr Met Asn Ser  Gln Gly Leu
    3815                 3820                 3825

Leu Pro  Pro Lys Asn Ser Ile  Asp Ala Phe Lys Leu  Asn Ile Lys
    3830                 3835                 3840

Leu Leu  Gly Val Gly Gly Lys  Pro Cys Ile Lys Val  Ala Thr Val
    3845                 3850                 3855

Gln Ser  Lys Met Ser Asp Val  Lys Cys Thr Ser Val  Val Leu Leu
    3860                 3865                 3870

Ser Val  Leu Gln Gln Leu Arg  Val Glu Ser Ser Ser  Lys Leu Trp
    3875                 3880                 3885

Ala Gln  Cys Val Gln Leu His  Asn Asp Ile Leu Leu  Ala Lys Asp
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    3890                3895                3900

Thr Thr  Glu Ala Phe Glu Lys  Met Val Ser Leu Leu  Ser Val Leu
    3905                3910                3915

Leu Ser  Met Gln Gly Ala Val  Asp Ile Asn Lys Leu  Cys Glu Glu
    3920                3925                3930

Met Leu  Asp Asn Arg Ala Thr  Leu Gln Ala Ile Ala  Ser Glu Phe
    3935                3940                3945

Ser Ser  Leu Pro Ser Tyr Ala  Ala Phe Ala Thr Ala  Gln Glu Ala
    3950                3955                3960

Tyr Glu  Gln Ala Val Ala Asn  Gly Asp Ser Glu Val  Val Leu Lys
    3965                3970                3975

Lys Leu  Lys Lys Ser Leu Asn  Val Ala Lys Ser Glu  Phe Asp Arg
    3980                3985                3990

Asp Ala  Ala Met Gln Arg Lys  Leu Glu Lys Met Ala  Asp Gln Ala
    3995                4000                4005

Met Thr  Gln Met Tyr Lys Gln  Ala Arg Ser Glu Asp  Lys Arg Ala
    4010                4015                4020

Lys Val  Thr Ser Ala Met Gln  Thr Met Leu Phe Thr  Met Leu Arg
    4025                4030                4035

Lys Leu  Asp Asn Asp Ala Leu  Asn Asn Ile Ile Asn  Asn Ala Arg
    4040                4045                4050

Asp Gly  Cys Val Pro Leu Asn  Ile Ile Pro Leu Thr  Thr Ala Ala
    4055                4060                4065

Lys Leu  Met Val Val Ile Pro  Asp Tyr Asn Thr Tyr  Lys Asn Thr
    4070                4075                4080

Cys Asp  Gly Thr Thr Phe Thr  Tyr Ala Ser Ala Leu  Trp Glu Ile
    4085                4090                4095

Gln Gln  Val Val Asp Ala Asp  Ser Lys Ile Val Gln  Leu Ser Glu
    4100                4105                4110

Ile Ser  Met Asp Asn Ser Pro  Asn Leu Ala Trp Pro  Leu Ile Val
    4115                4120                4125

Thr Ala  Leu Arg Ala Asn Ser  Ala Val Lys Leu Gln  Asn Asn Glu
    4130                4135                4140

Leu Ser  Pro Val Ala Leu Arg  Gln Met Ser Cys Ala  Ala Gly Thr
    4145                4150                4155

Thr Gln  Thr Ala Cys Thr Asp  Asp Asn Ala Leu Ala  Tyr Tyr Asn
    4160                4165                4170

Thr Thr  Lys Gly Gly Arg Phe  Val Leu Ala Leu Leu  Ser Asp Leu
    4175                4180                4185

Gln Asp  Leu Lys Trp Ala Arg  Phe Pro Lys Ser Asp  Gly Thr Gly
    4190                4195                4200

Thr Ile  Tyr Thr Glu Leu Glu  Pro Pro Cys Arg Phe  Val Thr Asp
    4205                4210                4215

Thr Pro  Lys Gly Pro Lys Val  Lys Tyr Leu Tyr Phe  Ile Lys Gly
    4220                4225                4230

Leu Asn  Asn Leu Asn Arg Gly  Met Val Leu Gly Ser  Leu Ala Ala
    4235                4240                4245

Thr Val  Arg Leu Gln Ala Gly  Asn Ala Thr Glu Val  Pro Ala Asn
    4250                4255                4260

Ser Thr  Val Leu Ser Phe Cys  Ala Phe Ala Val Asp  Ala Ala Lys
    4265                4270                4275
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Ala Tyr  Lys Asp Tyr Leu Ala  Ser Gly Gly Gln Pro  Ile Thr Asn
    4280                 4285                 4290

Cys Val  Lys Met Leu Cys Thr  His Thr Gly Thr Gly  Gln Ala Ile
    4295                 4300                 4305

Thr Val  Thr Pro Glu Ala Asn  Met Asp Gln Glu Ser  Phe Gly Gly
    4310                 4315                 4320

Ala Ser  Cys Cys Leu Tyr Cys  Arg Cys His Ile Asp  His Pro Asn
    4325                 4330                 4335

Pro Lys  Gly Phe Cys Asp Leu  Lys Gly Lys Tyr Val  Gln Ile Pro
    4340                 4345                 4350

Thr Thr  Cys Ala Asn Asp Pro  Val Gly Phe Thr Leu  Lys Asn Thr
    4355                 4360                 4365

Val Cys  Thr Val Cys Gly Met  Trp Lys Gly Tyr Gly  Cys Ser Cys
    4370                 4375                 4380

Asp Gln  Leu Arg Glu Pro Met  Leu Gln Ser Ala Asp  Ala Gln Ser
    4385                 4390                 4395

Phe Leu  Asn Arg Val Cys Gly  Val Ser Ala Ala Arg  Leu Thr Pro
    4400                 4405                 4410

Cys Gly  Thr Gly Thr Ser Thr  Asp Val Val Tyr Arg  Ala Phe Asp
    4415                 4420                 4425

Ile Tyr  Asn Asp Lys Val Ala  Gly Phe Ala Lys Phe  Leu Lys Thr
    4430                 4435                 4440

Asn Cys  Cys Arg Phe Gln Glu  Lys Asp Glu Asp Asp  Asn Leu Ile
    4445                 4450                 4455

Asp Ser  Tyr Phe Val Val Lys  Arg His Thr Phe Ser  Asn Tyr Gln
    4460                 4465                 4470

His Glu  Glu Thr Ile Tyr Asn  Leu Leu Lys Asp Cys  Pro Ala Val
    4475                 4480                 4485

Ala Lys  His Asp Phe Phe Lys  Phe Arg Ile Asp Gly  Asp Met Val
    4490                 4495                 4500

Pro His  Ile Ser Arg Gln Arg  Leu Thr Lys Tyr Thr  Met Ala Asp
    4505                 4510                 4515

Leu Val  Tyr Ala Leu Arg His  Phe Asp Glu Gly Asn  Cys Asp Thr
    4520                 4525                 4530

Leu Lys  Glu Ile Leu Val Thr  Tyr Asn Cys Cys Asp  Asp Asp Tyr
    4535                 4540                 4545

Phe Asn  Lys Lys Asp Trp Tyr  Asp Phe Val Glu Asn  Pro Asp Ile
    4550                 4555                 4560

Leu Arg  Val Tyr Ala Asn Leu  Gly Glu Arg Val Arg  Gln Ala Leu
    4565                 4570                 4575

Leu Lys  Thr Val Gln Phe Cys  Asp Ala Met Arg Asn  Ala Gly Ile
    4580                 4585                 4590

Val Gly  Val Leu Thr Leu Asp  Asn Gln Asp Leu Asn  Gly Asn Trp
    4595                 4600                 4605

Tyr Asp  Phe Gly Asp Phe Ile  Gln Thr Thr Pro Gly  Ser Gly Val
    4610                 4615                 4620

Pro Val  Val Asp Ser Tyr Tyr  Ser Leu Leu Met Pro  Ile Leu Thr
    4625                 4630                 4635

Leu Thr  Arg Ala Leu Thr Ala  Glu Ser His Val Asp  Thr Asp Leu
    4640                 4645                 4650
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Thr Lys  Pro Tyr Ile Lys Trp  Asp Leu Leu Lys Tyr  Asp Phe Thr
    4655                 4660                 4665

Glu Glu  Arg Leu Lys Leu Phe  Asp Arg Tyr Phe Lys  Tyr Trp Asp
    4670                 4675                 4680

Gln Thr  Tyr His Pro Asn Cys  Val Asn Cys Leu Asp  Asp Arg Cys
    4685                 4690                 4695

Ile Leu  His Cys Ala Asn Phe  Asn Val Leu Phe Ser  Thr Val Phe
    4700                 4705                 4710

Pro Pro  Thr Ser Phe Gly Pro  Leu Val Arg Lys Ile  Phe Val Asp
    4715                 4720                 4725

Gly Val  Pro Phe Val Val Ser  Thr Gly Tyr His Phe  Arg Glu Leu
    4730                 4735                 4740

Gly Val  Val His Asn Gln Asp  Val Asn Leu His Ser  Ser Arg Leu
    4745                 4750                 4755

Ser Phe  Lys Glu Leu Leu Val  Tyr Ala Ala Asp Pro  Ala Met His
    4760                 4765                 4770

Ala Ala  Ser Gly Asn Leu Leu  Leu Asp Lys Arg Thr  Thr Cys Phe
    4775                 4780                 4785

Ser Val  Ala Ala Leu Thr Asn  Asn Val Ala Phe Gln  Thr Val Lys
    4790                 4795                 4800

Pro Gly  Asn Phe Asn Lys Asp  Phe Tyr Asp Phe Ala  Val Ser Lys
    4805                 4810                 4815

Gly Phe  Phe Lys Glu Gly Ser  Ser Val Glu Leu Lys  His Phe Phe
    4820                 4825                 4830

Phe Ala  Gln Asp Gly Asn Ala  Ala Ile Ser Asp Tyr  Asp Tyr Tyr
    4835                 4840                 4845

Arg Tyr  Asn Leu Pro Thr Met  Cys Asp Ile Arg Gln  Leu Leu Phe
    4850                 4855                 4860

Val Val  Glu Val Val Asp Lys  Tyr Phe Asp Cys Tyr  Asp Gly Gly
    4865                 4870                 4875

Cys Ile  Asn Ala Asn Gln Val  Ile Val Asn Asn Leu  Asp Lys Ser
    4880                 4885                 4890

Ala Gly  Phe Pro Phe Asn Lys  Trp Gly Lys Ala Arg  Leu Tyr Tyr
    4895                 4900                 4905

Asp Ser  Met Ser Tyr Glu Asp  Gln Asp Ala Leu Phe  Ala Tyr Thr
    4910                 4915                 4920

Lys Arg  Asn Val Ile Pro Thr  Ile Thr Gln Met Asn  Leu Lys Tyr
    4925                 4930                 4935

