ANTIBODIES AGAINST SARS-COV-2

STATEMENT REGARDING SEQUENCE LISTING

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_409WO_SEQUENCE_LISTING.txt. The text file is 489 KB, was created on May 7, 2021, and is being submitted electronically via EFS-Web.

BACKGROUND

A novel betacoronavirus emerged in Wuhan, China, in late 2019. As of May 2, 2021, approximately 152 million cases of infection by this virus (termed, among other names, SARS-CoV-2 and Wuhan coronavirus) were confirmed worldwide, and had resulted in approximately 3.195 million deaths. Therapies for preventing or treating SARS-CoV-2 infection are needed.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A-1D show binding of certain antibodies to SARS-CoV-2 Spike protein RBD and SARS-CoV-1 Spike protein RBD. Human monoclonal antibodies isolated from patients who recovered from SARS-CoV-2 infection were recombinantly expressed and tested for RBD binding by ELISA. Figure 1A shows binding of five antibodies, Figure 1B and Figure 1C each show binding of seven antibodies, and Figure 1D shows binding of four antibodies. Two antibodies in the top panel of Figure 1B are shown using black symbols. In Figure 1B, S2X28 binding is represented by a line that stays at or near zero OD for the full range of concentrations tested. In Figure 1B (top), S2X41 binding is represented by the curve with an EC50 of approximarely 20.01 ng/ml. In each of Figures 1A-1D, the top panel shows binding to SARS-CoV-2 RBD and the bottom panel shows binding to SARS-CoV-1 RBD. The boxes on the right side of each figure, where present, indicate the calculated EC50 value for the indicated antibody.

Figure 2 shows inhibition of SARS-CoV-2 RBD binding to human ACE2 by recombinantly expressed monoclonal antibodies isolated from patients who recovered from SARS-CoV-2 infection. ELISA plates were coated with recombinant human ACE2 (produced in-house). Coating was carried out with ACE2 at 2ug/ml in PBS. Plates were incubated overnight at 4°C and blocking was performed with blocker Casein (1% Casein from Thermofisher) for 1 hour at room temperature.

Figures 3A-3F show results from neutralization of infection assays using certain antibodies against SARS-CoV-2 pseudotyped virus. Monoclonal antibodies isolated from patients who recovered from SARS-CoV-2 infection were expressed recombinantly and tested in neutralization assays against murine leukemia virus (MLV) pseudotyped with SARS-CoV-2 Spike protein. Figure 3A shows results for three antibodies. Figures 3B-3F each show results for four antibodies. Antibodies were tested at concentrations indicated in the x-axis. Boxes on the right side of each figure, where present, indicate the calculated IC50 for the indicated antibody.

Figures 4A-4N show binding of further antibodies to SARS-CoV-2 Spike protein, SARS-CoV-2 Spike protein RBD, and SARS-CoV-1 Spike protein RBD. Monoclonal antibodies isolated from patients who recovered from SARS-CoV-2 infection were expressed recombinantly and tested for RBD binding by ELISA. The boxes on the right side of each figure show the calculated EC50 value for the indicated antibody.

Figures 5A-5D show results from neutralization of infection assays using further antibodies against SARS-CoV-2 pseudotyped virus. Monoclonal antibodies isolated from patients who recovered from SARS-CoV-2 infection were expressed recombinantly and tested in neutralization assays (one antibody per assay) against murine leukemia virus (MLV) pseudotyped with SARS-CoV-2 Spike protein. Figures 5A and 5C each show results for three antibodies. Figure 5B shows results for two antibodies and Figure 5D shows results for four antibodies. Antibodies were tested at concentrations as indicated on the x-axis. Boxes on the right side of each figure, where present, show the calculated EC50 for the indicated antibody.

Figures 6A and 6B show results from neutralization of infection assays using monoclonal antibodies against authentic SARS-CoV-2 virus. Comparator antibody "S309-v2" comprises the VH amino acid sequence set forth in SEQ ID NO.: 342 and the VL amino acid sequence set forth in SEQ ID NO.: 346 (CDRH1-H3 and L1-L3 as set forth in SEQ ID NOs.:343-345 and 347-349, respectively), and is an engineered variant of an antibody isolated from a patient who recovered from SARS-CoV-1 infection. Vero E6 cells cultured in DMEM supplemented with 10% FBS (VWR) and 1x Penicillin/Streptomycin (Thermo Fisher Scientific) were seeded in white 96-well plates at 20,000 cells/well and attached overnight. Serial 1:4 dilutions of the antibodies were incubated with 200 pfu of SARS-CoV-2 (isolate USA-WA1/2020, passage 3, passaged in Vero E6 cells) for 30 minutes at 37°C in a BSL-3 facility. Cell supernatant was removed and the virus-antibody mixture was added to the cells. 24 hours post infection, cells were fixed with 4% paraformaldehyde for 30 minutes, followed by two PBS (pH 7.4) washes and permeabilization with 0.25% Triton X-100 in PBS for 30 minutes. After blocking in 5% milk powder/PBS for 30 minutes, cells were incubated with a primary antibody targeting SARS-CoV-2 nucleocapsid protein (Sino Biological, cat. 40143-R001) at a 1:2000 dilution for 1hour. After washing and incubation with a secondary Alexa647-labeled antibody mixed with 1 μg/ml Hoechst33342 for 1 hour, plates were imaged on an automated cell-imaging reader (Cytation 5, Biotek) and nucleocapsid-positive cells were counted using the manufacturer's supplied software. Data were processed using Prism software (GraphPad Prism 8.0).

Figures 7A-7D show results from neutralization of infection assays using further antibodies against SARS-CoV-2 pseudotyped virus. Monoclonal antibodies isolated from patients who recovered from SARS-CoV-2 infection were expressed recombinantly and tested in neutralization assays against murine leukemia virus (MLV) pseudotyped with SARS-CoV-2 Spike protein. Figures 7A and 7B each show results for four antibodies, along with comparator antibody S309 (VH amino acid sequence of SEQ ID NO.:139, VL amino acid sequence of SEQ ID NO.:143; CDRH1-H3 and L1-L3 as set forth in SEQ ID NOs.:140-142 and 144-146, respectively), isolated from a patient who recovered from SARS-CoV-1 infection. Figure 7C shows results for three

antibodies along with S309, and Figure 7D shows results for two antibodies along with S309. Antibody "S2H58" in Figure 7D comprises the VH amino acid sequence set forth in SEQ ID NO.: 228 and the VL amino acid sequence set forth in SEQ ID NO.: 238. Antibodies were tested at concentrations as indicated on the x-axis.

Figures 8A and 8B show binding of antibodies to SARS-CoV-2 Spike protein RBD and SARS-CoV-1 Spike protein RBD. Monoclonal antibodies isolated from patients who recovered from SARS-CoV-2 infection were expressed recombinantly and tested for RBD binding by ELISA. Figure 8A shows binding of five antibodies and one comparator antibody, S309 (VH amino acid sequence of SEQ ID NO.:139, VL amino acid sequence of SEQ ID NO.:143; CDRH1-H3 and L1-L3 as set forth in SEQ ID NOs.:140-142 and 144-146, respectively), isolated from a patient who recovered from SARS-CoV-1 infection. Figure 8B shows binding of four antibodies and S309. In each of Figures 8A and 8B, the left panel shows binding to SARS-CoV-2 RBD and the right panel shows binding to SARS-CoV-1 RBD. The boxes on the right side of each panel indicate the calculated EC50 value for the indicated antibody.

Figures 9A-9F show results from neutralization of infection assays using antibodies against SARS-CoV-2 pseudotyped virus. Monoclonal antibodies isolated from patients who recovered from SARS-CoV-2 infection were expressed recombinantly and tested in neutralization assays against murine leukemia virus (MLV) pseudotyped with SARS-CoV-2 Spike protein. Antibodies were tested at concentrations as indicated on the x-axis. Calculated IC50, IC80, and IC90 values (expressed as ng/ml) are shown below the graph in each figure.

Figures 10A-10E show binding of antibodies to SARS-CoV-2 Spike protein RBD and SARS-CoV-1 Spike protein RBD (SARS-CoV-1 Spike protein RBD being labeled "SARS RBD" in the lower graph in each figure). Monoclonal antibodies isolated from patients who recovered from SARS-CoV-2 infection were expressed recombinantly and tested for RBD binding by ELISA. In each of Figures 10A-10E, the top panel shows binding to SARS-CoV-2 RBD and the bottom panel shows binding to SARS-CoV-1 RBD. The boxes on the right side of each figure, where present, show the calculated EC50 value for the indicated antibody.

Figures 11A-11D show results from neutralization of infection assays using certain monoclonal antibodies. Antibodies were tested in neutralization assays against murine leukemia virus (MLV) pseudotyped with SARS-CoV-2 Spike protein. Figure 11A shows results for monoclonal antibodies S2X193 and S2X195. Figure 11B shows results for monoclonal antibodies S2X219 and S2X244. Figure 11C shows results for monoclonal antibodies S2X246 and S2X256. Figure 11D shows results for monoclonal antibody S2X278. The x-axis shows the total concentration of antibody. Calculated IC50, IC80, and IC90 values (expressed as ng/ml) are shown in the box on the right side of each figure.

Figures 12A-12D show results from neutralization of infection assays using certain monoclonal antibodies. Antibodies were expressed recombinantly and tested in neutralization assays against vesicular stomatitis virus (VSV) pseudotyped with SARS-CoV-2 Spike protein. Figure 12A shows results for monoclonal antibodies S2X193 and S2X195, along with comparator antibody S2X190. Figure 12B shows results for monoclonal antibody S2X219. Figure 12C shows results for monoclonal antibodies S2X244, S2X246, and S2X256. Figure 12D shows results for monoclonal antibodies S2X269 and S2X278. Antibodies were tested at concentrations indicated on the x-axis. Calculated IC50 and IC90 values (expressed as ng/ml) are shown at the bottom of each figure.

Figures 13A and 13B show the ability of certain monoclonal antibodies to inhibit binding by SARS-CoV-2 RBD to human ACE2. ELISA plates were coated with recombinant human ACE2 at 2 μg/ml in PBS. Serial dilutions of monoclonal antibodies were incubated with SARS-CoV-2 RBD at 20 ng/ml (RBD fused with mouse Fc, from Sino Biological) for 30 minutes at 37°C and then transferred onto the ACE2-coated plates for an additional 20 minute incubation at room temperature. Eleven serial dilutions were used, starting at 10 μg/ml and diluting at 1:3. Binding of RBD to ACE2 was detected using secondary antibody goat F(ab')2 anti-mouse IgG(H+L) antibody (Southern Biotech) conjugated to alkaline phosphatase, followed by addition of pNPP (Sigma Aldrich N2765-100TAB) in bicarbonate buffer and reading absorbance at 405nm.

Figure 13A shows results for monoclonal antibodies S2X193 and S2X195, along with four comparator antibodies. Figure 13B shows results for monoclonal antibodies S2X219, S2X244, S2X246, S2X256, S2X269, and S2X278. Calculated IC50 values are shown at or to the right of the graph in each figure.

Figures 14A-14H show binding affinity and avidity of certain monoclonal antibodies of the present disclosure to SARS-CoV-2 RBD, as measured by Octet. Antibody (as indicated at the bottom-right of each figure) was loaded on Protein A pins at 2.7 μg/ml. SARS-CoV-2 RBD was loaded for 5 minutes at 6 μg/ml, 1.5 μg/ml, or 0.4 μg/ml. Dissociation was measured for 7 minutes. The vertical dashed line in each figure indicates the start of the dissociation phase.