Ala Ile  Ser Ala Lys Asn Arg  Ala Arg Thr Val Ala  Gly Val Ser
    4940                 4945                 4950

Ile Cys  Ser Thr Met Thr Asn  Arg Gln Phe His Gln  Lys Leu Leu
    4955                 4960                 4965

Lys Ser  Ile Ala Ala Thr Arg  Gly Ala Thr Val Val  Ile Gly Thr
    4970                 4975                 4980

Ser Lys  Phe Tyr Gly Gly Trp  His Asn Met Leu Lys  Thr Val Tyr
    4985                 4990                 4995

Ser Asp  Val Glu Asn Pro His  Leu Met Gly Trp Asp  Tyr Pro Lys
    5000                 5005                 5010

Cys Asp  Arg Ala Met Pro Asn  Met Leu Arg Ile Met  Ala Ser Leu
    5015                 5020                 5025

Val Leu  Ala Arg Lys His Thr  Thr Cys Cys Ser Leu  Ser His Arg
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    5030                5035                5040

Phe Tyr  Arg Leu Ala Asn Glu  Cys Ala Gln Val Leu  Ser Glu Met
    5045                5050                5055

Val Met  Cys Gly Gly Ser Leu  Tyr Val Lys Pro Gly  Gly Thr Ser
    5060                5065                5070

Ser Gly  Asp Ala Thr Thr Ala  Tyr Ala Asn Ser Val  Phe Asn Ile
    5075                5080                5085

Cys Gln  Ala Val Thr Ala Asn  Val Asn Ala Leu Leu  Ser Thr Asp
    5090                5095                5100

Gly Asn  Lys Ile Ala Asp Lys  Tyr Val Arg Asn Leu  Gln His Arg
    5105                5110                5115

Leu Tyr  Glu Cys Leu Tyr Arg  Asn Arg Asp Val Asp  Thr Asp Phe
    5120                5125                5130

Val Asn  Glu Phe Tyr Ala Tyr  Leu Arg Lys His Phe  Ser Met Met
    5135                5140                5145

Ile Leu  Ser Asp Asp Ala Val  Val Cys Phe Asn Ser  Thr Tyr Ala
    5150                5155                5160

Ser Gln  Gly Leu Val Ala Ser  Ile Lys Asn Phe Lys  Ser Val Leu
    5165                5170                5175

Tyr Tyr  Gln Asn Asn Val Phe  Met Ser Glu Ala Lys  Cys Trp Thr
    5180                5185                5190

Glu Thr  Asp Leu Thr Lys Gly  Pro His Glu Phe Cys  Ser Gln His
    5195                5200                5205

Thr Met  Leu Val Lys Gln Gly  Asp Asp Tyr Val Tyr  Leu Pro Tyr
    5210                5215                5220

Pro Asp  Pro Ser Arg Ile Leu  Gly Ala Gly Cys Phe  Val Asp Asp
    5225                5230                5235

Ile Val  Lys Thr Asp Gly Thr  Leu Met Ile Glu Arg  Phe Val Ser
    5240                5245                5250

Leu Ala  Ile Asp Ala Tyr Pro  Leu Thr Lys His Pro  Asn Gln Glu
    5255                5260                5265

Tyr Ala  Asp Val Phe His Leu  Tyr Leu Gln Tyr Ile  Arg Lys Leu
    5270                5275                5280

His Asp  Glu Leu Thr Gly His  Met Leu Asp Met Tyr  Ser Val Met
    5285                5290                5295

Leu Thr  Asn Asp Asn Thr Ser  Arg Tyr Trp Glu Pro  Glu Phe Tyr
    5300                5305                5310

Glu Ala  Met Tyr Thr Pro His  Thr Val Leu Gln Ala  Val Gly Ala
    5315                5320                5325

Cys Val  Leu Cys Asn Ser Gln  Thr Ser Leu Arg Cys  Gly Ala Cys
    5330                5335                5340

Ile Arg  Arg Pro Phe Leu Cys  Cys Lys Cys Cys Tyr  Asp His Val
    5345                5350                5355

Ile Ser  Thr Ser His Lys Leu  Val Leu Ser Val Asn  Pro Tyr Val
    5360                5365                5370

Cys Asn  Ala Pro Gly Cys Asp  Val Thr Asp Val Thr  Gln Leu Tyr
    5375                5380                5385

Leu Gly  Gly Met Ser Tyr Tyr  Cys Lys Ser His Lys  Pro Pro Ile
    5390                5395                5400

Ser Phe  Pro Leu Cys Ala Asn  Gly Gln Val Phe Gly  Leu Tyr Lys
    5405                5410                5415
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Asn Thr  Cys Val Gly Ser Asp  Asn Val Thr Asp Phe  Asn Ala Ile
    5420                 5425                 5430

Ala Thr  Cys Asp Trp Thr Asn  Ala Gly Asp Tyr Ile  Leu Ala Asn
    5435                 5440                 5445

Thr Cys  Thr Glu Arg Leu Lys  Leu Phe Ala Ala Glu  Thr Leu Lys
    5450                 5455                 5460

Ala Thr  Glu Glu Thr Phe Lys  Leu Ser Tyr Gly Ile  Ala Thr Val
    5465                 5470                 5475

Arg Glu  Val Leu Ser Asp Arg  Glu Leu His Leu Ser  Trp Glu Val
    5480                 5485                 5490

Gly Lys  Pro Arg Pro Pro Leu  Asn Arg Asn Tyr Val  Phe Thr Gly
    5495                 5500                 5505

Tyr Arg  Val Thr Lys Asn Ser  Lys Val Gln Ile Gly  Glu Tyr Thr
    5510                 5515                 5520

Phe Glu  Lys Gly Asp Tyr Gly  Asp Ala Val Val Tyr  Arg Gly Thr
    5525                 5530                 5535

Thr Thr  Tyr Lys Leu Asn Val  Gly Asp Tyr Phe Val  Leu Thr Ser
    5540                 5545                 5550

His Thr  Val Met Pro Leu Ser  Ala Pro Thr Leu Val  Pro Gln Glu
    5555                 5560                 5565

His Tyr  Val Arg Ile Thr Gly  Leu Tyr Pro Thr Leu  Asn Ile Ser
    5570                 5575                 5580

Asp Glu  Phe Ser Ser Asn Val  Ala Asn Tyr Gln Lys  Val Gly Met
    5585                 5590                 5595

Gln Lys  Tyr Ser Thr Leu Gln  Gly Pro Pro Gly Thr  Gly Lys Ser
    5600                 5605                 5610

His Phe  Ala Ile Gly Leu Ala  Leu Tyr Tyr Pro Ser  Ala Arg Ile
    5615                 5620                 5625

Val Tyr  Thr Ala Cys Ser His  Ala Ala Val Asp Ala  Leu Cys Glu
    5630                 5635                 5640

Lys Ala  Leu Lys Tyr Leu Pro  Ile Asp Lys Cys Ser  Arg Ile Ile
    5645                 5650                 5655

Pro Ala  Arg Ala Arg Val Glu  Cys Phe Asp Lys Phe  Lys Val Asn
    5660                 5665                 5670

Ser Thr  Leu Glu Gln Tyr Val  Phe Cys Thr Val Asn  Ala Leu Pro
    5675                 5680                 5685

Glu Thr  Thr Ala Asp Ile Val  Val Phe Asp Glu Ile  Ser Met Ala
    5690                 5695                 5700

Thr Asn  Tyr Asp Leu Ser Val  Val Asn Ala Arg Leu  Arg Ala Lys
    5705                 5710                 5715

His Tyr  Val Tyr Ile Gly Asp  Pro Ala Gln Leu Pro  Ala Pro Arg
    5720                 5725                 5730

Thr Leu  Leu Thr Lys Gly Thr  Leu Glu Pro Glu Tyr  Phe Asn Ser
    5735                 5740                 5745

Val Cys  Arg Leu Met Lys Thr  Ile Gly Pro Asp Met  Phe Leu Gly
    5750                 5755                 5760

Thr Cys  Arg Arg Cys Pro Ala  Glu Ile Val Asp Thr  Val Ser Ala
    5765                 5770                 5775

Leu Val  Tyr Asp Asn Lys Leu  Lys Ala His Lys Asp  Lys Ser Ala
    5780                 5785                 5790
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Gln Cys  Phe Lys Met Phe Tyr  Lys Gly Val Ile Thr  His Asp Val
    5795                 5800                 5805

Ser Ser  Ala Ile Asn Arg Pro  Gln Ile Gly Val Val  Arg Glu Phe
    5810                 5815                 5820

Leu Thr  Arg Asn Pro Ala Trp  Arg Lys Ala Val Phe  Ile Ser Pro
    5825                 5830                 5835

Tyr Asn  Ser Gln Asn Ala Val  Ala Ser Lys Ile Leu  Gly Leu Pro
    5840                 5845                 5850

Thr Gln  Thr Val Asp Ser Ser  Gln Gly Ser Glu Tyr  Asp Tyr Val
    5855                 5860                 5865

Ile Phe  Thr Gln Thr Thr Glu  Thr Ala His Ser Cys  Asn Val Asn
    5870                 5875                 5880

Arg Phe  Asn Val Ala Ile Thr  Arg Ala Lys Val Gly  Ile Leu Cys
    5885                 5890                 5895

Ile Met  Ser Asp Arg Asp Leu  Tyr Asp Lys Leu Gln  Phe Thr Ser
    5900                 5905                 5910

Leu Glu  Ile Pro Arg Arg Asn  Val Ala Thr Leu Gln  Ala Glu Asn
    5915                 5920                 5925

Val Thr  Gly Leu Phe Lys Asp  Cys Ser Lys Val Ile  Thr Gly Leu
    5930                 5935                 5940

His Pro  Thr Gln Ala Pro Thr  His Leu Ser Val Asp  Thr Lys Phe
    5945                 5950                 5955

Lys Thr  Glu Gly Leu Cys Val  Asp Ile Pro Gly Ile  Pro Lys Asp
    5960                 5965                 5970

Met Thr  Tyr Arg Arg Leu Ile  Ser Met Met Gly Phe  Lys Met Asn
    5975                 5980                 5985

Tyr Gln  Val Asn Gly Tyr Pro  Asn Met Phe Ile Thr  Arg Glu Glu
    5990                 5995                 6000

Ala Ile  Arg His Val Arg Ala  Trp Ile Gly Phe Asp  Val Glu Gly
    6005                 6010                 6015

Cys His  Ala Thr Arg Glu Ala  Val Gly Thr Asn Leu  Pro Leu Gln
    6020                 6025                 6030

Leu Gly  Phe Ser Thr Gly Val  Asn Leu Val Ala Val  Pro Thr Gly
    6035                 6040                 6045

Tyr Val  Asp Thr Pro Asn Asn  Thr Asp Phe Ser Arg  Val Ser Ala
    6050                 6055                 6060

Lys Pro  Pro Pro Gly Asp Gln  Phe Lys His Leu Ile  Pro Leu Met
    6065                 6070                 6075

Tyr Lys  Gly Leu Pro Trp Asn  Val Val Arg Ile Lys  Ile Val Gln
    6080                 6085                 6090

Met Leu  Ser Asp Thr Leu Lys  Asn Leu Ser Asp Arg  Val Val Phe
    6095                 6100                 6105

Val Leu  Trp Ala His Gly Phe  Glu Leu Thr Ser Met  Lys Tyr Phe
    6110                 6115                 6120

Val Lys  Ile Gly Pro Glu Arg  Thr Cys Cys Leu Cys  Asp Arg Arg
    6125                 6130                 6135

Ala Thr  Cys Phe Ser Thr Ala  Ser Asp Thr Tyr Ala  Cys Trp His
    6140                 6145                 6150

His Ser  Ile Gly Phe Asp Tyr  Val Tyr Asn Pro Phe  Met Ile Asp
    6155                 6160                 6165

Val Gln  Gln Trp Gly Phe Thr  Gly Asn Leu Gln Ser  Asn His Asp
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    6170                6175                6180

Leu Tyr  Cys Gln Val His Gly  Asn Ala His Val Ala  Ser Cys Asp
    6185                6190                6195

Ala Ile  Met Thr Arg Cys Leu  Ala Val His Glu Cys  Phe Val Lys
    6200                6205                6210

Arg Val  Asp Trp Thr Ile Glu  Tyr Pro Ile Ile Gly  Asp Glu Leu
    6215                6220                6225

Lys Ile  Asn Ala Ala Cys Arg  Lys Val Gln His Met  Val Val Lys
    6230                6235                6240

Ala Ala  Leu Leu Ala Asp Lys  Phe Pro Val Leu His  Asp Ile Gly
    6245                6250                6255

Asn Pro  Lys Ala Ile Lys Cys  Val Pro Gln Ala Asp  Val Glu Trp
    6260                6265                6270

Lys Phe  Tyr Asp Ala Gln Pro  Cys Ser Asp Lys Ala  Tyr Lys Ile
    6275                6280                6285

Glu Glu  Leu Phe Tyr Ser Tyr  Ala Thr His Ser Asp  Lys Phe Thr
    6290                6295                6300

Asp Gly  Val Cys Leu Phe Trp  Asn Cys Asn Val Asp  Arg Tyr Pro
    6305                6310                6315

Ala Asn  Ser Ile Val Cys Arg  Phe Asp Thr Arg Val  Leu Ser Asn
    6320                6325                6330

Leu Asn  Leu Pro Gly Cys Asp  Gly Gly Ser Leu Tyr  Val Asn Lys
    6335                6340                6345

His Ala  Phe His Thr Pro Ala  Phe Asp Lys Ser Ala  Phe Val Asn
    6350                6355                6360

Leu Lys  Gln Leu Pro Phe Phe  Tyr Tyr Ser Asp Ser  Pro Cys Glu
    6365                6370                6375

Ser His  Gly Lys Gln Val Val  Ser Asp Ile Asp Tyr  Val Pro Leu
    6380                6385                6390

Lys Ser  Ala Thr Cys Ile Thr  Arg Cys Asn Leu Gly  Gly Ala Val
    6395                6400                6405

Cys Arg  His His Ala Asn Glu  Tyr Arg Leu Tyr Leu  Asp Ala Tyr
    6410                6415                6420

Asn Met  Met Ile Ser Ala Gly  Phe Ser Leu Trp Val  Tyr Lys Gln
    6425                6430                6435

Phe Asp  Thr Tyr Asn Leu Trp  Asn Thr Phe Thr Arg  Leu Gln Ser
    6440                6445                6450

Leu Glu  Asn Val Ala Phe Asn  Val Val Asn Lys Gly  His Phe Asp
    6455                6460                6465

Gly Gln  Gln Gly Glu Val Pro  Val Ser Ile Ile Asn  Asn Thr Val
    6470                6475                6480

Tyr Thr  Lys Val Asp Gly Val  Asp Val Glu Leu Phe  Glu Asn Lys
    6485                6490                6495

Thr Thr  Leu Pro Val Asn Val  Ala Phe Glu Leu Trp  Ala Lys Arg
    6500                6505                6510

Asn Ile  Lys Pro Val Pro Glu  Val Lys Ile Leu Asn  Asn Leu Gly
    6515                6520                6525

Val Asp  Ile Ala Ala Asn Thr  Val Ile Trp Asp Tyr  Lys Arg Asp
    6530                6535                6540

Ala Pro  Ala His Ile Ser Thr  Ile Gly Val Cys Ser  Met Thr Asp
    6545                6550                6555
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Ile Ala  Lys Lys Pro Thr Glu  Thr Ile Cys Ala Pro  Leu Thr Val
    6560                 6565                 6570

Phe Phe  Asp Gly Arg Val Asp  Gly Gln Val Asp Leu  Phe Arg Asn
    6575                 6580                 6585

Ala Arg  Asn Gly Val Leu Ile  Thr Glu Gly Ser Val  Lys Gly Leu
    6590                 6595                 6600

Gln Pro  Ser Val Gly Pro Lys  Gln Ala Ser Leu Asn  Gly Val Thr
    6605                 6610                 6615

Leu Ile  Gly Glu Ala Val Lys  Thr Gln Phe Asn Tyr  Tyr Lys Lys
    6620                 6625                 6630

Val Asp  Gly Val Val Gln Gln  Leu Pro Glu Thr Tyr  Phe Thr Gln
    6635                 6640                 6645

Ser Arg  Asn Leu Gln Glu Phe  Lys Pro Arg Ser Gln  Met Glu Ile
    6650                 6655                 6660

Asp Phe  Leu Glu Leu Ala Met  Asp Glu Phe Ile Glu  Arg Tyr Lys
    6665                 6670                 6675

Leu Glu  Gly Tyr Ala Phe Glu  His Ile Val Tyr Gly  Asp Phe Ser
    6680                 6685                 6690

His Ser  Gln Leu Gly Gly Leu  His Leu Leu Ile Gly  Leu Ala Lys
    6695                 6700                 6705

Arg Phe  Lys Glu Ser Pro Phe  Glu Leu Glu Asp Phe  Ile Pro Met
    6710                 6715                 6720

Asp Ser  Thr Val Lys Asn Tyr  Phe Ile Thr Asp Ala  Gln Thr Gly
    6725                 6730                 6735

Ser Ser  Lys Cys Val Cys Ser  Val Ile Asp Leu Leu  Leu Asp Asp
    6740                 6745                 6750

Phe Val  Glu Ile Ile Lys Ser  Gln Asp Leu Ser Val  Val Ser Lys
    6755                 6760                 6765

Val Val  Lys Val Thr Ile Asp  Tyr Thr Glu Ile Ser  Phe Met Leu
    6770                 6775                 6780

Trp Cys  Lys Asp Gly His Val  Glu Thr Phe Tyr Pro  Lys Leu Gln
    6785                 6790                 6795

Ser Ser  Gln Ala Trp Gln Pro  Gly Val Ala Met Pro  Asn Leu Tyr
    6800                 6805                 6810

Lys Met  Gln Arg Met Leu Leu  Glu Lys Cys Asp Leu  Gln Asn Tyr
    6815                 6820                 6825

Gly Asp  Ser Ala Thr Leu Pro  Lys Gly Ile Met Met  Asn Val Ala
    6830                 6835                 6840

Lys Tyr  Thr Gln Leu Cys Gln  Tyr Leu Asn Thr Leu  Thr Leu Ala
    6845                 6850                 6855

Val Pro  Tyr Asn Met Arg Val  Ile His Phe Gly Ala  Gly Ser Asp
    6860                 6865                 6870

Lys Gly  Val Ala Pro Gly Thr  Ala Val Leu Arg Gln  Trp Leu Pro
    6875                 6880                 6885

Thr Gly  Thr Leu Leu Val Asp  Ser Asp Leu Asn Asp  Phe Val Ser
    6890                 6895                 6900

Asp Ala  Asp Ser Thr Leu Ile  Gly Asp Cys Ala Thr  Val His Thr
    6905                 6910                 6915

Ala Asn  Lys Trp Asp Leu Ile  Ile Ser Asp Met Tyr  Asp Pro Lys
    6920                 6925                 6930
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Thr Lys  Asn Val Thr Lys Glu  Asn Asp Ser Lys Glu  Gly Phe Phe
    6935                 6940                 6945

Thr Tyr  Ile Cys Gly Phe Ile  Gln Gln Lys Leu Ala  Leu Gly Gly
    6950                 6955                 6960

Ser Val  Ala Ile Lys Ile Thr  Glu His Ser Trp Asn  Ala Asp Leu
    6965                 6970                 6975

Tyr Lys  Leu Met Gly His Phe  Ala Trp Trp Thr Ala  Phe Val Thr
    6980                 6985                 6990

Asn Val  Asn Ala Ser Ser Ser  Glu Ala Phe Leu Ile  Gly Cys Asn
    6995                 7000                 7005

Tyr Leu  Gly Lys Pro Arg Glu  Gln Ile Asp Gly Tyr  Val Met His
    7010                 7015                 7020

Ala Asn  Tyr Ile Phe Trp Arg  Asn Thr Asn Pro Ile  Gln Leu Ser
    7025                 7030                 7035

Ser Tyr  Ser Leu Phe Asp Met  Ser Lys Phe Pro Leu  Lys Leu Arg
    7040                 7045                 7050

Gly Thr  Ala Val Met Ser Leu  Lys Glu Gly Gln Ile  Asn Asp Met
    7055                 7060                 7065

Ile Leu  Ser Leu Leu Ser Lys  Gly Arg Leu Ile Ile  Arg Glu Asn
    7070                 7075                 7080

Asn Arg  Val Val Ile Ser Ser  Asp Val Leu Val Asn  Asn
    7085                 7090                 7095


<210> SEQ ID NO 371
<211> LENGTH: 1273
<212> TYPE: PRT
<213> ORGANISM: betacoronavirus SARS coronavirus 2

<400> SEQUENCE: 371

Met Phe Val Phe Leu Val Leu Leu Pro Leu Val Ser Ser Gln Cys Val
1               5                   10                  15

Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe
            20                  25                  30

Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu
        35                  40                  45

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
    50                  55                  60

Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp
65                  70                  75                  80

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
                85                  90                  95

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
            100                 105                 110

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
        115                 120                 125

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
    130                 135                 140

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
145                 150                 155                 160

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
                165                 170                 175

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
            180                 185                 190
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Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
        195                 200                 205

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
    210                 215                 220

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
225                 230                 235                 240

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
                245                 250                 255