Figure 15 shows binding affinity and avidity of monoclonal antibodies S2X219 (first panel) and S2X193, S2X195, S2X244, S2X246, S2X256, S2X269, and S2X278, along with four comparator antibodies (second panel), to SARS-CoV-1 RBD as measured by Octet. Antibody was loaded on Protein A pins at 2.7 μg/ml. SARS-CoV-1 RBD was loaded for 5 minutes at 6 μg/ml. Dissociation was measured for 7 minutes. The vertical dashed line in each graph indicates the start of the dissociation phase. In the second panel, the order of the curves curves (top to bottom) corresponds to the antibodies listed to the right of the graph (top to bottom). By way of illustration, the top curve corresponds to S2X127 and the bottom curve corresponds to S2X278.

Figures 16A-16D show neutralization of SARS-CoV-2 infection by certain monoclonal antibodies, as assessed by inhibition of nucleocapsid (NP) expression at 24 hours post infection. Figure 16A shows neutralization of SARS-CoV-2 infection by monoclonal antibodies S2N22, S2N12, S2N28, S2N25, S2H58-v2, along with comparator antibody S309-v2 (VH amino acid sequence of SEQ ID NO.:342, VL amino acid sequence of SEQ ID NO.:346; CDRH1-H3 and L1-L3 as set forth in SEQ ID NOs.:343-345 and 347-349, respectively). Figure 16B shows neutralization of SARS-CoV-2 infection by monoclonal antibodies S2E9, S2E6, S2E13, S2K4, S2E14, S2E7, and S2E12 (VH amino acid sequence of SEQ ID NO.:399, VL amino acid sequence of SEQ ID NO.:403; CDRH1-H3 and L1-L3 as set forth in SEQ ID NOs.:400, 766, 402 and 404-406, respectively), along with comparator antibody S309-v2. Figure

16C shows neutralization of SARS-CoV-2 infection by monoclonal antibodies S2H37, S2H73, S2H40, S2H70, and S2H71, along with comparator antibody S309-v2 (with M428L/N434S Fc mutations). Figure 16D shows neutralization of SARS-CoV-2 infection by monoclonal antibodies S2X30, S2H58-v1, S2H66, S2H62, and S2H30, along with comparator antibody S309-v2. Calculated IC50 values are shown below each graph.

Figures 17A-17C show results from neutralization of infection assays using certain monoclonal antibodies. Figure 17A shows results for monoclonal antibodies S2M11 and S2M28. Figure 17B shows results for monoclonal antibody S2M16. Figure 17C shows results for monoclonal antibodies S2M7 and S2L49. Antibodies were tested in neutralization assays against murine leukemia virus (MLV) pseudotyped with SARS-CoV-2 Spike protein. The x-axis shows the total concentration of antibody. Calculated IC50, IC80, and IC90 values (expressed as ng/ml) are shown in the box below each graph.

Figures 18A-18E show binding of certain monoclonal antibodies to SARS-CoV-2 Spike protein, SARS-CoV-2 Spike protein RBD, SARS-CoV-1 Spike protein, and SARS-CoV-1 Spike protein RBD. Antibodies isolated from patients who recovered from SARS-CoV-2 infection were expressed recombinantly and tested for Spike and Spike RBD binding by ELISA. The boxes on the right side of each figure show calculated EC50 values (expressed as ng/ml).

Figures 19A-19E show results from neutralization of infection assays using certain monoclonal antibodies. Antibodies were tested in neutralization assays against murine leukemia virus (MLV) pseudotyped with SARS-CoV-2 Spike protein. Figure 19A shows results for monoclonal antibodies S2X149 and S2X179. Figure 19B shows results for monoclonal antibody S2D65. Figure 19C shows results for monoclonal antibody S2D97. Figure 19D shows results for monoclonal antibody S2D106. Figure 19E shows results for monoclonal antibody S2H101. The x-axis shows the total concentration of antibody. Calculated IC50, IC80, and IC90 values are shown in the box on the right side of each figure, in the left-hand column of the box.

Figures 20A and 20B show binding of human monoclonal antibody S2X149 and comparator antibody S309-v2 LS (VH amino acid sequence of SEQ ID NO.:342, VL amino acid sequence of SEQ ID NO.:346; CDRH1-H3 and L1-L3 as set forth in SEQ ID NOs.:343-345 and 347-349, respectively; expressed as rIgG1 with M428L and N434S Fc mutations) to SARS-CoV-1 Spike protein, SARS-CoV-1 Spike protein RBD, and SARS-CoV-2 Spike protein RBD. Human monoclonal antibodies were expressed recombinantly and binding was tested by ELISA. Figure 20A shows binding of antibodies to SARS-CoV-1 Spike protein RBD (top panel) and SARS-CoV-1 Spike protein (bottom panel). Figure 20B shows binding of antibodies to SARS-CoV-2 Spike protein RBD (top panel) and to an uncoated control plate (bottom panel). The boxes to the right of the graphs show calculated EC50 values.

Figures 21A and 21B show binding of human monoclonal antibody S2X179 and comparator antibody S2X200 to SARS-CoV-1 Spike protein, SARS-CoV-1 Spike protein RBD, and SARS-CoV-2 Spike protein RBD. Human monoclonal antibodies were expressed recombinantly and binding was tested by ELISA. Figure 21A shows binding of antibodies to SARS-CoV-1 Spike protein RBD (top panel) and SARS-CoV-1 Spike protein (bottom panel). Figure 21B shows binding of antibodies to SARS-CoV-2 Spike protein RBD (top panel) and to an uncoated control plate (bottom panel). The box to the right of the top graph in Figure 21B shows calculated EC50 values for binding SARS-CoV-2 RBD.

Figures 22A and 22B show binding of human monoclonal antibodies S2H101, S2D65 (22A), S2D97, and S2D106 (22B) to SARS-CoV-2 Spike protein RBD. Antibodies were expressed recombinantly and binding was tested by ELISA. The boxes to the right of the graphs show calculated EC50 values.

Figures 23A and 23B show antibody inhibition of binding by SARS-CoV-2 RBD to human ACE2, as measured by ELISA. Figure 23A shows results for monoclonal antibody S2X149. Figure 24B shows results for monoclonal antibody S2X179 and comparator antibody S2X200. Calculated IC50 values are shown to the right of each graph.

Figure 24 summarizes results of quantitative epitope-specific serology studies using monoclonal antibody S309 and other anti-Spike antibodies, as determined by binding competition, cryo-EM, and crystallography data. Underlined antibodies are cross-reactive with SARS-CoV-1.

Figures 25A and 25B show neutralization of SARS-CoV-2 infection by certain monoclonal antibodies. Figure 25A shows results for four antibodies of the present disclosure, along with comparator antibodies S309 N55Q LS and S2X193. S309 N55Q LS comprises the VH amino acid sequence set forth in SEQ ID NO:342 and the VL amino acid sequence set forth in SEQ ID NO: 346, and comprises an MLNS modification in the Fc region. Figure 25B shows results for antibodies S2X129 and S2X132, along with four comparator antibodies. Calculated IC50 values are shown in the boxes below each graph. Calculated EC50 and EC90 values are shown at the bottom of each figure.

Figure 26 shows neutralization of SARS-CoV-2 infection by certain monoclonal antibodies using a VSV pseudovirus. Data are from one single experiment, triplicate wells VSV-luc(spike D19) pseudovirus. "LS" = Fc mutations M428L + N434S.

Figure 27 shows neutralization of infection by live SARS-CoV-2 by certain monoclonal antibodies. Data are from triplicate wells SARS-CoV-2-luc, MOI 0.1, 6h infection.

Figures 28A and 28B show activation of FcγRIIIa (V158 allele) (Figure 28A) and FcγRIIa (H131 allele) (Figure 28B) by certain monoclonal antibodies. Data show experiments using CHO target cells expressing SARS CoV2 S protein.

Figures 29A and 29B show binding (ELISA) of certain antibodies to SARS-CoV-2 RBD and Spike protein.

Figures 30A and 30B show binding of certain antibodies against SARS-CoV-2 RBD, SARS-CoV-2 S protein, and SARS-CoV-1 RBD.

Figures 31A and 31B show binding of antibody S2D106 to SARS-CoV-2 RBD in the presence of different concentrations of AAPH (2,2'-azobis(2-amidinopropane) dihydrochloride) or after UV irradiation. Both AAPH and UV radiation are used to

induce oxidation stress in the antibody. Figure 31A shows binding of S2D106 to RBD as measured by indirect ELISA. Figure 31B shows binding of S2D106 as measured by sandwich ELISA; x-axis = concentration of RBD.

Figures 32A-32C show neutralization of infection (pseudovirus particles) by S2E12 and engineered variants thereof (*see* Table 22 in Example 9 for VH and VL sequences of S2E12 antibodies). Figure 32A and Figure 32B show results from two repetitions of the same experiment. Figure 32C shows results for a third experiment using S2E12 and other variants thereof.

Figures 33A and 33B show binding of certain antibodies to SARS-CoV-2 RBD as measured by indirect ELISA. Figure 33A shows results for eight antibodies. Figure 33B shows the average of results from duplicate experiments for six antibodies.

Figures 34A and 34B show binding of certain antibodies to SARS-CoV-2 RBD as measured by sandwich ELISA. Figure 34A shows results for eight antibodies. Figure 34B shows the average of results from duplicate experiments for six antibodies.

Figure 35 shows neutralization of infection using live SARS-CoV-2 virus by five antibodies. The curve labeled "S2E12-11" was generated using antibody present in the supernatant of CHO cells transformed to express S2E12 antibody. The curve labeled "S2E12 wt" was generated using purified antibody produced in transformed HEK cells.

Figure 36 shows binding of certain antibodies to SARS-CoV-2 Spike protein expressed on the surface of CHO cells, as measured by flow cytometry. The calculated EC50 values for each antibody are shown in the legend to the right of each antibody name. The curve labeled "S2E12-11" was generated using antibody present in the supernatant of CHO cells transformed to express S2E12 antibody. The curve labeled "S2E12" was generated using purified antibody produced in transformed HEK cells.

Figures 37A and 37B show neutralization of infection using pseudovirus particles by certain monoclonal antibodies. Figure 37A and Figure 37B show results from two repetitions of the same experiment.

Figures 38A and 38B show binding of certain antibodies to SARS-CoV-2 RBD. Binding of comparator antibody S309-14 (S309 with VH W105F mutation,

having similar affinity to RBD as S309) is also shown. Figure 38A shows binding as measured by indirect ELISA. Figure 38B shows binding as measured by sandwich ELISA. Each of Figures 38A and 38B show the average of results from duplicate experiments.

Figures 39A and 39B show characteristics of certain engineered S2E12 antibodies as compared to parental monoclonal antibody S2E12 (S2E12 values indicated as "WT" on the y-axis). Comparative data were generated using the assays listed in the legend on the right of each figure.

Figure 40 shows characteristics of certain engineered S2D106 antibodies as compared to parental monoclonal antibody S2D106 (S2D106 values indicated as "WT" on the y-axis). Comparative data were generated using the assays listed in the legend on the right of each figure.

Figure 41 shows expression (immunofluorescence) of DC-SIGN/L-SIGN, DC-SIGN, and ACE2 transgenes in HEK293T cells engineered to overexpress the indicated protein(s). See Example 14.

Figure 42 shows VSV pseudovirus infection levels in wild-type HEK293T cells and in HEK293T cells engineered to overexpress DC-SIGN, L-SIGN, or ACE2. The pseudovirus expressed a recombinant SARS-CoV-2 spike protein with luciferase reporter. See Example 14.

Figure 43 shows neutralization by monoclonal antibody S309 (VH of SEQ ID NO.:139, VL of SEQ ID NO.:143) of VSV pseudovirus infection in HEK293T cells engineered to overexpress DC-SIGN, L-SIGN, or ACE2. In this example, antibody S309 includes M428L and N434S Fc mutations. See Example 14.

Figure 44 shows live SARS-CoV-2 infection levels in wild-type HEK293T cells and in HEK293T cells engineered to overexpress DC-SIGN, L-SIGN, or ACE2. Infection was determined using a recombinant S protein with luciferase reporter. See Example 14.

Figure 45 shows neutralization by monoclonal antibody S309 (VH of SEQ ID NO.:139, VL of SEQ ID NO.:143) of live SARS-CoV-2 infection in HEK293T cells

engineered to overexpress DC-SIGN, L-SIGN, or ACE2. In this example, antibody S309 includes M428L and N434S Fc mutations. See Example 14.

Figure 46 shows expression (immunofluorescence) of DC-SIGN/L-SIGN, DC-SIGN, SIGLEC1, and ACE2 transgenes in HEK293T cells engineered to overexpress the indicated protein(s). See Example 14.

Figure 47 shows live SARS-CoV-2 infection levels in wild-type HEK293T cells and in HEK293T cells engineered to overexpress DC-SIGN, L-SIGN, SIGLEC-1, or ACE2. Infection was determined using a recombinant S protein with luciferase reporter. See Example 14.

Figure 48 shows neutralization by monoclonal antibody S309 (VH of SEQ ID NO.:139, VL of SEQ ID NO.:143) of live SARS-CoV-2 infection in HEK293T cells engineered to overexpress DC-SIGN, L-SIGN, SIGLEC-1, or ACE2. In this example, antibody S309 includes M428L and N434S Fc mutations. See Example 14.

Figure 49 shows neutralization by monoclonal antibody S2E12-LS (VH of SEQ ID NO.:399, VL of SEQ ID NO.:403n M428L/N434S Fc mutations) of live SARS-CoV-2 infection in HEK293T cells engineered to overexpress DC-SIGN, L-SIGN, SIGLEC-1, or ACE2. In this example, antibody S2E12 includes M428L and N434S Fc mutations. See Example 14.

Figures 50A and 50B shows expression analysis of receptor proteins including CD209 (DC-SIGN) and SIGLEC proteins in several cell types. Size of dot correlates with the percentage of cells of the indicated type that express the protein, and intensity of dot shading correlates with the expression level of the protein. See Example 14.

Figure 51 shows infection by live SARS-CoV-2 expressing N-luciferase in HEK293T cells ("parental") or HEK293T cells stably expressing DC-SIGN, L-SIGN, SIGLEC-1, or ACE2. Data represent experiments testing SARS-CoV-2 at three multiplicities of infection (MOI). See Example 14.

Figure 52 shows infection by SARS-CoV-2 pseudotyped VSV in HEK293T cells, HeLa cells, and MRC5 cells transiently transduced with lentivirus to express DC-SIGN, L-SIGN, SIGLEC-1, or ACE2. Uninfected cells are shown as negative control. See Example 14.

Figure 53 shows neutralization of infection by S2E12. A panel of 7 cell lines (HeLa, 293T (wt), Vero E6, Huh7, 293T ACE2, MRC 5-ACE2-TMPRSS2, A549-ACE2-TMPRSS2 clone 5, A549-ACE2-TMPRSS2 clone 10) were infected with SARS-CoV-2-Nluc in the presence of S2E12. Luciferase signal was quantified 24h post infection.

Figure 54 shows neutralization of infection by S2E12. A panel of 7 cell lines (HeLa, 293T (wt), Vero E6, Huh7, 293T ACE2, MRC 5-ACE2-TMPRSS2, A549-ACE2-TMPRSS2 clone 5, A549-ACE2-TMPRSS2 clone 10) were infected with VSV pseudotyped with the SARS-CoV-2 spike protein in the presence of S2E12-LS. Luciferase signal was quantified 24h post infection.

Figure 55 shows binding of purified, fluorescently-labeled SARS-CoV-2 spike protein binding to each of 7 cell lines as quantified by flow cytometry. HeLa and 239T WT cells had he lowest MFIs, followed by Huh7 and VeroE6 cells. 293T ACE2 cells (highest), MRC 5-ACE2-TMPRSS2 (third-highest), A549-ACE2-TMPRSS2 clone 5 (fourth-highest), and A549-ACE2-TMPRSS2 clone 10 (second-highest) had higher MFIs.

Figures 56A and 56B show that both S309 (VH SEQ ID NO.:139; VL SEQ ID NO.:143) or the combination of S309 and S2E12-LS provide robust *in vivo* protection against SARS-CoV-2 challenge. Syrian hamsters were injected with the indicated amount of mAb 48 hours before intra-nasal challenge with SARS-CoV-2. Fig. 56A, top row, shows quantification of viral RNA in the lungs 4 days post-infection. Fig 56A, middle row, shows quantification of replicating virus in lung homogenates harvested 4 days post infection using a TCID50 assay. Fig 56A, bottom row, shows histological score of the lung tissue assessed 4 days post infection. Fig. 56B shows that the concentration of mAbs measured in the serum before infection (day 0) inversely correlates with the viral RNA load in the lung 4 days post infection. See Example 14.

Figure 57 shows infection of HEK293T cells transfected to over-express ACE2 or one of a panel of selected lectins and receptor candidates by VSV-SARS-CoV-2 pseudovirus.

Figure 58 shows micrographs of stable HEK293T cell lines overexpressing DC-SIGN, L-SIGN, SIGLEC1, or ACE2 infected with authentic SARS-CoV-2 (MOI of 0.1), then fixed and immunostained for 24 hours for SARS-CoV-2 nucleoprotein (red)

Figure 59 shows quantification of luciferase levels in stable HEK293T cell lines overexpressing DC-SIGN, L-SIGN, SIGLEC1, or ACE2, as measured 24 hours after infection with SARS-CoV-2-Nluc.

Figure 60 shows quantification of luciferase levels in stable HEK293T cell lines overexpressing DC-SIGN, L-SIGN, SIGLEC1, or ACE2 after incubation with different concentrations of anti-SIGLEC1 monoclonal antibody (clone 7-239) and infection with SARS-CoV-2-Nluc.

Figure 61 shows infection of cells transiently transduced to overexpress DC-SIGN, L-SIGN, SIGLEC1, or ACE2 by VSV-SARS-CoV-2 pseudovirus. Results for HEK293T cells (left panel), HeLa cells (center panel), and MRC5 cells (right panel) are shown.

Figure 62 shows infection of stable HEK293T cell lines overexpressing DC-SIGN, L-SIGN, SIGLEC1, or ACE2 after treatment with ACE2 siRNA followed by infection with VSV-SARS-CoV-2 pseudovirus.

Figure 63 shows infection of stable HEK293T cell lines overexpressing DC-SIGN, L-SIGN, SIGLEC1, or ACE2 after treatment with different concentrations of anti-ACE2 antibody (polyclonal serum) followed by infection with VSV-SARS-CoV-2 pseudovirus.

Figure 64 shows the distribution and expression of ACE2, DC-SIGN (CD209), L-SIGN (CLEC4M), and SIGLEC1 in the human lung cell atlas.

Figure 65 shows analysis of major cell types with detectable SARS-CoV-2 genome in bronchoalveolar lavage fluid or sputum of severe COVID-19 patients. The single cell gene expression profiles are shown as a t-SNE (t-distributed stochastic neighbor embedding) plot, colored by cell type and sized by viral load.

Figure 66 shows analysis of major cell types with detectable SARS-CoV-2 genome in bronchoalveolar lavage fluid or sputum of severe COVID-19 patients. The cumulative fraction of cells (y-axis) with detected viral RNA per cell up to the

corresponding logCPM (log(counts per million); x-axis) is shown for each of the indicated cell types.

Figure 67 shows a heatmap matrix of counts for cells with detected transcripts for the receptor genes shown on the x-axis and SARS-CoV-2+ cell types on the y-axis. Total n=3,085 cells from eight subjects. See Ren, X. et al. COVID-19 immune features revealed by a large-scale single cell transcriptome atlas. Cell, doi:10.1016/j.cell.2021.01.053 (2021).

Figure 68 shows the correlation of receptor transcript counts (y-axis of each plot) with SARS-CoV-2 RNA counts (x-axis of each plot) in macrophages and in secretory cells. Correlation is based on counts before log transformation from Ren et al.

Figure 69 shows, at right, results of trans-infection with VSV-SARS-CoV-2. A schematic of the trans-infection process is shown in the left panel. HeLa cells transduced with DC-SIGN, L-SIGN, or SIGLEC1 were incubated with VSV-SARS-CoV-2, extensively washed, and co-cultured with Vero-E6-TMPRSS2 susceptible target cells. Results in the presence or absence of target cells are shown in the right panel.

Figure 70 shows the results of trans-infection, where VSV-SARS-CoV-2 viral adsorption was performed in the presence or absence of an anti-SIGLEC1 blocking antibody.

Figure 71 shows neutralization of SARS-CoV-2 infection of Vero-E6 cells by antibodies S309, S2E12-LS, and S2X33. S2E12-LS comprises the VH sequence of SEQ ID NO:399 and the VL sequence of SEQ ID NO:403, and M428L/N434S in Fc.

Figure 72 shows neutralization of SARS-CoV-2 infection of Vero-E6-TMPRSS2 cells by antibodies S309, S2E12-LS, and S2X33.

Figure 73 shows quantification of binding of purified, fluorescently-labeled SARS-CoV-2 spike protein or RBD to the indicated cell lines, as measured by flow cytometry. "A" indicates cell line overexpressing ACE2; "T" indicates cell line overexpressing TMPRSS2.

Figure 74 shows quantification of cellular ACE2 and TMPRSS2 transcripts in the indicated cell lines, as measured by RT-qPCR. "A" indicates cell line overexpressing ACE2; "T" indicates cell line overexpressing TMPRSS2.

Figure 75 shows neutralization of SARS-CoV-2-Nluc infection by antibodies S309, S2E12-LS, or S2X333. Each of the seven cell lines indicated was tested. Luciferase signal was quantified 24 hours post infection.

Figure 76 shows neutralization of VSV-SARS-CoV-2 pseudovirus infection by antibodies S309, S2E12-LS, or S2X333. Each of the seven cell lines indicated was tested. Luciferase signal was quantified 24 hours post infection.

Figure 77 shows cell-cell fusion of CHO cells expressing SARS-CoV-2 S protein (CHO-S) on the plasma membrane in the absence (top panels) or presence (bottom panels) of 5 μg/ml of antibody S2E12-LS, as measured by immune-fluorescence. Nuclei were stained with Hoechst dye; cytoplasm was stained with CellTracker Green.

Figure 78 shows CHO-S cell-cell fusion mediated by different spike-specific antibodies. Fusion was quantified using the Cytation 5 Imager (BioTek) and an object detection protocol that detected nuclei as objects and measured their size. The area of the objects in fused cells divided by the total area of all the objects multiplied by 100 provides the percentage of fused cells.