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
            260                 265                 270

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
        275                 280                 285

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
    290                 295                 300

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
305                 310                 315                 320

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
                325                 330                 335

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
            340                 345                 350

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
        355                 360                 365

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
    370                 375                 380

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
385                 390                 395                 400

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
                405                 410                 415

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
            420                 425                 430

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
        435                 440                 445

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
    450                 455                 460

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
465                 470                 475                 480

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
                485                 490                 495

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
            500                 505                 510

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
        515                 520                 525

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
    530                 535                 540

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
545                 550                 555                 560

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
                565                 570                 575

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
            580                 585                 590
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Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
        595                 600                 605

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
    610                 615                 620

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
625                 630                 635                 640

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
                645                 650                 655

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
            660                 665                 670

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
        675                 680                 685

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
    690                 695                 700

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
705                 710                 715                 720

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
                725                 730                 735

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
            740                 745                 750

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
        755                 760                 765

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
    770                 775                 780

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
785                 790                 795                 800

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
                805                 810                 815

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
            820                 825                 830

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
        835                 840                 845

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
    850                 855                 860

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
865                 870                 875                 880

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
                885                 890                 895

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
            900                 905                 910

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
        915                 920                 925

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
    930                 935                 940

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
945                 950                 955                 960

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
                965                 970                 975

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
            980                 985                 990

Ile Asp Arg Leu Ile Thr Gly Arg  Leu Gln Ser Leu Gln  Thr Tyr Val
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        995                 1000                1005

Thr Gln  Gln Leu Ile Arg Ala  Ala Glu Ile Arg Ala  Ser Ala Asn
    1010                1015                1020

Leu Ala  Ala Thr Lys Met Ser  Glu Cys Val Leu Gly  Gln Ser Lys
    1025                1030                1035

Arg Val  Asp Phe Cys Gly Lys  Gly Tyr His Leu Met  Ser Phe Pro
    1040                1045                1050

Gln Ser  Ala Pro His Gly Val  Val Phe Leu His Val  Thr Tyr Val
    1055                1060                1065

Pro Ala  Gln Glu Lys Asn Phe  Thr Thr Ala Pro Ala  Ile Cys His
    1070                1075                1080

Asp Gly  Lys Ala His Phe Pro  Arg Glu Gly Val Phe  Val Ser Asn
    1085                1090                1095

Gly Thr  His Trp Phe Val Thr  Gln Arg Asn Phe Tyr  Glu Pro Gln
    1100                1105                1110

Ile Ile  Thr Thr Asp Asn Thr  Phe Val Ser Gly Asn  Cys Asp Val
    1115                1120                1125

Val Ile  Gly Ile Val Asn Asn  Thr Val Tyr Asp Pro  Leu Gln Pro
    1130                1135                1140

Glu Leu  Asp Ser Phe Lys Glu  Glu Leu Asp Lys Tyr  Phe Lys Asn
    1145                1150                1155

His Thr  Ser Pro Asp Val Asp  Leu Gly Asp Ile Ser  Gly Ile Asn
    1160                1165                1170

Ala Ser  Val Val Asn Ile Gln  Lys Glu Ile Asp Arg  Leu Asn Glu
    1175                1180                1185

Val Ala  Lys Asn Leu Asn Glu  Ser Leu Ile Asp Leu  Gln Glu Leu
    1190                1195                1200

Gly Lys  Tyr Glu Gln Tyr Ile  Lys Trp Pro Trp Tyr  Ile Trp Leu
    1205                1210                1215

Gly Phe  Ile Ala Gly Leu Ile  Ala Ile Val Met Val  Thr Ile Met
    1220                1225                1230

Leu Cys  Cys Met Thr Ser Cys  Cys Ser Cys Leu Lys  Gly Cys Cys
    1235                1240                1245

Ser Cys  Gly Ser Cys Cys Lys  Phe Asp Glu Asp Asp  Ser Glu Pro
    1250                1255                1260

Val Leu  Lys Gly Val Lys Leu  His Tyr Thr
    1265                1270


<210> SEQ ID NO 372
<211> LENGTH: 375
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VH

<400> SEQUENCE: 372

caagtgcaac tcgtggagtc cggcggcggc gtcgtccagc caggtcggtc tctaaggctg      60

tcgtgcgctg caagtgggtt tacattctct aattatggta tgcattgggt gaggcaggct     120

cccggcaagg ggctggaatg gctcgctgtg atttcaagcg atggtcgaat taaattttat     180

gctgactctg ttaaaggcag atttactatg agtagagact catcaaaaaa cactctgtac     240

ctgcaaatga atagcctgcg cgccgaggat acggctgtct actactgcgc caaagaccgg     300
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ttccaattcg caagatcatg gtatggagac tacttcgatt attgggggca aggtactcag    360

gtgactgtct cctca                                                     375


<210> SEQ ID NO 373
<211> LENGTH: 375
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VH-v3

<400> SEQUENCE: 373

caggtgcaac ttgtggaaag tggcggaggc gtggtgcagc cggggcgatc cttgcgcctc     60

tcctgtgccg ccagcgggtt tacattttcc aattatggca tgcactgggt gcgtcaggcc    120

cccgggaagg gcctggaatg gcttgccgtg atcagcagtg acggacgcat taaattctac    180

gccgattctg tcaagggtcg gttcaccatg agtagagact cctcaaagaa cactctgtac    240

ctgcagatga atagcctgcg ggccgaagac accgctgtgt actactgtgc taaggaccgg    300

tttcaatttg ctagatcatt ctacggggac tacttcgact attggggcca aggcacgcag    360

gtgacagtca gctca                                                     375


<210> SEQ ID NO 374
<211> LENGTH: 125
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VH-v3

<400> SEQUENCE: 374

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 Asn Tyr
            20                  25                  30

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

Ala Val Ile Ser Ser Asp Gly Arg Ile Lys Phe Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Met Ser Arg Asp Ser 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 Lys Asp Arg Phe Gln Phe Ala Arg Ser Phe Tyr Gly Asp Tyr Phe
            100                 105                 110

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


<210> SEQ ID NO 375
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VH-v3 CDRH3

<400> SEQUENCE: 375

Ala Lys Asp Arg Phe Gln Phe Ala Arg Ser Phe Tyr Gly Asp Tyr Phe
1               5                   10                  15

Asp Tyr
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<210> SEQ ID NO 376
<211> LENGTH: 375
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VH-v4

<400> SEQUENCE: 376

caagtccagc ttgtcgagtc tggagggggc gtagtgcagc ccgggcgcag tttgagatta 60

agctgcgccg cctctggttt cacgttctcc aattacggta tgcactgggt gcgacaggca 120

cccggcaagg ggctggaatg gctggccgtc attagttcag acgggcggat caaattttac 180

gctgacagtg tgaagggtag gtttaccatg tcaagagact ccagcaaaaa cacattatac 240

ctgcagatga acagcctgcg cgccgaggac accgccgtat attattgcgc taaggaccgc 300

tttcagttcg ctaggtctgc ctacggtgac tattttgatt attggggaca gggaactcag 360

gtaacggtca gctca 375

<210> SEQ ID NO 377
<211> LENGTH: 125
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VH-v4

<400> SEQUENCE: 377

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 Asn Tyr
20 25 30

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

Ala Val Ile Ser Ser Asp Gly Arg Ile Lys Phe Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Met Ser Arg Asp Ser 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 Lys Asp Arg Phe Gln Phe Ala Arg Ser Ala Tyr Gly Asp Tyr Phe
100 105 110

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

<210> SEQ ID NO 378
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VH-v4

<400> SEQUENCE: 378

Ala Lys Asp Arg Phe Gln Phe Ala Arg Ser Ala Tyr Gly Asp Tyr Phe
1 5 10 15

Asp Tyr

<210> SEQ ID NO 379

-continued

<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VL (Vk)

<400> SEQUENCE: 379

gcggttgcaa tgactcagtc cccactctcc ttgcccgtga cactcgggca accggcctcc 60

atctcttgcc ggagcaatca gtcccttgtt tatagcgacg ggaatatcta tctgaattgg 120

ttccagcaga ggcccgggca gtcaccaatg cgcctcatct atcgggtgtc caaccgggat 180

tcaggtgtgc ccgaccggtt ttctggcagc ggatcaggaa cggactttac actcaaaatt 240

tcccgcgtgg aggctgagga tgtcggaatc tattattgca tgcagggcac gcactggcct 300

ccaaccttcg gcggaggaac caaggtggag atcaag 336

<210> SEQ ID NO 380
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VL-v3 (Vk)

<400> SEQUENCE: 380

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Gln Gln Ser Leu Val Tyr Ser
20 25 30

Asp Gly Asn Ile Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Met Arg Leu Ile Tyr Arg Val Ser Asn Arg Asp 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 Ile Tyr Tyr Cys Met Gln Gly
85 90 95

Thr His Trp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> SEQ ID NO 381
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VL-v3 (Vk)

<400> SEQUENCE: 381

gatgtggtaa tgacccaaag ccccctgtca ttgccagtga cactgggcca gccggcctca 60

attagttgca ggtctcagca gtcactggtg tactccgatg gcaatatcta cctaaactgg 120

ttccagcagc ggcctgggca atctcctatg cgacttatat atagagtgag taaccgggac 180

agtggggtcc ctgatagatt ttcaggtagc ggcagtggca cagatttcac cctgaagata 240

tctcgggtag aagcagagga cgtggggata tattattgca tgcagggaac gcactggccc 300

cctaccttcg gcggcggaac aaaagtggaa ataaaa 336

<210> SEQ ID NO 382
<211> LENGTH: 220

-continued

<212> TYPE: PRT
<213> ORGANISM: betacoronavirus SARS coronavirus 2

<400> SEQUENCE: 382

Asn Ile Thr Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Arg
1 5 10 15

Phe Ala Ser Val Tyr Ala Trp Asn Arg Lys Arg Ile Ser Asn Cys Val
20 25 30

Ala Asp Tyr Ser Val Leu Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys
35 40 45

Cys Tyr Gly Val Ser Pro Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn
50 55 60

Val Tyr Ala Asp Ser Phe Val Ile Arg Gly Asp Glu Val Arg Gln Ile
65 70 75 80

Ala Pro Gly Gln Thr Gly Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro
85 90 95

Asp Asp Phe Thr Gly Cys Val Ile Ala Trp Asn Ser Asn Asn Leu Asp
100 105 110

Ser Lys Val Gly Gly Asn Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys
115 120 125

Ser Asn Leu Lys Pro Phe Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln
130 135 140

Ala Gly Ser Thr Pro Cys Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe
145 150 155 160

Pro Leu Gln Ser Tyr Gly Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln
165 170 175