Figure 79 shows inhibition of S2E12-LS -induced cell-cell fusion of CHO-S cells by 15 μg/ml of the indicated antibodies.

Figure 80 shows S2E12-LS -induced uni-directional fusion (also referred to as trans-fusion) of S-positive CHO-S cells with fluorescently-labelled S-negative CHO cells in the absence of ACE2. Nuclei were stained with Hoechst dye; cytoplasm was stained with CellTracker Green.

Figure 81 shows neutralization of infection of a stable HEK293T cell line overexpressing ACE2 by authentic SARS-CoV-2 pre-incubated with the indicated antibodies. Infection was measured by immunostaining at 24 hours for the SARS-CoV-2 nucleoprotein.

Figure 82 shows neutralization of infection of a stable HEK293T cell line overexpressing SIGLEC1 by authentic SARS-CoV-2 pre-incubated with the indicated antibodies. Infection was measured by immunostaining at 24 hours for the SARS-CoV-2 nucleoprotein.

Figure 83 shows neutralization of infection of a stable HEK293T cell line overexpressing DC-SIGN by authentic SARS-CoV-2 pre-incubated with the indicated monoclonal antibodies. Infection was measured by immunostaining at 24 hours for the SARS-CoV-2 nucleoprotein.

Figure 84 shows neutralization of infection of a stable HEK293T cell line overexpressing L-SIGN by authentic SARS-CoV-2 pre-incubated with the indicated monoclonal antibodies. Infection was measured by immunostaining at 24 hours for the SARS-CoV-2 nucleoprotein.

Figure 85 shows a summary of the mechanisms of action of different classes of spike-specific antibodies. "Fusion inhibition" refers to antibody-mediated inhibition of fusion between CHO-S cells and ACE2+ Vero-E6 cells. Assessment of effector functions is based on antibody-dependent activation of human FcγRs, as measured using a bioluminescent reporter assay. RBM Ia-IIa antibodies include S2E12, S2X259, S2X58, S2D106, Ly-CoV016, CT-P59, and REGN10933. RBM Ib antibodies include Ly-CoV555, REGN10987, and S2M11. NTD antibodies include S2X333. Stem helix antibodies include S2P6.

Figure 86 shows analysis of binding of antibodies targeting DC/L-SIGN, DC-SIGN, SIGLEC1, or ACE2 on HEK293T cells stably over-expressing the respective attachment receptor, as measured by flow cytometry.

Figure 87 shows analysis of binding of antibodies targeting DC/L-SIGN, DC-SIGN, SIGLEC1, or ACE2 on HEK293T cells stably over-expressing the respective attachment receptor, as measured by immunofluorescence.

Figure 88 shows infection of HEK293T cells stably over-expressing the indicated attachment receptor by VSV-SARS-CoV-2 pseudotyped with wild type spike protein (grey bars), or VSV-SARS-CoV-2 pseudotyped with spike protein bearing the

mutations of the B1.1.7 lineage (red bars). Luminescence was analyzed one day post infection.

Figure 89 shows neutralization of SARS-CoV-2 infection of Vero-E6 or Vero-E6-TMPRSS2 cells by 10 μg/ml of S309, S2E12-v2, and S2X333. Cells were infected with SARS-CoV-2 (isolate USA-WA1/2020) at MOI 0.01 in the presence of the indicated antibodies. Cells were fixed 24h post infection and viral nucleocapsid protein was immunostained.

Figure 90 shows quantification of binding of purified, fluorescently-labelled SARS-CoV-2 spike protein (left panels) or RBD (right panels) to the indicated cell lines, as measured by flow cytometry.

Figure 91 shows quantification of binding of purified, fluorescently-labelled SARS-CoV-2 spike protein (left panels) or RBD (right panels) to the indicated cell lines, as measured by flow cytometry.

Figure 92 shows analysis of the protective effect of antibody S309 (left panels) or a combination of antibodies S309 and S2E12-v2 (right panels) against SARS-CoV-2 challenge in Syrian hamsters. Top panels show quantification of viral RNA in the lungs four days post infection. Bottom panels show quantification of replicating virus in lung homogenates harvested four days post infection using a TCID50 assay.

Figure 93 shows analysis of the protective effect of antibody S309 (left panels) or a combination of antibodies S309 and S2E12-LS (right panels) against SARS-CoV-2 challenge in Syrian hamsters. Top panels show histopathological score of lung tissue assessed four days post infection. Bottom panels show efficacy plots based on the correlation between the level of serum antibody measured at the time of infection (x-axis) and the level of SARS-CoV-2 viral RNA measured in lungs (y-axis) on day four after infection. The dotted lines represent the EC50 and EC90 for viral reduction. EC90 of S309 alone is 9 μg/ml; EC90 of S309+S2E12-v2 is 11 μg/ml.

Figure 94 shows binding of immunocomplexes to hamster splenocytes. Alexa-488 fluorescent immunocomplexes (IC) were titrated (0-200 nM range) and incubated with total naïve hamster splenocytes. Binding was revealed with a cytometer upon exclusion of dead/apoptotic cells and physical gating on bona fide monocyte

population. Left panel shows the fluorescent intensity associated to hamster cells of IC made with either hamster or human Fc antibodies (Human S309 shown in green; GH-S309 shown in dark grey; GH-S309-N297A shown in blue). A single replicate of two is shown. Right panel shows the relative Alexa-488 mean fluorescent intensity of the replicates measured on the entire monocyte population.

Figure 95 shows analysis of the role of host effector function in SARS-CoV-2 challenge. Syrian hamsters were injected with the indicated amount (mg/kg) of hamster IgG2a S309, either wt or Fc silenced (S309-N297A). Top panel shows quantification of viral RNA in the lung 4 days post infection. Center panel shows quantification of replicating virus in the lung 4 days post infection. Bottom panel shows histopathological score in the lung 4 days post infection. Control animals (white symbols) were injected with 4 mg/kg unrelated control isotype antibody. * $p< 0.05$, ** $p< 0.01$, *** $p< 0.001$, **** $p< 0.0001$ vs control animals, using Mann-Whitney test.

Figure 96 shows inhibition of infection by SARS-CoV-2-Nluc in HeLa cells stably expressing DC-SIGN in the presence of the indicated antibodies. Cells were infected at MOI of 0.04. Infection was analyzed by quantification of luminescent signal at 24 hours post infection.

Figure 97 shows neutralization of SARS-CoV-2 infection of HEK293T cells stably expressing ACE2 (top panel) or DC-SIGN (bottom panel) in the presence of the indicated antibodies. Cells were infected at MOI of 0.02. Cells were fixed 24h post infection, viral nucleocapsid protein was immunostained and positive cells were quantified.

Figure 98 shows neutralization of SARS-CoV-2 infection of HEK293T cells stably expressing SIGLEC1 (top panel) or L-SIGN (bottom panel) in the presence of the indicated antibodies. Cells were infected at MOI of 0.02. Cells were fixed 24h post infection, viral nucleocapsid protein was immunostained and positive cells were quantified.

Figure 99 shows a concentration curve for S2E12 engineered variant 409_11_4_v2, comprising LS mutations in Fc, in female non-human primates over 64 days.

Figure 100 shows 409_11_4_v2-LS pharmacokinetics values from the non-human primate study.

DETAILED DESCRIPTION

Provided herein are antibodies and antigen-binding fragments that bind to SARS-CoV-2 coronavirus (*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 the SARS-CoV-2 coronavirus). 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 an animal 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 a SARS-CoV-2 infection in a subject.

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.

As used herein, "SARS-CoV-2", also referred to herein as "Wuhan seafood market phenomia 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, and dyspnea.

The genomic sequence of SARS-CoV-2 isolate Wuhan-Hu-1 is provided in SEQ ID NO.:1 (*see also* GenBank MN908947.3, January 23, 2020), and the amino acid translation of the genome is provided in SEQ ID NO.:2 (*see also* GenBank QHD43416.1, January 23, 2020). Like other coronaviruses (*e.g.*, SARS- CoV-1), 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.

The amino acid sequence of the Wuhan-Hu-1 surface glycoprotein is provided in SEQ ID NO.:3. The amino acid sequence of Wuhan-Hu-1 RBD is provided in SEQ ID NO.:4. SARS-CoV-2 S protein has approximately 73% amino acid sequence identity with SARS-CoV-1. The amino acid sequence of Wuhan-Hu-1 RBM is provided in SEQ ID NO.:5. Wuhan-Hu-1 RBD has approximately 75% to 77% amino acid sequence similarity to SARS–CoV-1RBD, and Wuhan-Hu-1 RBM has approximately 50% amino acid sequence similarity to SARS-CoV-1 RBM.

Unless otherwise indicated herein, SARS-CoV-2 Wuhan Hu-1 refers to a virus comprising the amino acid sequence set forth in any one or more of SEQ ID NOs.:2, 3, and 4, optionally with the genomic sequence set forth in SEQ ID NO.:1.

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; (del69-70, del144, N501Y, A570D, D614G, P681H, T716I, S982A, and D1118H mutations)) and B.1.351 (also known as 20H/501Y.V2; L18F, D80A, D215G, R246I, K417N, E484K, N501Y, D614G, and A701V mutations), 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 include 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 of variants of SARS-CoV-2 in the Americas*, January 20, 2021, available at 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). The foregoing SARS-CoV-2 variants, and the amino acid and nucleotide sequences thereof, are incorporated herein by reference. Accordingly, it will be understood that SARS-CoV-2 includes Wuhan Hu-1 and variants thereof, including presently disclosed variants.

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.

"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.

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.

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).

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.

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).

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.

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.

"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.

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.

"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.

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.

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).

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).

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).

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.

As used herein, "heterologous" or "non-endogenous" or "exogenous" refers to any gene, protein, compound, 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.

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 a fusion protein, or any combination thereof.

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.

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).

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.

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.

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).

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.

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).

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 if they are contiguous with the gene of interest and expression control sequences that act in *trans* or at a distance to control the gene of interest.

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 ortho-myxovirus (*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).

"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.

"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.

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. Patent 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).

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).

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.

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

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).

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).

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

"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 cytotoxicicity, 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 a 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.

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, Antigen-Binding Fragments, and Compositions

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.

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.

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-1) present in the sample, but not significantly associating or uniting 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.

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_d) 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_d) of a particular binding interaction with units of M (*e.g.,* 10^{-5} M to 10^{-13} M).

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 (*e.g.*, direct, indirect, or sandwich), 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. Patent Nos. 5,283,173, 5,468,614, or the equivalent). Assays for assessing affinity or apparent affinity or relative affinity are also known.

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 cytometery (*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.

In some embodiments an antibody or antigen-binding fragment of the present disclosure binds to SARS-CoV-2 S protein, as measured using biolayer interferometry.

In certain embodiments, an antibody or antigen-binding fragment of the present disclosure binds to SARS-CoV-2 S protein with a K_D of less than about $4.5x10^{-9}$ M, less than about $5x10^{-9}$ M, less than about $1x10^{-10}$ M, less than about $5x10^{-10}$ M, less than about $1x10^{-11}$ M, less than about $5x10^{-11}$ M, less than about $1x10^{-12}$ M, or less than about $5x10^{-12}$ M. In some embodiments, an antibody or antigen-binding fragment of the present disclosure binds to SARS-CoV-2 S protein RBD with a K_D of less than about $4.5x10^{-9}$ M, less than about $5x10^{-9}$ M, less than about $1x10^{-10}$ M, less than about $5x10^{-10}$ M, less than about $1x10^{-11}$ M, less than about $5x10^{-11}$ M, less than about $1x10^{-12}$ M, or less than about $5x10^{-12}$ M.

Certain characteristics of presently disclosed antibodies or antigen-binding fragments may be described using IC50 or EC50 values. In certain embodiments, the IC50 is the concentration of a composition (*e.g.*, antibody) that results in half-maximal inhibition of the indicated biological or biochemical function, activity, or response. In certain embodiments, the EC50 is the concentration of a composition that provides the half-maximal response in the assay. In some embodiments, *e.g.*, for describing the ability of a presently disclosed antibody or antigen-binding fragment to neutralize infection by SARS-CoV-2, IC50 and EC50 are used interchangeably.

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 (*e.g.*, using a Syrian hamster model with intranasal delivery of SARS-CoV-2) and/or in a human.

In some embodiments, an antibody or antigen-binding fragment of the present disclosure is capable of neutralizing a SARS-CoV-2 infection or infection by a virus pseudotyped with SARS-CoV-2 S protein with an IC50 of about 16 to about 20 μg/ml.

In some embodiments, an antibody or antigen-binding fragment is capable of neutralizing a SARS-CoV-2 infection, or a virus pseudotyped with SARS-CoV-2 S protein, with an IC50 of about 3 to about 4 μg/ml. In any of the presently disclosed embodiments, an antibody or antigen-binding fragment is capable of neutralizing a SARS-CoV-2 infection, or a virus pseudotyped with SARS-CoV-2 S protein, with an IC50, an IC80, and/or an IC90 as shown in Table 4.

In some embodiments, an antibody or antigen-binding fragment, or a composition comprising two or more antibodies or antigen-binding fragments, of the present disclosure is capable of neutralizing a SARS-CoV-2 infection, or a virus pseudotyped with SARS-CoV-2 S protein, with an IC50 of about 0.8 to about 0.9 μg/ml. In some embodiments, an antibody or antigen-binding fragment, or a composition comprising two or more antibodies or antigen-binding fragments, of the present disclosure is capable of neutralizing a SARS-CoV-2 infection, or a virus pseudotyped with SARS-CoV-2 S protein, with an IC50 of about 0.5 to about 0.6 μg/ml. In some embodiments, an antibody or antigen-binding fragment, or a composition comprising two or more antibodies or antigen-binding fragments, of the present disclosure is capable of neutralizing a SARS-CoV-2 infection, or a virus pseudotyped with SARS-CoV-2, with an IC50 of about 0.1 to about 0.2 μg/ml.

In certain embodiments, the antibody or antigen-binding fragment (i) recognizes an epitope in the ACE2 receptor binding motif (RBM, SEQ ID NO.:5) of SARS-CoV-2; (ii) is capable of blocking an interaction between SARS-CoV-2 and human ACE2 (*i.e.* partially or fully blocking the interaction, via binding to SARS-CoV-2); (ii) is capable of binding to SARS-CoV-2 S protein; (iv) recognizes an epitope that is conserved in the ACE2 RBM of SARS-CoV-2 and in an ACE2 RBM of SARS-CoV-1; (v) is cross-reactive against SARS-CoV-2 and SARS-CoV-1; (vi) recognizes an epitope in the SARS-CoV-2 surface glycoprotein that is not in the ACE2 RBM; or (vii) any combination of (i)-(vii).

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 inter-connected 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.

The terms "V_L" or "VL" and "V_H" 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 (λ) 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.

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.

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 Plückthun, *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 CDRs of a VH sequence according to any one of SEQ ID NOs.: 22, 32, 42, 52, 62, 72, 74, 84, 96, 106, 119, 129, 139, 150, 163, 173, 175, 178, 186, 189, 191, 198, 208, 218, 228, 240, 254, 264, 274, 284, 298, 312, 322, 332, 350, 351, 353, 359, 361, 363, 365, 367, 368, 369, 379, 389, 399, 409, 419, 429, 434, 444, 454, 464, 474, 484, 494, 504, 514, 524, 534, 544, 554, 564, 574, 584, 594, 604, 614, 624, 626, 628, 630, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, 684, 692, 740, 741, 742, 743, 748, 749, 750, 752, 754, 756, 758, 759, 761, 762, and 764 and of a VL sequence according to any one of SEQ ID NOs.: 26, 36, 46, 56, 66, 78, 88, 94, 100, 110, 123, 133

143, 154, 157, 168, 194, 196, 202, 212, 222, 232, 238, 244, 250, 252, 258, 268, 278, 288, 294, 296, 302, 308, 310, 316, 326, 336, 355, 357, 373, 383, 393, 403, 413, 423, 438, 448, 458, 468, 478, 488, 498, 508, 518, 528, 538, 548, 558, 568, 578, 588, 598, 608, 618, 686, 696, 738, 744, and 746, 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).

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.: 23, 33, 43, 53, 63, 75, 85, 97, 107, 120, 130, 140, 147, 160, 170, 174, 183, 190, 199, 209, 219, 229, 241, 255, 265, 275, 285, 299, 313, 323, 333, 370, 380, 390, 400, 410, 420, 430, 435, 445, 455, 465, 475, 485, 495, 505, 515, 525, 535, 545, 555, 565, 575, 585, 595, 605, 615, 631, 693, 740, 741, 742, and 743, 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.: 24, 34, 44, 54, 64, 76, 86, 98, 108, 121, 131, 141, 148, 151, 161, 171, 184, 200, 210, 220, 230, 242, 256, 266, 276, 286, 300, 314, 324, 334, 352, 360, 362, 364, 366, 371, 381, 391, 401, 411, 421, 431, 436, 446, 456, 466, 476, 486, 496, 506, 516, 526, 536, 546, 556, 566, 576, 586, 596, 606, 616, 625, 632, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 675, 677, 679, 681, 683, 685, and 694, 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.: 25, 35, 45, 55, 65, 77, 87, 99, 109, 122, 132, 142, 149, 162, 164, 165, 172, 176, 177, 179, 180, 185, 187, 188, 201, 211, 221, 231, 243, 257, 267, 277, 287, 301, 315, 325, 335, 354, 372, 382, 392, 402, 412, 422, 432, 437, 447, 457, 467, 477, 487, 497, 507, 517, 527, 537, 547, 557, 567, 577, 587, 597, 607, 617, 627, 633, 695, 751, 753, 755, 757, 760, 763, 765, and 766, 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.: 27, 37, 47, 57, 67, 79, 89, 101, 111, 124, 134, 144, 152, 155, 156, 158, 159, 166, 181, 192, 203, 213, 223, 233, 245, 259, 269, 279, 289, 303, 317, 327, 337, 356, 374, 384, 394, 404, 414, 424, 439, 449, 459, 469, 479, 489, 499, 509, 519, 529, 539, 549, 559, 569, 579, 589, 599, 609, 619, 687, and 697, 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.: 28, 38, 48, 58, 68, 80, 90, 102, 112, 125, 135, 145, 153, 167, 182, 193, 204, 214, 224, 234, 246, 260, 270, 280, 290, 304, 318, 328, 338, 375, 385, 395, 405, 415, 425, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 688, and 698, 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.: 29, 39, 49, 59, 69, 81, 91, 103, 113, 126, 136, 146, 169, 195, 197, 205, 215, 225, 235, 247, 261, 271, 281, 291, 305, 319, 329, 339, 358, 376, 386, 396, 406, 416, 426, 441, 451, 461, 471, 481, 491, 501, 511, 521, 531, 541, 551, 561, 571, 581, 591, 601, 611, 621, 689, 699, 745, and 747, 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.

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.

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) 23-25 and 27-29, respectively; (ii) 33-35 and 37-39, respectively; (iii) 43-45 and 47-49, respectively; (iv) 53-55 and 57-59, respectively; (v) 63-65 and 67-69, respectively; (vi) 75-77 and 79-81, respectively; (vii) 85-87 and 89-91, respectively; (viii) 97-99 and 101-103, respectively; (ix) 107-109 and 111-113, respectively; (x) 120-122 and 124-126, respectively; (xi) 130-132 and 134-136, respectively; (xii) 23 or 147, any one of 24, 148 or 151, 25 or 149, any one of 27, 152, 155, 156, 158, or 159, 28 or 153, and 29, respectively; (xiii) 43 or 160, 44 or 161, any one of 45, 162, 164, or 165, 47 or 166, 48 or 167, and 49 or 169, respectively; (xiv) any one of 130, 170, or 174, 130, 131, 132, 134 or 181, 135 or 182, and 136, respectively; (xv) any one of 53, 183, or 190, 54 or 184, any one of 55, 185, 187, or 188, 57 or 192, 58 or 193, and any one of 59, 195, or 197, respectively; (xvi) 199-201 and 203-205, respectively; (xvii) 209-211 and 213-215, respectively; (xviii) 219-221 and 223-225, respectively; (xix) 229-231 and 233-235, respectively; (xx) 241-243 and 245-247, respectively; (xxi) 255-257 and 259-261, respectively; (xxii) 265-267 and 269-271, respectively; (xxiii) 275-277 and 279-281, respectively; (xxiv) 285-287 289-291, respectively, (xxv) 299-301 and 303-305, respectively; (xxvi) 313-315 and 317-319, respectively; (xxvii) 323-325 and 327-329, respectively; (xxviii) 333-335 and 337-339, respectively; (xxix) 229, 230 or 352, 231 or 354, and 233 or 356, 234, and 235 or 358, respectively; (xxx) 313, any one of 314, 360, 362, 364, or 366, 315, and 317-319, respectively; (xxxi) 370-372 and 374-376, respectively; (xxxii) 380-382 and 384-386, respectively; (xxxiii) 390-392 and 394-396, respectively; (xxxiv) 400-402 and 404-406, respectively; (xxxv) 410-412 and 414-416, respectively; (xxxvi) 420-422 and 424-426,

respectively; (xxxvii) 435-437 and 439-441, respectively; (xxxviii) 445-447 and 449-451, respectively; (xxxix) 455-457 and 459-461, respectively; (xxxx) 465-467 and 469-471, respectively; (xxxxi) 475-477 and 479-481, respectively; (xxxxii) 485-487 and 489-491, respectively; (xxxxiii) 494-497 and 499-501, respectively; (xxxxiv) 505-507 and 509-511, respectively; (xxxxv) 515-517 and 519-521, respectively; (xxxxvi) 525-527 and 529-531, respectively; (xxxxvii) 535-537 and 539-541, respectively; (xxxxviii) 545-547 and 549-551, respectively; (xxxxix) 555-557 and 559-561, respectively; (xxxxx) 565-567 and 569-571, respectively; (xxxxxi) 575-577 and 579-581, respectively; (xxxxxii) 585, 586 or 625, 587 or 627, and 589-591, respectively; (xxxxxiii) 595-597 and 599-601, respectively; (xxxxxiv) 605-607 and 609-611, respectively; (xxxxxv) 615-617 and 619-621, respectively, (xxxxxvi) 631, 632 or 635 or 637 or 639 or 641 or 643 or 645 or 647 or 649 or 651 or 653 or 655 or 657 or 659 or 661 or 663 or 665 or 667 or 669 or 671 or 673 or 675 or 677 or 679 or 681 or 683 or 685, 633, and 697-699, respectively; (xxxxxvii) 693-695 and 697-699, respectively; (xxxxxviii) 400, 401 and any one of 751, 753, 755, 757, or 760 and 404, 405, and any one of 745 or 747, respectively; (xxxxxxix) 585, 586, and 762 or 764 and 589-591, respectively; or (xxxxxxx) 400, 401, 766, and 404-406, respectively.