Pro Tyr Arg Val Val Val Leu Ser Phe Glu Leu Leu His Ala Pro Ala
180 185 190

Thr Val Cys Gly Pro Lys Lys Ser Thr Asn Leu Val Lys Asn Lys Cys
195 200 205

Val Asn Phe Asn Phe Asn Gly Leu Thr Gly Thr Gly
210 215 220

<210> SEQ ID NO 383
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VL-v3 (Vk)

<400> SEQUENCE: 383

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Ser
20 25 30

Asp Gly Asn Ile Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Met Arg Leu Ile Tyr Arg Val Ser Asn Arg Asp 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 Ile Tyr Tyr Cys Met Gln Gly
85 90 95

Thr His Trp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

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            100                 105                 110


<210> SEQ ID NO 384
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VL-v4 (Vk)

<400> SEQUENCE: 384

gacgtggtga tgacacagag cccactatcc cttccggtca ccttgggcca gccagcaagc     60

atttcctgtc ggtcgagcca gtctctggtc tatagtgacg gaaacattta tttgaattgg    120

tttcaacaga ggcccggaca gtcaccaatg cgcctcatct accgcgtctc taacagagac    180

tctggagtcc ccgatcgctt ttccggtagc gggtctggga ccgattttac attgaagatc    240

tccagggtgg aagccgagga cgttggtatc tactactgca tgcagggtac ccattggcca    300

ccgaccttcg gcgggggcac caaagtggag atcaaa                              336


<210> SEQ ID NO 385
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VL-v5 (Vk)

<400> SEQUENCE: 385

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1               5                   10                  15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Ser
            20                  25                  30

Asp Gly Asn Ile Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
        35                  40                  45

Pro Met Arg Leu Ile Tyr Arg Val Ser Asn Arg Asp 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 Ile Tyr Tyr Cys Met Gln Gly
                85                  90                  95

Thr His Phe Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> SEQ ID NO 386
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VL-v5 (Vk) CDRL3

<400> SEQUENCE: 386

Met Gln Gly Thr His Phe Pro Pro Thr
1               5


<210> SEQ ID NO 387
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VL-v5 (Vk)
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<400> SEQUENCE: 387

gatgtcgtga tgacacagtc gccactgagt ctaccggtga cactggggca gccggcctcc 60

atttcatgta ggagcagtca gtcgttagtg tactctgacg gtaacatcta tcttaattgg 120

ttccagcaaa gacctggcca gtcacctatg cggctgatat atagagtttc caacagagac 180

tccggggtgc cagacaggtt ctctggaagt ggctctggaa ctgactttac actgaagatc 240

agcagggtgg aggcagagga cgtgggtatc tattactgta tgcaagggac tcatttccct 300

ccaacattcg gaggagggac aaaagtggag ataaaa 336

<210> SEQ ID NO 388
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VL-v6 (Vk)

<400> SEQUENCE: 388

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Gln Gln Ser Leu Val Tyr Ser
20 25 30

Asp Gly Asn Ile Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Met Arg Leu Ile Tyr Arg Val Ser Asn Arg Asp 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 Ile Tyr Tyr Cys Met Gln Gly
85 90 95

Thr His Phe Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> SEQ ID NO 389
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VL-v6 (Vk)

<400> SEQUENCE: 389

gacgtggtga tgactcaatc acccctctcc ctaccggtca cactgggcca gccagcaagc 60

atttcatgcc gttcgcagca gtccctcgtc tattcggacg gcaatattta cctcaactgg 120

tttcagcagc gacccgggca gtcacccatg cgacttatct acagggtgag caacagagat 180

tccggggtcc ccgatcgctt ctcaggcagt ggcagcggca ccgatttcac cctaaaaatt 240

agccgcgtgg aagcggaaga tgtgggtatc tactactgca tgcagggaac tcactttcca 300

cccacttttg gagggggac caaagttgaa atcaag 336

<210> SEQ ID NO 390
<211> LENGTH: 72
<212> TYPE: PRT
<213> ORGANISM: betacoronavirus SARS coronavirus 2

<400> SEQUENCE: 390

Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn Tyr Asn Tyr Leu

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1               5                   10                  15

Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe Glu Arg Asp Ile
            20                  25                  30

Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys Asn Gly Val Glu
        35                  40                  45

Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly Phe Gln Pro Thr
    50                  55                  60

Asn Gly Val Gly Tyr Gln Pro Tyr
65                  70


<210> SEQ ID NO 391
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV10 mAb CL (Ck), k1m3,
      IGKC-01

<400> SEQUENCE: 391

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1               5                   10                  15

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
            20                  25                  30

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

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
    50                  55                  60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65                  70                  75                  80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
                85                  90                  95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
            100                 105


<210> SEQ ID NO 392
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VL-v7 (Vk)

<400> SEQUENCE: 392

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1               5                   10                  15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Ser
            20                  25                  30

Asp Gly Asn Ile Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
        35                  40                  45

Pro Met Arg Leu Ile Tyr Arg Val Ser Asn Arg Asp 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 Ile Tyr Tyr Cys Met Gln Gly
                85                  90                  95

Thr His Tyr Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110
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<210> SEQ ID NO 393
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VL-v8 (Vk)

<400> SEQUENCE: 393

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Ser
20 25 30

Glu Gly Asn Ile Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Met Arg Leu Ile Tyr Arg Val Ser Asn Arg Asp 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 Ile Tyr Tyr Cys Met Gln Gly
85 90 95

Thr His Tyr Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> SEQ ID NO 394
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VL-v7/8 (Vk)
CDRL3

<400> SEQUENCE: 394

Met Gln Gly Thr His Tyr Pro Pro Thr
1 5

<210> SEQ ID NO 395
<211> LENGTH: 330
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCov10 CH1-CH3 G1m17;
IgHG1-01_MLNS

<400> SEQUENCE: 395

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

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys

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            100                 105                 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
        115                 120                 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
    130                 135                 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145                 150                 155                 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
                165                 170                 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
            180                 185                 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195                 200                 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    210                 215                 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225                 230                 235                 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
                245                 250                 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
            260                 265                 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
        275                 280                 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
    290                 295                 300

Val Phe Ser Cys Ser Val Leu His Glu Ala Leu His Ser His Tyr Thr
305                 310                 315                 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330


<210> SEQ ID NO 396
<211> LENGTH: 125
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VH-v5

<400> SEQUENCE: 396

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 Asn Tyr
            20                  25                  30

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

Ala Val Ile Ser Ser Asp Gly Arg Ile Lys Phe Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Met Ser Arg Asp Ser 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 Lys Asp Arg Phe Gln Phe Ala Arg Ser Tyr Tyr Gly Asp Tyr Phe
            100                 105                 110

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


<210> SEQ ID NO 397
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VH-v5 CDRH3

<400> SEQUENCE: 397

Ala Lys Asp Arg Phe Gln Phe Ala Arg Ser Tyr Tyr Gly Asp Tyr Phe
1               5                   10                  15

Asp Tyr


<210> SEQ ID NO 398
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VL-v8 (Vk) CDRL1

<400> SEQUENCE: 398

Gln Ser Leu Val Tyr Ser Glu Gly Asn Ile Tyr
1               5                   10


<210> SEQ ID NO 399
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VL-v9

<400> SEQUENCE: 399

Gln Ala Leu Val Tyr Ser Asp Gly Asn Ile Tyr
1               5                   10


<210> SEQ ID NO 400
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequencenCoV-10 mAb VL-v9 (Vk)

<400> SEQUENCE: 400

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Asn Gln Ala Leu Val Tyr Ser
            20                  25                  30

Asp Gly Asn Ile Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
        35                  40                  45

Pro Met Arg Leu Ile Tyr Arg Val Ser Asn Arg Asp 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 Ile Tyr Tyr Cys Met Gln Gly
                85                  90                  95

Thr His Trp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> SEQ ID NO 401
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<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VL-v10 (Vk)
CDRL1

<400> SEQUENCE: 401

Gln Gly Leu Val Tyr Ser Asp Gly Asn Ile Tyr
1 5 10

<210> SEQ ID NO 402
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VL-v10 (Vk)

<400> SEQUENCE: 402

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Asn Gln Gly Leu Val Tyr Ser
20 25 30

Asp Gly Asn Ile Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Met Arg Leu Ile Tyr Arg Val Ser Asn Arg Asp 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 Ile Tyr Tyr Cys Met Gln Gly
85 90 95

Thr His Trp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> SEQ ID NO 403
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VL-v11 (Vk)
CDRL1

<400> SEQUENCE: 403

Gln Val Leu Val Tyr Ser Asp Gly Asn Ile Tyr
1 5 10

<210> SEQ ID NO 404
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VL-v11

<400> SEQUENCE: 404

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Asn Gln Val Leu Val Tyr Ser
20 25 30

Asp Gly Asn Ile Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

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Pro Met Arg Leu Ile Tyr Arg Val Ser Asn Arg Asp 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 Ile Tyr Tyr Cys Met Gln Gly
                85                  90                  95

Thr His Trp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> SEQ ID NO 405
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence  nCoV-10 mAb VL-v12 (Vk)
      CDRL1

<400> SEQUENCE: 405

Pro Ser Leu Val Tyr Ser Asp Gly Asn Ile Tyr
1               5                   10


<210> SEQ ID NO 406
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VL-v12 (Vk)

<400> SEQUENCE: 406

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Asn Pro Ser Leu Val Tyr Ser
            20                  25                  30

Asp Gly Asn Ile Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
        35                  40                  45

Pro Met Arg Leu Ile Tyr Arg Val Ser Asn Arg Asp 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 Ile Tyr Tyr Cys Met Gln Gly
                85                  90                  95

Thr His Trp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> SEQ ID NO 407
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VL-v13 (Vk)

<400> SEQUENCE: 407

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Asp Gln Ser Leu Val Tyr Ser
            20                  25                  30

Asp Gly Asn Ile Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
        35                  40                  45
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Pro Met Arg Leu Ile Tyr Arg Val Ser Asn Arg Asp 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 Ile Tyr Tyr Cys Met Gln Gly
                85                  90                  95

Thr His Trp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> SEQ ID NO 408
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VL-v14 (Vk)

<400> SEQUENCE: 408

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Glu Gln Ser Leu Val Tyr Ser
            20                  25                  30

Asp Gly Asn Ile Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
        35                  40                  45

Pro Met Arg Leu Ile Tyr Arg Val Ser Asn Arg Asp 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 Ile Tyr Tyr Cys Met Gln Gly
                85                  90                  95

Thr His Trp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> SEQ ID NO 409
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VL-v15 (Vk)

<400> SEQUENCE: 409

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1               5                   10                  15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Asn Gln Ala Leu Val Tyr Ser
            20                  25                  30

Asp Gly Asn Ile Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
        35                  40                  45

Pro Met Arg Leu Ile Tyr Arg Val Ser Asn Arg Asp 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 Ile Tyr Tyr Cys Met Gln Gly
                85                  90                  95

Thr His Trp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> SEQ ID NO 410
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<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VL-v16 (Vk)

<400> SEQUENCE: 410

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Asn Gln Gly Leu Val Tyr Ser
20 25 30

Asp Gly Asn Ile Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Met Arg Leu Ile Tyr Arg Val Ser Asn Arg Asp 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 Ile Tyr Tyr Cys Met Gln Gly
85 90 95

Thr His Trp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> SEQ ID NO 411
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VL-v17 (Vk)

<400> SEQUENCE: 411

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Asn Gln Val Leu Val Tyr Ser
20 25 30

Asp Gly Asn Ile Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Met Arg Leu Ile Tyr Arg Val Ser Asn Arg Asp 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 Ile Tyr Tyr Cys Met Gln Gly
85 90 95

Thr His Trp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> SEQ ID NO 412
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VL-v18 (Vk)

<400> SEQUENCE: 412

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Asn Pro Ser Leu Val Tyr Ser
20 25 30

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Asp Gly Asn Ile Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
        35                  40                  45

Pro Met Arg Leu Ile Tyr Arg Val Ser Asn Arg Asp 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 Ile Tyr Tyr Cys Met Gln Gly
                85                  90                  95

Thr His Trp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> SEQ ID NO 413
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VL-v19 (Vk)

<400> SEQUENCE: 413

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1               5                   10                  15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Asp Gln Ser Leu Val Tyr Ser
            20                  25                  30

Asp Gly Asn Ile Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
        35                  40                  45

Pro Met Arg Leu Ile Tyr Arg Val Ser Asn Arg Asp 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 Ile Tyr Tyr Cys Met Gln Gly
                85                  90                  95

Thr His Trp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> SEQ ID NO 414
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VL-v20 (Vk)

<400> SEQUENCE: 414

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1               5                   10                  15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Glu Gln Ser Leu Val Tyr Ser
            20                  25                  30

Asp Gly Asn Ile Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
        35                  40                  45

Pro Met Arg Leu Ile Tyr Arg Val Ser Asn Arg Asp 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 Ile Tyr Tyr Cys Met Gln Gly
                85                  90                  95

Thr His Trp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110
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<210> SEQ ID NO 415
<211> LENGTH: 125
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VH-v21

<400> SEQUENCE: 415

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 Asn Tyr
20 25 30

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

Ala Val Ile Ser Phe Asp Gly Arg Ile Lys Phe Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Met Ser Arg Asp Ser 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 Lys Asp Arg Phe Gln Phe Ala Arg Ser Trp Tyr Gly Asp Tyr Phe
100 105 110

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

<210> SEQ ID NO 416
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VH-v21 CDRH2

<400> SEQUENCE: 416

Ile Ser Phe Asp Gly Arg Ile Lys
1 5

<210> SEQ ID NO 417
<211> LENGTH: 421
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic sequence nCoV-10 mAb VH-v21

<400> SEQUENCE: 417

gccagtgtca ggtgcagctg gtggagtctg ggggaggcgt ggtccagcct gggaggtccc 60

tgagactctc ctgtgcagcc tctggattca ccttcagtaa ctatggcatg cactgggtcc 120

gccaggctcc aggcaagggg ctggagtggc tggcagttat atcatttgat ggaagaatta 180

agttctatgc agactccgtg aagggccgat tcaccatgtc cagagacagt tccaagaaca 240

cgctgtatct gcaaatgaac agcctgagag ctgaggacac ggctgtgtat tactgtgcga 300

aagatcggtt ccagtttgcc agaagctggt acggtgacta ctttgactac tggggccagg 360

gaacccaggt caccgtctcc tcagcctcca ccaagggccc atcggtcttc cccctggcac 420

c 421

1. An antibody, or an antigen-binding fragment thereof, comprising a heavy chain variable domain (VH) comprising a CDRH1, a CDRH2, and a CDRH3, and a light chain variable domain (VL) comprising a CDRL1, a CDRL2, and a CDRL3, wherein the antibody or antigen binding fragment is capable of binding to a surface glycoprotein of SARS-CoV-2 expressed on a cell surface of a host cell and/or on a virion.

2. The antibody, or an antigen-binding fragment of claim **1**, wherein the antibody or antigen binding fragment is capable of binding to the Receptor Binding Domain (RBD) of a surface glycoprotein of SARS-CoV-2 and/or SARS-CoV expressed on a cell surface of a host cell and/or on a virion.

3. The antibody or antigen-binding fragment of claim **1**, which is capable of neutralizing a SARS-CoV-2 infection in an in vitro model of infection and/or in an in vivo animal model of infection and/or in a human.

4. An antibody, or antigen-binding fragment thereof, comprising a heavy chain variable domain (VH) comprising a CDRH1, a CDRH2, and a CDRH3, and a light chain variable domain (VL) comprising a CDRL1, a CDRL2, and a CDRL3, wherein:

(i) the CDRH1 comprises or consists of the amino acid sequence according to any one of SEQ ID NOs.: 6, 22, 38, 54, 70, 86, 102, 118, 134, 150, 166, 182, 198, 214, 230, 246, 262, 278, 294, 310, 326, 342, or 358, or a sequence variant thereof comprising one, two, or three acid substitutions, one or more of which substitutions is optionally a conservative substitution and/or is a substitution to a germline-encoded amino acid;

(ii) the CDRH2 comprises or consists of the amino acid sequence according to any one of SEQ ID NOs.: 7, 23, 39, 55, 71, 87, 103, 119, 135, 151, 167, 183, 199, 215, 231, 247, 263, 279, 295, 311, 327, 343, 359, or 416, or a sequence variant thereof comprising one, two, or three amino acid substitutions, one or more of which substitutions is optionally a conservative substitution and/or is a substitution to a germline-encoded amino acid;

(iii) the CDRH3 comprises or consists of the amino acid sequence according to any one of SEQ ID NOs.: 8, 24, 40, 56, 72, 88, 104, 120, 136, 152, 168, 184, 200, 216, 232, 248, 264, 280, 296, 312, 328, 344, 360, 375, 378, or 397, or a sequence variant thereof comprising one, two, or three amino acid substitutions, one or more of which substitutions is optionally a conservative substitution and/or is a substitution to a germline-encoded amino acid;

(iv) the CDRL1 comprises or consists of the amino acid sequence according to any one of SEQ ID NOs.: 14, 30, 46, 62, 78, 94, 110, 126, 142, 158, 174, 190, 206, 222, 238, 254, 270, 286, 302, 318, 334, 350, 366, 398, 399, 401, 403, or 405, or a sequence variant thereof comprising one, two, or three amino acid substitutions, one or more of which substitutions is optionally a conservative substitution and/or is a substitution to a germline-encoded amino acid;

(v) the CDRL2 comprises or consists of the amino acid sequence according to any one of SEQ ID NOs.: 15, 31, 47, 63, 79, 95, 111, 127, 143, 159, 175, 191, 207, 223, 239, 255, 271, 287, 303, 319, 335, 351, or 367, or a sequence variant thereof comprising one, two, or three amino acid substitutions, one or more of which substitutions is optionally a conservative substitution and/or is a substitution to a germline-encoded amino acid; and/or

(vi) the CDRL3 comprises or consists of the amino acid sequence according to any one of SEQ ID NOs.: 16, 32, 48, 64, 80, 96, 112, 128, 144, 160, 176, 192, 208, 224, 240, 256, 272, 288, 304, 320, 336, 352, 358, 386, or 394, or a sequence variant thereof comprising having one, two, or three amino acid substitutions, one or more of which substitutions is optionally a conservative substitution and/or is a substitution to a germline-encoded amino acid,

wherein the antibody or antigen binding fragment is capable of binding to a surface glycoprotein of SARS-CoV-2 expressed on a cell surface of a host cell and/or on a virion.

5. The antibody or antigen-binding fragment of claim **4**, which is capable of neutralizing a SARS-CoV-2 infection in an in vitro model of infection and/or in an in vivo animal model of infection and/or in a human.

6. The antibody or antigen-binding fragment of claim **4**, comprising CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 amino acid sequences according to SEQ ID NOs.:

(i) 6-8 and 14-16, respectively;
(ii) 22-24 and 30-32, respectively;
(iii) 22-24, 398, 31, and 32, respectively;
(iv) 22-24, 399, 31, and 32, respectively;
(v) 22-24, 401, 31, and 32, respectively;
(vi) 22-24, 403, 31, and 32, respectively;
(v) 22-24, 405, 31, and 32, respectively;
(vi) 38-40 and 46-48, respectively;
(vii) 38-40, 398, 47, and 48, respectively;
(viii) 38-40, 399, 47, and 48, respectively;
(viv) 38-40, 401, 47, and 48, respectively;
(x) 38-40, 403, 47, and 48, respectively;
(xi) 38-40, 405, 47, and 48, respectively;
(xii) 54-56 and 62-64, respectively;
(xiii) 70-72 and 78-80, respectively;
(xiv) 86-88 and 94-96, respectively;
(xv) 102-104 and 110-112, respectively;
(xvi) 118-120 and 126-128, respectively;
(xvii) 134-136 and 142-144, respectively;
(xviii) 150-152 and 158-160, respectively;
(xix) 166-168 and 174-176, respectively;
(xx) 182-184 and 190-192, respectively;
(xxi) 198-200 and 206-208, respectively;
(xxii) 214-216 and 222-224, respectively;
(xxiii) 230-232 and 238-240, respectively;
(xxiv) 246-248 and 254-256, respectively;
(xxv) 262-264 and 270-272, respectively;
(xxxvi) 278-280 and 286-288, respectively;
(xxvii) 294-296 and 302-304, respectively;
(xxviii) 310-312 and 318-320, respectively;
(xxix) 326-328 and 334-336, respectively;
(xxx) 342-344 and 350-352, respectively;
(xxxi) 358-360 and 366-368, respectively;
(xxxii) 22, 23, 375, and 30-32, respectively;
(xxxiii) 22, 23, 375, 398, 31, and 32, respectively;
(xxxiv) 22, 23, 375, 399, 31, and 32, respectively;
(xxxv) 22, 23, 375, 401, 31, and 32, respectively;
(xxxvi) 22, 23, 375, 403, 31, and 32, respectively;
(xxxvii) 22, 23, 375, 405, 31, and 32, respectively;
(xxxviii) 22, 23, 378, and 30-32, respectively;