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.:631, 632 or 635 or 637 or 639 or 641 or 643 or 645 or 647 or 649 or 651 or 653 or 655 or 657 or 659 or 661 or 663 or 665 or 667 or 669 or 671 or 673 or 675 or 677 or 679 or 681 or 683 or 685, 633, and 697-699, respectively. 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.:693-695 and 697-699, respectively.

In certain embodiments, the antibody or antigen-binding fragment comprises CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 amino acid sequences according to SEQ ID NOs.:400-402, and 404-406, respectively. In certain embodiments, the antibody or antigen-binding fragment comprises CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 amino acid sequences according to SEQ ID

NOs.:400, 401, 766, and 404-406, respectively. In certain embodiments, the antibody or antigen-binding fragment comprises CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 amino acid sequences according to SEQ ID NOs.:400-402, 404, 405, and 745, respectively. In certain embodiments, the antibody or antigen-binding fragment comprises CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 amino acid sequences according to SEQ ID NOs.:400, 401, 766, 404, 405, and 745, respectively. In certain embodiments, the antibody or antigen-binding fragment comprises CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 amino acid sequences according to SEQ ID NOs.:400-402, 404, 405, and 747, respectively. In certain embodiments, the antibody or antigen-binding fragment comprises CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 amino acid sequences according to SEQ ID NOs.:400, 401, 766, 404, 405, and 747, respectively. In certain embodiments, the antibody or antigen-binding fragment comprises CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 amino acid sequences according to SEQ ID NOs.:400, 401, 751, and 404-406, respectively. In certain embodiments, the antibody or antigen-binding fragment comprises CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 amino acid sequences according to SEQ ID NOs.:400, 401, 753, and 404-406, respectively. In certain embodiments, the antibody or antigen-binding fragment comprises CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 amino acid sequences according to SEQ ID NOs.:400, 401, 755, and 404-406, respectively. In certain embodiments, the antibody or antigen-binding fragment comprises CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 amino acid sequences according to SEQ ID NOs.:400, 401, 757, and 404-406, respectively. In certain embodiments, the antibody or antigen-binding fragment comprises CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 amino acid sequences according to SEQ ID NOs.:400, 401, 760, and 404-406, 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 SARS-CoV-2 S2X16-v1 mAb, SARS-CoV-2 S2X16-v2 mAb, SARS-CoV-2 S2X16-v3 mAb, SARS-CoV-2 S2X16-v4 mAb, SARS-CoV-2 S2X16-v5 mAb, SARS-CoV-2

S2X16-v6 mAb, SARS-CoV-2 S2X16-v7 mAb, SARS-CoV-2 S2X16-v8 mA,b SARS-CoV-2 S2X28-v1 mAb, SARS-CoV-2 S2X30-v1 mAb, SARS-CoV-2 S2X30-v2 mAb, SARS-CoV-2 S2X30-v3 mAb, SARS-CoV-2 S2X30-v4 mAb, SARS-CoV-2 S2X30-v5 mAb, SARS-CoV-2 S2X30-v6 mAb, SARS-CoV-2 S2X47-v1 mAb, SARS-CoV-2 S2X47-v2 mAb, SARS-CoV-2 S2X47-v3 mAb, SARS-CoV-2 S2X47-v4 mAb, SARS-CoV-2 S2X47-v5 mAb, SARS-CoV-2 S2X47-v6 mAb, SARS-CoV-2 S2X47-v7 mAb, SARS-CoV-2 S2X47-v8 mAb, SARS-CoV-2 S2X47-v9 mAb, SARS-CoV-2 S2X55-v1 mAb, SARS-CoV-2 S2X55-v2 mAb, SARS-CoV-2 S2X56-v1 mAb, SARS-CoV-2 S2X58-v1 mAb, SARS-CoV-2 S2X58-v2 mAb, SARS-CoV-2 S2X71-v1 mAb SARS-CoV-2 S2X76-v1 mAb, SARS-CoV-2 S2X76-v2 mAb, SARS-CoV-2 S2X76-v3 mAb, SARS-CoV-2 S2X76-v4 mAb, SARS-CoV-2 S2X11-v1 mAb, or SARS-CoV-2 S2X35-v1 mAb, SARS-CoV-2 S2X35-v2 mAb, SARS-CoV-2 S2X35-v3 mAb, SARS-CoV-2 S2X35-v4 mAb, SARS-CoV-2 S2X35-v5 mAb, SARS-CoV-2 S2X35-v6 mAb, SARS-CoV-2 S2X35-v7 mAb, SARS-CoV-2 S2X35-v8 mAb, SARS-CoV-2 S2H30-v1 mAb, SARS-CoV-2 S2H37-v1 mAb, SARS-CoV-2 S2H40-v1 mAb, SARS-CoV-2 S2H58-v1 mAb, SARS-CoV-2 S2H58-v2 mAb, SARS-CoV-2 S2H58-v3 mAb, SARS-CoV-2 S2H58-v4 mAb, SARS-CoV-2 S2H58-v5 mAb, SARS-CoV-2 S2H58-v6 mAb, SARS-CoV-2 S2H58-v7 mAb, SARS-CoV-2 S2H62-v1 mAb, SARS-CoV-2 S2H62-v2 mAb, SARS-CoV-2 S2H62-v3 mAb, SARS-CoV-2 S2H66-v1 mAb, SARS-CoV-2 S2H66-v2 mAb, SARS-CoV-2 S2H66-v3 mAb, SARS-CoV-2 S2H70-v1 mAb, SARS-CoV-2 S2H71-v1 mAb, SARS-CoV-2 S2H73-v1 mAb, SARS-CoV-2 S2N12-v1 mAb, SARS-CoV-2 S2N12-v2 mAb, SARS-CoV-2 S2N12-v3 mAb, SARS-CoV-2 S2N22-v1 mAb, SARS-CoV-2 S2N22-v2 mAb, SARS-CoV-2 S2N22-v3 mAb, SARS-CoV-2 S2N22-v4 mAb, SARS-CoV-2 S2N22-v5 mAb, SARS-CoV-2 S2N22-v6 mAb, SARS-CoV-2 S2N22-v7 mAb, SARS-CoV-2 S2N25-v1 mAb, SARS-CoV-2 S2N28-v1 mAb, SARS-CoV-2 S2E6-v1 mAb, SARS-CoV-2 S2E7-v1 mAb, SARS-CoV-2 S2E9-v1 mAb, SARS-CoV-2 S2E12-v1 mAb, SARS-CoV-2 S2E12-v2 mAb, SARS-CoV-2 S2E13-v1 mAb, SARS-CoV-2 S2E14-v1 mAb, SARS-CoV-2 S2K4-v1 mAb, SARS-CoV-2 S2X193-v1 mAb, SARS-CoV-2 S2X195-v1 mAb, SARS-CoV-2 S2X219-v1 mAb, SARS-CoV-2 S2X244-v1 mAb, SARS-CoV-2 S2X246-v1 mAb, SARS-CoV-2

S2X256-v1 mAb, SARS-CoV-2 S2X269-v1 mAb, SARS-CoV-2 S2X278-v1 mAb, SARS-CoV-2 S2M7-v1 mAb, SARS-CoV-2 S2M11-v1 mAb, SARS-CoV-2 S2M16-v1 mAb, SARS-CoV-2 S2M28-v1 mAb, SARS-CoV-2 S2L49-v1 mAb, SARS CoV-2 S2D65-v1 mAb, SARS CoV-2 S2D97-v1 mAb, SARS CoV-2 S2D106-v1 mAb, SARS CoV-2 S2X149-v1 mAb, SARS CoV-2 S2X179-v1 mAb, SARS-CoV-2 S2H101 mAb, Antibody 409_11_1_v2, Antibody 409_11_1_v3, Antibody 409_11_1_v4, Antibody 409_11_1_v5, Antibody 409_11_1_v6, Antibody 409_11_2_v1, Antibody 409_11_2_v2, Antibody 409_11_2_v3, Antibody 409_11_2_v4, Antibody 409_11_2_v5, Antibody 409_11_2_v6, Antibody 409_11_2_v7, Antibody 409_11_2_v8, Antibody 409_11_2_v9, Antibody 409_11_2_v10, Antibody 409_11_2_v11, Antibody 409_11_2_v12, Antibody 409_11_2_v13, Antibody 409_11_2_v14, Antibody 409_11_2_v15, Antibody 409_11_2_v16, Antibody 409_11_2_v17, Antibody 409_11_2_v18, Antibody 409_11_2_v19, Antibody 409_11_2_v20, Antibody 409_11_2_v21, Antibody Antibody 409_11_2_v22, Antibody 409_11_2_v23, Antibody 409_11_2_v24, Antibody 409_11_2_v25, Antibody 409_11_2_v26, Antibody 409_11_2_v27, Antibody 409_11_3_v1, Antibody 409_11_4_v2, Antibody 409_11_4_v3, Antibody 409_11_4_v4, Antibody 409_11_4_v5, Antibody 409_11_4_v6, Antibody 409_11_4_v7, Antibody 409_11_4_v8, Antibody 409_11_4_v9, Antibody 409_11_4_v10, Antibody 409_11_4_v11, Antibody 409_11_4_v12, or Antibody 409_11_4_v13, as provided in Table 2. That is, all combinations of CDRs from SARS-CoV-2 mAbs and the variant sequences thereof provided in Table 2 are contemplated.

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 anti-SARS-CoV-2 antibodies of the present disclosure are provided in Table 2 herein.

Exemplary antibodies of the present disclosure include antibody S2E12 and engineered variants thereof. Engineered S2E12 variants include "Antibody 409_11_4_v2", "Antibody 409_11_4_v3", "Antibody 409_11_4_v4", "Antibody 409_11_4_v5", "Antibody 409_11_4_v6", "Antibody 409_11_4_v7", "Antibody 409_11_4_v8", "Antibody 409_11_4_v9", "Antibody 409_11_4_v10", "Antibody 409_11_4_v11", "Antibody 409_11_4_v12", "Antibody 409_11_4_v13". In particular embodiments, an antibody or antigen-binding fragment comprises a CDRH1, a CDRH2, a CDRH3, a CDRL1, a CDRL2, and/or a CDRL3 selected from any of the CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 amino acid sequences (respectively) provided in Table 1. Table 1 also provides amino acid sequences that comprise S2E12 CDRH3 sequences and two amino acids (Ala-Ser) that are immediately N-terminal to CDRH3 in S2E12.

In some embodiments, an antibody or antigen-binding fragment comprises: a CDRH1, a CDRH2, and/or a CDRH3 of the VH amino acid sequence set forth in any one of SEQ ID NOs.:399, 748, 749, 750, 752, 754, 756, 758, 759, and 761; and a CDRL1, a CDRL2, and/or a CDRL3 of the VL amino acid sequence set forth in any one of SEQ ID NOs.:403, 738, 744, and 746 (*i.e.*, according to any CDR numbering or determination method known in the art, such as IMGT, Kabat, Chothia, AHo, North, Contact, CCG, EU, or Martin (Enhanced Chothia)). For example, in some embodiments, the antibody or antigen-binding fragment comprises the CDRH1, the CDRH2, and/or the CDRH3 of the VH amino acid sequence set forth in SEQ ID

NO.:399, and the CDRL1, the CDRL2, and/or the CDRL3 of the VL amino acid sequence set forth in SEQ ID NO.:738, wherein the CDRs are according to IMGT. As another non-limiting example, in some embodiments, the antibody or antigen-binding fragment comprises the CDRH1, the CDRH2, and the CDRH3 of the VH amino acid sequence set forth in SEQ ID NO.:399, and the CDRL1, the CDRL2, and the CDRL3 of the VL amino acid sequence set forth in SEQ ID NO.:738, wherein the CDRs are according to IMGT.