(xxxix) 22, 23, 378, 398, 31, and 32, respectively;
(xl) 22, 23, 378, 399, 31, and 32, respectively;
(xli) 22, 23, 378, 401, 31, and 32, respectively;
(xlii) 22, 23, 378, 403, 31, and 32, respectively;
(xliii) 22, 23, 378, 405, 31, and 32, respectively;
(xliv) 22-24, 30, 31, and 386, respectively;
(xlv) 22-24, 398, 31, and 386, respectively;
(xlvi) 22-24, 399, 31, and 386, respectively;
(xlvii) 22-24, 401, 31, and 386, respectively;
(xlviii) 22-24, 403, 31, and 386, respectively;
(xlix) 22-24, 405, 31, and 386, respectively;
(l) 38-40, 46, 47, and 386, respectively;
(li) 38-40, 398, 47, and 386, respectively;
(lii) 38-40, 399, 47, and 386, respectively;
(liii) 38-40, 401, 47, and 386, respectively;
(liv) 38-40, 403, 47, and 386, respectively;
(lv) 38-40, 405, 47, and 386, respectively;
(lvi) 22-24, 30, 31, and 394, respectively;
(lvii) 22-24, 398, 31, and 394, respectively;
(lviii) 22-24, 399, 31, and 394, respectively;
(lix) 22-24, 401, 31, and 394, respectively;
(lx) 22-24, 403, 31, and 394, respectively;
(lxi) 22-24, 405, 31, and 394, respectively;
(lxii) 22, 23, 375, 30, 31, and 394, respectively;
(lxiii) 22, 23, 375, 30, 31, and 386, respectively;
(lxiv) 22, 23, 375, 398, 31, and 386, respectively;
(lxv) 22, 23, 375, 399, 31, and 386, respectively;
(lxvi) 22, 23, 375, 401, 31, and 386, respectively;
(lxvii) 22, 23, 375, 403, 31, and 386, respectively;
(lxviii) 22, 23, 375, 405, 31, and 386, respectively;
(lxix) 22, 23, 378, 30, 31, and 394, respectively;
(lxx) 22, 23, 378, 398, 31, and 394, respectively;
(lxxi) 22, 23, 378, 399, 31, and 394, respectively;
(lxxii) 22, 23, 378, 401, 31, and 394, respectively;
(lxxiii) 22, 23, 378, 403, 31, and 394, respectively;
(lxxiv) 22, 23, 378, 405, 31, and 394, respectively;
(lxxv) 22, 23, 378, 30, 31, and 386, respectively;
(lxxvi) 22, 23, 378, 398, 31, and 386, respectively;
(lxxvii) 22, 23, 378, 399, 31, and 386, respectively;
(lxxviii) 22, 23, 378, 401, 31, and 386, respectively;
(lxxix) 22, 23, 378, 403, 31, and 386, respectively;
(lxxx) 22, 23, 378, 405, 31, and 386, respectively;
(lxxxi) 22, 23, 397, and 30-32, respectively;
(lxxxii) 22, 23, 397, 398, 31, and 32, respectively;
(lxxxiii) 22, 23, 397, 399, 31, and 32, respectively;
(lxxxiv) 22, 23, 397, 401, 31, and 32, respectively;
(lxxxv) 22, 23, 397, 403, 31, and 32, respectively;
(lxxxvi) 22, 23, 397, 405, 31, and 32, respectively;
(lxxxvii) 22, 23, 397, 30, 31, and 386, respectively;
(lxxxviii) 22, 23, 397, 398, 31, and 386, respectively;
(lxxxix) 22, 23, 397, 399, 31, and 386, respectively;
(xc) 22, 23, 397, 401, 31, and 386, respectively;
(xci) 22, 23, 397, 403, 31, and 386, respectively;
(xcii) 22, 23, 397, 405, 31, and 386, respectively;
(xciii) 22, 23, 397, 30, 31, and 394, respectively;
(xciv) 22, 23, 397, 398, 31, and 394, respectively;
(xcv) 22, 23, 397, 399, 31, and 394, respectively;
(xcvi) 22, 23, 397, 401, 31, and 394, respectively;
(xcvii) 22, 23, 397, 403, 31, and 394, respectively;
(xcviii) 22, 23, 397, 405, 31, and 394, respectively;
(xcix) 22, 416, 24, 30, 31, and 32, respectively;
(c) 22, 416, 24, 30, 31, and 386, respectively;
(ci) 22, 416, 24, 30, 31, and 394, respectively;
(cii) 22, 416, 24, 398, 31, and 32, respectively;
(ciii) 22, 416, 24, 398, 31, and 386, respectively;
(civ) 22, 416, 24, 398, 31, and 394, respectively;
(cv) 22, 416, 24, 399, 31, and 32, respectively;
(cvi) 22, 416, 24, 399, 31, and 386, respectively;
(cvii) 22, 416, 24, 399, 31, and 394, respectively;
(cviii) 22, 416, 24, 401, 31, and 32, respectively;
(cix) 22, 416, 24, 401, 31, and 386, respectively;
(cx) 22, 416, 24, 401, 31, and 394, respectively;
(cxi) 22, 416, 24, 403, 31, and 32, respectively;
(cxii) 22, 416, 24, 403, 31, and 386, respectively;
(cxiii) 22, 416, 24, 403, 31, and 394, respectively;
(cxiv) 22, 416, 24, 405, 31, and 32, respectively;
(cxv) 22, 416, 24, 405, 31, and 386, respectively;
(cxvi) 22, 416, 24, 405, 31, and 394, respectively;
(cxvii) 22, 416, 375, 30, 31, and 32, respectively;
(cxviii) 22, 416, 375, 398, 31, and 386, respectively;
(cxix) 22, 416, 375, 398, 31, and 394, respectively;
(cxx) 22, 416, 375, 399, 31, and 386, respectively;
(cxxi) 22, 416, 375, 399, 31, and 394, respectively;
(cxxii) 22, 416, 375, 401, 31, and 386, respectively;
(cxxiii) 22, 416, 375, 401, 31, and 394, respectively;
(cxxiv) 22, 416, 375, 403, 31, and 386, respectively;
(cxxv) 22, 416, 375, 403, 31, and 394, respectively;
(cxxvi) 22, 416, 375, 405, 31, and 386, respectively;
(cxxvii) 22, 416, 375, 405, 31, and 394, respectively;
(cxxviii) 22, 416, 378, 30, 31, and 32, respectively;
(cxxix) 22, 416, 378, 398, 31, and 386, respectively;
(cxxx) 22, 416, 378, 398, 31, and 394, respectively;
(cxxxi) 22, 416, 378, 399, 31, and 386, respectively;
(cxxxii) 22, 416, 378, 399, 31, and 394, respectively;
(cxxxiii) 22, 416, 378, 401, 31, and 386, respectively;
(cxxxiv) 22, 416, 378, 401, 31, and 394, respectively;
(cxxxv) 22, 416, 375, 403, 31, and 386, respectively;
(cxxxvi) 22, 416, 378, 403, 31, and 394, respectively;
(cxxxvii) 22, 416, 378, 405, 31, and 386, respectively;
(cxxxviii) 22, 416, 378, 405, 31, and 394, respectively;
(cxxxix) 22, 416, 397, 30, 31, and 32, respectively;
(cxl) 22, 416, 397, 398, 31, and 386, respectively;
(cxli) 22, 416, 397, 398, 31, and 394, respectively;
(cxlii) 22, 416, 397, 399, 31, and 386, respectively;
(ccxliii) 22, 416, 397, 399, 31, and 394, respectively;
(cxliv) 22, 416, 397, 401, 31, and 386, respectively;
(cxlv) 22, 416, 397, 401, 31, and 394, respectively;
(cxlvi) 22, 416, 375, 403, 31, and 386, respectively;
(cxlvii) 22, 416, 397, 403, 31, and 394, respectively;
(cxlviii) 22, 416, 397, 405, 31, and 386, respectively; or
(cxlix) 22, 416, 397, 405, 31, and 394, respectively.

7. The antibody or antigen-binding fragment of claim **1**, wherein:

(i) the VH comprises or consists of an amino acid sequence having at least 85% identity to the amino acid sequence according to any one of SEQ ID NOs.: 5, 21, 37, 53, 69, 85, 101, 117, 133, 149, 165, 181, 197, 213, 229, 245, 261, 277, 293, 309, 325, 341, 357, 374, 377, 396, and 415, wherein the variation, if present, is optionally limited to one or more framework regions and/or the variation, if present, comprises one or more substitution to a germline-encoded amino acid; and/or

(ii) the VL comprises or consists of an amino acid sequence having at least 85% identity to the amino acid sequence according to any one of SEQ ID NOs.: 13, 29, 45, 61, 77, 93, 109, 125, 141, 157, 173, 189, 205, 221, 237, 253, 269, 285, 301, 317, 333, 349, 365, 380, 383, 385, 388, 392, 393, 400, 402, 404, and 406-414,

wherein the variation, if present, is optionally limited to one or more framework regions and/or the variation, if present, comprises one or more substitution to a germline-encoded amino acid.

8. The antibody or antigen-binding fragment of claim **1**, wherein the VH comprises or consists of any VH amino acid sequence set forth in Table 1, and wherein the VL comprises or consists of any VL amino acid sequence set forth in Table 1, wherein, optionally, the VH and the VL comprise or consist of the amino acid sequences according to SEQ ID NOs.:

(i) 5 and 13, respectively;
(ii) 21 and any one of 29, 45, 380, 383, 385, 388, 392, 393, 400, 402, 404, 406, 407, 408, 409, 410, 411, 412, 413, and 414, respectively;
(iii) 415 and any one of 29, 45, 380, 383, 385, 388, 392, 400, 402, 404, 406, 407, 408, 409, 410, 411, 412, 413, and 414, respectively;
(iv) 37 and any one of 29, 45, 380, 383, 385, 388, 392, 400, 402, 404, 406, 407, 408, 409, 410, 411, 412, 413, and 414, respectively;
(v) 53 and 61, respectively;
(vi) 69 and 77, respectively;
(vii) 85 and 93, respectively;
(viii) 101 and 109, respectively;
(ix) 117 and any one of 125, 141, and 157, respectively;
(x) 133 and any one of 125, 141, and 157, respectively;
(xi) 149 and any one of 125, 141, and 157, respectively;
(xii) 165 and 173, respectively;
(xiii) 181 and 189, respectively;
(xiv) 197 and 205, respectively;
(xv) 213 and 221, respectively;
(xvi) 229 and 237, respectively;
(xvii) 245 and 253, respectively;
(xviii) 261 and 269, respectively;
(xix) 277 and 285, respectively;
(xx) 293 and 301, respectively;
(xxi) 309 and 317, respectively;
(xxii) 325 and 333, respectively;
(xxiii) 341 and 349, respectively;
(xxiv) 357 and 365, respectively;
(xxv) 374 and any one of 29, 45, 380, 383, 385, 392, 393, 400, 402, 404, 406, 407, 408, 409, 410, 411, 412, 413, and 414, respectively;
(xxvi) 377 and any one of 29, 45, 380, 383, 385, 392, 393, 400, 402, 404, 406, 407, 408, 409, 410, 411, 412, 413, and 414, respectively;
(xxvii) 415 and any one of 29, 45, 380, 383, 385, 392, 393, 400, 402, 404, 406, 407, 408, 409, 410, 411, 412, 413, and 414, respectively; or
(xxviii) 396 and any one of 29, 37, 45, 380, 383, 385, 388, 392, 393, 400, 402, 404, 406, 407, 408, 409, 410, 411, 412, 413, and 414, respectively.