In further embodments, the antibody or antigen-binding fragment comprises a VH having at least 85% identity (*e.g.*, 85%, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100%) identity to a VH amino acid sequence provided in Table 1 and/or a VL having at least 85% identity (*e.g.*., 85%, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100%) identity to a VL amino acid sequence provided in Table 1. In still further embodments, the antibody or antigen-binding fragment comprises a VH having at least 90% identity identity to a VH amino acid sequence provided in Table 1 and/or a VL having at least 90% identity to a VL amino acid sequence provided in Table 1. In still further embodments, the antibody or antigen-binding fragment comprises a VH having at least 95% identity identity to a VH amino acid sequence provided in Table 1 and/or a VL having at least 95% identity to a VL amino acid sequence provided in Table 1. In still further embodments, the antibody or antigen-binding fragment comprises a VH having at least 99% identity identity to a VH amino acid sequence provided in Table 1 and/or a VL having at least 99% identity to a VL amino acid sequence provided in Table 1. In some embodiments, the antibody or antigen-binding fragment comprises a VH amino acid sequence selected from the VH amino acid sequences provided in Table 1 and a VL amino acid sequence selected from the VL amino acid sequence provided in Table 1. In some embodiments, S2E12 antibodies comprise a kappa light chain, *e.g.*, k1m3, IGKC*01.

Table 1. CDR (IMGT) and Variable Region Amino Acid Sequences of Certain S2E12 Antibodies

CDRH1	GFTFTSSA (SEQ ID NO.:400)

CDRH2	IVVGSGNT (SEQ ID NO.:401)
CDRH3	PYCSGGSCSDGFDI (SEQ ID NO.:766) PYCSGGSCSDAFDI (SEQ ID NO.:769) PYSSGGSSSDGFDI (SEQ ID NO.:770) PYPSGGSPSDGFDI (SEQ ID NO.:771) PYASGGSASDGFDI (SEQ ID NO.:772) PYCSGGSCSEGFDI (SEQ ID NO.:773)
CDRH3 and N-terminal adjacent alanine and serine amino acids	ASPYCSGGSCSDGFDI (SEQ ID NO.:402) ASPYCSGGSCSDAFDI (SEQ ID NO.:751) ASPYSSGGSSSDGFDI (SEQ ID NO.:753) ASPYPSGGSPSDGFDI (SEQ ID NO.:755) ASPYASGGSASDGFDI (SEQ ID NO.:757) ASPYCSGGSCSEGFDI (SEQ ID NO.:760)
VH	QVQLVQSGPEVKKPGTSVRVSCKASGFTFTSSAVQWVRQAR GQRLEWVGWIVVGSGNTNYAQKFHERVTITRDMSTSTAYM ELSSLRSEDTAVYYCASPYCSGGSCSDGFDIWGQGTMVTVSS (SEQ ID NO.:399) QVQLVQSGPEVKKPGTSVRVSCKASGFTFTSSAVQWVRQAR GQRLEWVGFIVVGSGNTNYAQKFHERVTITRDMSTSTAYME LSSLRSEDTAVYYCASPYCSGGSCSDGFDIWGQGTMVTVSS (SEQ ID NO.:748) QVQLVQSGPEVKKPGTSVRVSCKASGFTFTSSAVQWVRQAR GQRLEWVGYIVVGSGNTNYAQKFHERVTITRDMSTSTAYME LSSLRSEDTAVYYCASPYCSGGSCSDGFDIWGQGTMVTVSS (SEQ ID NO.:749)

	QVQLVQSGPEVKKPGTSVRVSCKASGFTFTSSAVQWVRQAR GQRLEWVGWIVVGSGNTNYAQKFHERVTITRDMSTSTAYM ELSSLRSEDTAVYYCASPYCSGGSCSDAFDIWGQGTMVTVSS (SEQ ID NO.:750) QVQLVQSGPEVKKPGTSVRVSCKASGFTFTSSAVQWVRQAR GQRLEWVGWIVVGSGNTNYAQKFHERVTITRDMSTSTAYM ELSSLRSEDTAVYYCASPYSSGGSSSDGFDIWGQGTMVTVSS (SEQ ID NO.:752) QVQLVQSGPEVKKPGTSVRVSCKASGFTFTSSAVQWVRQAR GQRLEWVGWIVVGSGNTNYAQKFHERVTITRDMSTSTAYM ELSSLRSEDTAVYYCASPYPSGGSPSDGFDIWGQGTMVTVSS (SEQ ID NO.:754) QVQLVQSGPEVKKPGTSVRVSCKASGFTFTSSAVQWVRQAR GQRLEWVGWIVVGSGNTNYAQKFHERVTITRDMSTSTAMEL SSLRSEDTAVYYCASPYASGGSASDGFDIWGQGTMVTVSS (SEQ ID NO.:756) QVQLVQSGPEVKKPGTSVRVSCKASGFTFTSSAVQWVRQAR GQRLEWVGFIVVGSGNTNYAQKFHERVTITRDMSTSTAYME LSSLRSEDTAVYYCASPYCSGGSCSEGFDIWGQGTMVTVSS (SEQ ID NO.:758) QVQLVQSGPEVKKPGTSVRVSCKASGFTFTSSAVQWVRQAR GQRLEWVGWIVVGSGNTNYAQKFHERVTITRDMSTSTAYM ELSSLRSEDTAVYYCASPYCSGGSCSEGFDIWGQGTMVTVSS (SEQ ID NO.:759)

	QVQLVQSGPEVKKPGTSVRVSCKASGFTFTSSAVQWVRQAR GQRLEWVGAIVVGSGNTNYAQKFHERVTITRDMSTSTAYME LSSLRSEDTAVYYCASPYCSGGSCSDGFDIWGQGTMVTVSS (SEQ ID NO.:761)
CDRL1	QSVSSSY (SEQ ID NO.:404)
CDRL2	GAS (SEQ ID NO.:405)
CDRL3	QQYVGLTGWT (SEQ ID NO.:406) QQYVGLTGFT (SEQ ID NO.:745) QQYVGLTGYT (SEQ ID NO.:747)
VL	DIVLTQTPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPG QAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQYVGLTGWTFGQGTKVEIK (SEQ ID NO.:403) DIVLTQTPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPG QAPRALIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQYVGLTGWTFGQGTKVEIK (SEQ ID NO.:738) DIVLTQTPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPG QAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQYVGLTGFTFGQGTKVEIK (SEQ ID NO.:744) DIVLTQTPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPG QAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQYVGLTGYTFGQGTKVEIK (SEQ ID NO.:746)

In some embodiments, an antibody, or an antigen-binding fragment thereof, comprises a heavy chain variable domain (VH) comprising complementarity determining region (CDR)H1, CDRH2, and CDRH3, and a light chain variable domain (VL) comprising CDRL1, CDRL2, and CDRL3, wherein CDRH1, CDRH2, CDRH3,

CDRL1, CDRL2, and CDRL3 comprise or consist of the amino acid sequences set forth in: (a) SEQ ID NOs.:400, 401, 766, 404, 405, and 406, respectively; (b) SEQ ID NOs.:400, 401, 769, 404, 405, and 406, respectively; (c) SEQ ID NOs.:400, 401, 770, 404, 405, and 406, respectively; (d) SEQ ID NOs.:400, 401, 771, 404, 405, and 406, respectively; (e) SEQ ID NOs.:400, 401, 772, 404, 405, and 406, respectively; (f) SEQ ID NOs.:400, 401, 773, 404, 405, and 406, respectively; (g) SEQ ID NOs.:400, 401, 766, 404, 405, and 745, respectively; (h) SEQ ID NOs.:400, 401, 769, 404, 405, and 745, respectively; (i) SEQ ID NOs.:400, 401, 770, 404, 405, and 745, respectively; (j) SEQ ID NOs.:400, 401, 771, 404, 405, and 745, respectively; (k) SEQ ID NOs.:400, 401, 772, 404, 405, and 745, respectively; (l) SEQ ID NOs.: 400, 401, 773, 405, 405, and 745, respectively; (m) SEQ ID NOs.:400, 401, 766, 404, 405, and 747, respectively; (n) SEQ ID NOs.:400, 401, 769, 404, 405, and 747, respectively; (o) SEQ ID NOs.:400, 401, 770, 404, 405, and 747, respectively; (p) SEQ ID NOs.:400, 401, 771, 404, 405, and 747, respectively; (q) SEQ ID NOs.:400, 401, 772, 404, 405, and 747, respectively; or (r) SEQ ID NOs.:400, 401, 773, 404, 405, and 747, respectively.

In further embodiments, the antibody or antigen-binding fragment comprises the amino acid sequences set forth in: (a) SEQ ID NOs.:400, 401, 402, 404, 405, and 406; (b) SEQ ID NOs.:400, 401, 751, 404, 405, and 406; (c) SEQ ID NOs.:400, 401, 753, 404, 405, and 406; (d) SEQ ID NOs.:400, 401, 755, 404, 405, and 406; (e) SEQ ID NOs.:400, 401, 757, 404, 405, and 406; (f) SEQ ID NOs.:400, 401, 760, 404, 405, and 406; (g) SEQ ID NOs.:400, 401, 402, 404, 405, and 745; (h) SEQ ID NOs.:400, 401, 751, 404, 405, and 745; (i) SEQ ID NOs.:400, 401, 753, 404, 405, and 745; (j) SEQ ID NOs.:400, 401, 755, 404, 405, and 745; (k) SEQ ID NOs.:400, 401, 757, 404, 405, and 745; (l) SEQ ID NOs.: 400, 401, 760, 405, 405, and 745; (m) SEQ ID NOs.:400, 401, 402, 404, 405, and 747; (n) SEQ ID NOs.:400, 401, 751, 404, 405, and 747; (o) SEQ ID NOs.:400, 401, 753, 404, 405, and 747; (p) SEQ ID NOs.:400, 401, 755, 404, 405, and 747; (q) SEQ ID NOs.:400, 401, 757, 404, 405, and 747; or (r) SEQ ID NOs.:400, 401, 760, 404, 405, and 747. In each of (a)-(r) above, it will be understood that the first three recited SEQ ID NOs. are VH amino acid sequences, and the latter three recited SEQ ID NOs. are VL amino acid sequences. For example, in (a), SEQ ID NOs.:400,

401, and 402 are amino acid sequences in VH, and SEQ ID NOs.:404, 405, and 406 are amino acid sequences in VL.