9. The antibody or antigen-binding fragment of claim **1**, which:

(i) recognizes an epitope in the ACE2 receptor binding motif (RBM, SEQ ID NO.:390) of SARS-CoV-2;
(ii) is capable of blocking an interaction between SARS-CoV-2 (e.g., SARS-CoV-2 RBM) and ACE2;
(ii) is capable of binding to SARS-CoV-2 S protein with greater avidity than to SARS coronavirus S protein;
(iv) is capable of staining about 30%, about 35%, about 40%, about 50%, about 55%, about 56%, about 57%, about 58%, about 59%, about 60%, or more of target cells expressing SARS-CoV-2 surface glycoprotein in a sample comprising about 50,000 of the target cells in approximately 100 μL when the antibody or antigen-binding fragment is present at 10 μg/ml;
(v) recognizes an epitope that is conserved in the ACE2 RBM of SARS-CoV-2 and in an ACE2 RBM of SARS coronavirus;
(vi) is cross-reactive against SARS-CoV-2 and SARS coronavirus;
(vii) recognizes an epitope in the SARS-CoV-2 surface glycoprotein that is not in the ACE2 RBM; or
(viii) any combination of (i)-(vii).

10. The antibody or antigen-binding fragment of claim **4**, which is a IgG, IgA, IgM, IgE, or IgD isotype.

11. The antibody or antigen-binding fragment of claim **4**, which is an IgG isotype selected from IgG1, IgG2, IgG3, and IgG4.

12. The antibody or antigen-binding fragment of claim **4**, which is human, humanized, or chimeric.

13. The antibody or antigen-binding fragment of claim **4**, wherein the antibody, or the antigen-binding fragment, comprises a human antibody, a monoclonal antibody, a purified antibody, a single chain antibody, a Fab, a Fab', a F(ab')2, a Fv, or a scFv.

14. The antibody or antigen-binding fragment of claim **4**, wherein the antibody or antigen-binding fragment is a multi-specific antibody or antigen binding fragment.

15. The antibody or antigen-binding fragment of claim **14**, wherein the antibody or antigen binding fragment is a bispecific antibody or antigen-binding fragment.

16. The antibody or antigen-binding fragment of claim **14**, comprising:

(i) a first VH and a first VL; and
(ii) a second VH and a second VL,

wherein the first VH and the second VH are different and each independently comprise an amino acid sequence having at least 85% identity to the amino acid sequence set forth in any one of SEQ ID NOs.: 5, 21, 37, 53, 69, 85, 101, 117, 133, 149, 165, 181, 197, 213, 229, 245, 261, 277, 293, 309, 325, 341, 357, 374, 377, 396, and 415, and

wherein the first VL and the second VL are different and each independently comprise an amino acid sequence having at least 85% identity to the amino acid sequence set forth in any one of SEQ ID NOs.: 13, 29, 45, 61, 77, 93, 109, 125, 141, 157, 173, 189, 205, 221, 237, 253, 269, 285, 301, 317, 333, 349, 365, 380, 383, 385, 388, 392, 393, 400, 402, 404, and 406-414,

and wherein the first VH and the first VL together form a first antigen-binding site, and wherein the second VH and the second VL together form a second antigen-binding site.

17. The antibody or antigen-binding fragment of claim **16**, wherein:

(i) the first VH comprises or consists of the amino acid sequence set forth in any one of SEQ ID NOs.:21, 37, 374, 377, 396, and 415, and the first VL comprises or consists of the amino acid sequence set forth in any one of SEQ ID NOs.:29, 45, 380, 383, 385, 388, 392, 393, 400, 402, 404, and 406-414; and
(ii) the second VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:69 and the second VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.: 77.

18. The antibody or antigen-binding fragment of claim **4**, wherein the antibody or antigen-binding fragment further comprises a Fc polypeptide or a fragment thereof.

19. The antibody or antigen-binding fragment of claim **18**, wherein the Fc polypeptide or fragment thereof comprises:

(i) a mutation that enhances binding to a FcRn as compared to a reference Fc polypeptide that does not comprise the mutation; and/or

(ii) a mutation that enhances binding to a FcγR as compared to a reference Fc polypeptide that does not comprise the mutation.

20. The antibody or antigen-binding fragment of claim **19**, wherein the mutation that enhances binding to a FcRn comprises: M428L; N434S; N434H; N434A; N434S; M252Y; S254T; T256E; T250Q; P257I; Q311I; D376V; T307A; E380A; or any combination thereof.

21. The antibody or antigen-binding fragment of claim **19**, wherein the mutation that enhances binding to FcRn comprises:

(i) M428L/N434S;

(ii) M252Y/S254T/T256E;

(iii) T250Q/M428L;

(iv) P257I/Q311I;

(v) P257I/N434H;

(vi) D376V/N434H;

(vii) T307A/E380A/N434A; or

(viii) any combination of (i)-(vii).

22. The antibody or antigen-binding fragment of claim **19**, wherein the mutation that enhances binding to FcRn comprises M428L/N434S.

23. The antibody or antigen-binding fragment of claim **19**, wherein the mutation that enhances binding to a FcγR comprises: S239D; I332E; A330L; G236A; or any combination thereof.

24. The antibody or antigen-binding fragment of claim **19**, wherein the mutation that enhances binding to a FcγR comprises:

(i) S239D/I332E;

(ii) S239D/A330L/I332E;

(iii) G236A/S239D/I332E; or

(iv) G236A/A330L/I332E.

25. The antibody or antigen-binding fragment claim **4**, which comprises a mutation that alters glycosylation, wherein the mutation that alters glycosylation comprises N297A, N297Q, or N297G, and/or which is aglycosylated and/or afucosylated.

26. An isolated polynucleotide encoding the antibody or antigen-binding fragment of claim **1**, or encoding a VH, a heavy chain, a VL, and/or a light chain of the antibody or the antigen-binding fragment.

27. The polynucleotide of claim **28**, wherein the polynucleotide comprises deoxyribonucleic acid (DNA) or ribonucleic acid (RNA), wherein the RNA optionally comprises messenger RNA (mRNA).

28. The polynucleotide of claim **26**, which is codon-optimized for expression in a host cell.

29. The polynucleotide of claim **26**, comprising a polynucleotide having at least 50% identity to the polynucleotide sequence according to any one or more of SEQ ID NOs.:1-4, 9-12, 17-20, 25-28, 33-36, 41-44, 49-52, 57-60, 65-68, 73-76, 81-84, 89-92, 97-100, 105-108, 113-116, 121-124, 129-132, 137-140, 145-148, 153-156, 161-164, 169-172, 177-180, 185-188, 193-196, 201-204, 209-212, 217-220, 225-228, 233-236, 241-244, 249-252, 257-260, 265-268, 273-276, 281-284, 289-292, 297-300, 305-308, 313-316, 321-324, 329-332, 337-340, 345-348, 353-356, 361-364, 372, 373, 376, 379, 381, 384, 387, 389 and 417.

30. A recombinant vector comprising the polynucleotide of claim **29**.

31. A host cell comprising the polynucleotide of claim **26**, wherein the polynucleotide is heterologous to the host cell.

32. A human B cell comprising the polynucleotide of claim **26**, wherein the polynucleotide is heterologous to the human B cell and/or wherein the human B cell is immortalized.

33. A composition comprising:

the antibody or antigen-binding fragment of claim **4**,

and a pharmaceutically acceptable excipient, carrier, or diluent.

34. The composition of claim **33**, comprising two or more different antibodies or antigen-binding fragments of claim **4**.

35. The composition of claim **34**, comprising a first antibody or antigen-binding fragment and a second antibody or antigen-binding fragment, wherein:

(i) the first antibody or antigen-binding fragment comprises a VH comprising or consisting of the amino acid sequence set forth in any one of SEQ ID NOs.:21, 37, 374, 377, 396 and 415, and a VL comprising or consisting of the amino acid sequence set forth in any one of SEQ ID NOs.:29, 45, 380, 383, 385, 388, 392, 393, 400, 402, 404, and 406-414; and

(ii) the second antibody or antigen-binding fragment comprises a VH comprising or consisting of the amino acid sequence set forth in SEQ ID NO.:69, and a VL comprising or consisting of the amino acid sequence set forth in SEQ ID NO.:77.

36. A composition comprising the polynucleotide of claim **26** encapsulated in a carrier molecule, wherein the carrier molecule optionally comprises a lipid, a lipid-derived delivery vehicle, such as a liposome, a solid lipid nanoparticle, an oily suspension, a submicron lipid emulsion, a lipid microbubble, an inverse lipid micelle, a cochlear liposome, a lipid microtubule, a lipid microcylinder, lipid nanoparticle (LNP), or a nanoscale platform.

37. A method of treating a SARS-CoV-2 infection in a subject, the method comprising administering to the subject an effective amount of

the antibody or antigen-binding fragment of claim **4**.

38. The method of claim **37**, comprising administering to the subject

(a) a first antibody or antigen-binding fragment of claim **4**, when the subject has received a second antibody or antigen-binding fragment of claim **4**;

(b) a second antibody or antigen-binding fragment of claim **4**, when the subject has received a first antibody or antigen-binding fragment of claim **4**; or

(c) a first antibody or antigen-binding fragment of claim **4**, and a second antibody or antigen-binding fragment of claim **4**,

wherein

(i) the first antibody or antigen-binding fragment comprises a VH comprising or consisting of the amino acid sequence set forth in any one of SEQ ID NOs.:21, 37, 374, 377, 396 and 415, and a VL comprising or consisting of the amino acid sequence set forth in any one of SEQ ID NOs.:29, 45, 380, 383, 385, 388, 392, 393, 400, 402, 404, and 406-414; and

(ii) the second antibody or antigen-binding fragment comprises a VH comprising or consisting of the amino acid sequence set forth in SEQ ID NO.:69, and a VL comprising or consisting of the amino acid sequence set forth in SEQ ID NO.:77.

39.-**40**. (canceled)

41. A method for in vitro diagnosis of a sarbecovirus infection, the method comprising:

(i) contacting a sample from a subject with an antibody or antigen-binding fragment of claim **4**; and

(ii) detecting a complex comprising an antigen and the antibody, or comprising an antigen and the antigen-binding fragment.

42. The method of claim **41**, wherein the sarbecovirus is SARS-CoV or SARS-CoV-2.

43. The method of claim **41**, wherein the sample comprises blood isolated from the subject.

44. A method of treating a SARS-CoV-2 infection in a subject, the method comprising administering to the subject an effective amount of the antibody or antigen-binding fragment of claim **1**.

* * * * *