Other exemplary antibodies include S2M11, S2D106, S2H58, and engineered variants thereof. In some embodiments, an antibody or antigen-binding fragment comprises CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 amino acid sequences as set forth in SEQ ID NOs.:525-527 and 529-531, respectively. In further embodiments, the antibody or antigen-binding fragment comprises a VH having at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or comprising or consisting of, the amino acid sequence set forth in SEQ ID NO.:524, and a VL having at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or comprising or consisting of, the amino acid sequence set forth in SEQ ID NO.:528. In other embodiments, an antibody or antigen-binding fragment comprises CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 amino acid sequences as set forth in SEQ ID NOs.: 585, 586, 587, 589, 590, and 591, respectively, or as set forth in SEQ ID NOs.:585, 625, 627, 589, 590, and 591, respectively. In further embodiments, the antibody or antigen-binding fragment comprises a VH having at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or comprising or consisting of, the amino acid sequence set forth in any one of SEQ ID NOs.:584, 624, 626, and 628, and a VL having at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or comprising or consisting of, the amino acid sequence set forth in SEQ ID NO.:588. In other embodiments, an antibody or antigen-binding fragment comprises CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 amino acid sequences as set forth in SEQ ID NOs.: 229, 230, 231, 233, 234, and 235, respectively. In further embodiments, the antibody or antigen-binding fragment comprises a VH having at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or comprising or consisting of, the amino acid sequence set forth in any one of SEQ ID NOs.:228, 740, 741, 742, and 743, and a VL having at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or comprising or consisting of, the amino acid sequence set forth in SEQ ID NO.:232. In other embodiments, , the antibody or antigen-binding fragment comprises a VH having at least 80%, at least 85%, at least

90%, at least 95%, at least 97%, at least 99%, or comprising or consisting of, the amino acid sequence set forth in any one of SEQ ID NOs.:228, 740, 741, 742, and 743, and a VL having at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99%, or comprising or consisting of, the amino acid sequence set forth in SEQ ID NO.:238.

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.

Variant antibodies provided herein include those that comprise one or more amino acid alterations in a variable region (*e.g.*, VH, VL, framework or CDR) as compared to a presently disclosed antibody having a specific sequence, wherein the variant antibody is capable of binding to a SARS-CoV-2 antigen.

In certain embodiments, the VH comprises or consists of an amino acid sequence having at least 85% (*e.g.*, having 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.: 22, 32, 42, 52, 62, 72, 74, 84, 96, 106, 119, 129, 139, 150, 163, 173, 175, 178, 186, 189, 191, 198, 208, 218, 228, 240, 254, 264, 274, 284, 298, 312, 322, 332, 350, 351, 353, 359, 361, 363, 365, 367, 368, 369, 379, 389, 399, 409, 419, 429, 434, 444, 454, 464, 474, 484, 494, 504, 514, 524, 534, 544, 554, 564, 574, 584, 594, 604, 614, 624, 626, 628, 630, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, 684, 692, 740, 741, 742, 743, 748, 749, 750, 752, 754, 756, 758, 759, 761, 762, and 765, wherein the variation is optionally limited to one or more framework regions and/or the variation 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% (*e.g.*, having 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.: 26, 36, 46, 56, 66, 78, 88, 94, 100, 110, 123, 133, 143, 154, 157, 168, 194, 196, 202, 212, 222, 232, 238, 244, 250, 252, 258, 268, 278, 288, 294, 296, 302, 308, 310, 316, 326, 336, 355, 357, 373, 383, 393, 403, 413, 423, 438, 448,

458, 468, 478, 488, 498, 508, 518, 528, 538, 548, 558, 568, 578, 588, 598, 608, 618, 686, 696, 738, 744, and 746, wherein the variation is optionally limited to one or more framework regions and/or the variation comprises one or more substitution to a germline-encoded amino acid.

In further embodments, the VH has at least 85% (*e.g.*, having 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.:399, 748, 749, 750, 752, 754, 756, 758, 759, and 761, and the VL has at least 85% (*e.g.*, having 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.:403, 738, 744, and 746.

In further embodments, the VH has at least 85% (*e.g.*, having 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.:399, 748, 749, 750, 752, 754, 756, 758, 759, and 761, and the VL has at least 85% (*e.g.*, having 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 SEQ ID NO.:403.

In further embodments, the VH has at least 85% (*e.g.*, having 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.:399, 748, 749, 750, 752, 754, 756, 758, 759, and 761, and the VL has at least 85% (*e.g.*, having 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 SEQ ID NO.:738.

In further embodments, the VH has at least 85% (*e.g.*, having 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.:399, 748, 749, 750, 752, 754, 756, 758, 759, and 761, and the VL has at least 85% (*e.g.*, having 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 SEQ ID NO.:744.

In further embodments, the VH has at least 85% (*e.g.*, having 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.:399, 748, 749, 750, 752, 754, 756, 758, 759, and 761, and the VL has at least 85% (*e.g.*, having 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 SEQ ID NO.:746.

In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:399 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:403. In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:399 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:738. In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:399 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:744. In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:399 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:746.

In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:748 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:403. In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:748 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:738. In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:748 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:744. In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:748 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:746.

In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:749 and the VL comprises or consists of the amino acid

sequence set forth in SEQ ID NO.:403. In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:749 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:738. In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:749 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:744. In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:749 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:746.

In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:750 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:403. In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:750 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:738. In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:750 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:744. In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:750 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:746.

In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:750 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:403. In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:752 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:738. In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:752 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:744. In some embodments, the VH comprises or consists of the amino acid sequence set forth

in SEQ ID NO.:752 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:746.

In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:754 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:403. In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:754 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:738. In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:754 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:744. In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:754 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:746.

In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:756 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:403. In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:756 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:738. In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:756 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:744. In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:756 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:746.

In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:758 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:403. In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:758 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:738. In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:758 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:744. In some embodments, the VH comprises or consists of the amino

acid sequence set forth in SEQ ID NO.:758 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:746.

In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:759 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:403. In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:759 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:738. In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:759 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:744. In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:759 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:746.

In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:761 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:403. In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:761 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:738. In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:761 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:744. In some embodments, the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO.:761 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO.:746.

In some embodiments, the VH comprises or consists of any VH amino acid sequence set forth in Table 2, and the VL comprises or consists of any VL amino acid sequence set forth in Table 2. In particular embodiments, the VH and the VL comprise or consist of the amino acid sequences according to SEQ ID NOs.: (i) 22 and 26, respectively; (ii) 32 and 36, respectively; (iii) 42 and 46, respectively; (iv) 52 and 56, respectively; (v) 62 and 66, respectively; (vi) 72

and 66, respectively; (vii) 74 and 78, respectively; (viii) 84 and 88, respectively; (ix) 84 and 94, respectively; (x) 96 and 100, respectively; (xi) 106 and 110, respectively; (xii) 119 and 123, respectively; (xiii) 129 and 133, respectively; (xiv) 22 or 150 and 26, 154, or 157, respectively; (xv) 42 or 163 and 46 or 168, respectively; (xvi) any one of 129, 173, 175, or 178 and 133, respectively; (xvii) any one of 52, 186, 189, or 191 and any one of 56, 194, or 196, respectively; (xviii) 198 and 202, respectively; (xix) 208 and 212, respectively; (xx) 218 and 222, respectively; (xxi) 228 and 232 or 238, respectively; (xxii) 240 and any one of 244, 250, or 252, respectively; (xxiii) 254 and 258, respectively; (xxiv) 264 and 268, respectively; (xxv) 274 and 278, respectively; (xxvi) 284 and any one of 288, 294, or 296, respectively; (xxvii) 298 and any one of 302, 308, or 310, respectively; (xxviii) 312 and 316, respectively; (xxix) 322 and 326, respectively; (xxx) 332 and 336, respectively, (xxxi) any one of 228, 350, 351, or 353 and any one of 232, 238, 355, or 357, respectively; (xxxii) any one of 312, 359, 361, 363, 365, 367, or 368 and 316, respectively; (xxxiii) 369 and 373, respectively; (xxxiv) 379 and 383, respectively; (xxxv) 389 and 393, respectively; (xxxvi) 399 and 403 or 738, respectively; (xxxvii) 409 and 413, respectively; (xxxviii) 419 and 423, respectively; (xxxix) 434 and 438, respectively; (xxxx) 444 and 448, respectively; (xxxxi) 454 and 458, respectively; (xxxxii) 464 and 468, respectively; (xxxxiii) 474 and 478, respectively; (xxxxiv) 484 and 488, respectively; (xxxxv) 494 and 498, respectively; (xxxxvi) 504 and 508, respectively; (xxxxvii) 514 and 518, respectively; (xxxxviii) 524 and 528, respectively; (xxxxix) 534 and 538, respectively; (xxxxx) 544 and 548, respectively; (xxxxxi) 554 and 558, respectively; (xxxxxii) 564 and 568, respectively; (xxxxxiii) 574 and 578, respectively; (xxxxxiv) 584 and 588, respectively; (xxxxxv) 594 and 598, respectively; (xxxxxvi) 604 and 608, respectively; (xxxxxvii) 614 and 618, respectively; (xxxxxviii) 624, 626, or 628 and 588, respectively; (xxxxxix) 630, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, or 684, and 686, respectively; (xxxxxx) 692 and 696, respectively; (xxxxxxi) any one of 740-743 and 238, respectively, (xxxxxxii) any one of 399, 748, 749, 750, 752, 754, 756, 758, 759 or 761

and any one of 403, 744, or 746, respectively; or (xxxxxxiii) 762 or 764 and 588, respectively.

In certain embodiments, the VH and the VL comprise or consist of the amino acid sequences according to SEQ ID NOs.: 624, 626, or 628 and 588, respectively. In certain embodiments, the VH and the VL comprise or consist of the amino acid sequences according to SEQ ID NOs.: 630, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, or 684, and 686, respectively. In certain embodiments, the VH and the VL comprise or consist of the amino acid sequences according to SEQ ID NOs.:692 and 696, respectively.

In certain embodiments, the VH and the VL comprise or consist of the amino acid sequences according to SEQ ID NOs.: 399 and 738, respectively. In certain embodiments, the VH and the VL comprise or consist of the amino acid sequences according to SEQ ID NOs.:399 and 403, respectively. In certain embodiments, the VH and the VL comprise or consist of the amino acid sequences according to SEQ ID NOs.:399 and 738, respectively. In certain embodiments, the VH and the VL comprise or consist of the amino acid sequences according to SEQ ID NOs.:399 and 744, respectively. In certain embodiments, the VH and the VL comprise or consist of the amino acid sequences according to SEQ ID NOs.:399 and 746, respectively. In certain embodiments, the VH and the VL comprise or consist of the amino acid sequences according to SEQ ID NOs.:748 and 403, respectively. In certain embodiments, the VH and the VL comprise or consist of the amino acid sequences according to SEQ ID NOs.:749 and 403, respectively. In certain embodiments, the VH and the VL comprise or consist of the amino acid sequences according to SEQ ID NOs.:750 and 403, respectively. In certain embodiments, the VH and the VL comprise or consist of the amino acid sequences according to SEQ ID NOs.:752 and 403, respectively. In certain embodiments, the VH and the VL comprise or consist of the amino acid sequences according to SEQ ID NOs.:754 and 403, respectively. In certain embodiments, the VH and the VL comprise or consist of the amino acid sequences according to SEQ ID NOs.:756 and 403, respectively. In certain embodiments, the VH

and the VL comprise or consist of the amino acid sequences according to SEQ ID NOs.:758 and 403, respectively. In certain embodiments, the VH and the VL comprise or consist of the amino acid sequences according to SEQ ID NOs.:759 and 403, respectively. In certain embodiments, the VH and the VL comprise or consist of the amino acid sequences according to SEQ ID NOs.:761 and 403, respectively.

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: a 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.:8 or SEQ ID NO.: 9. In certain embodiments, a CH1-CH2-CH3 (also referred-to as a CH1-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.:6 or SEQ ID NO.:7.

In certain embodiments, an antibody or antigen-binding fragment of the present disclosure comprises a heavy chain polypeptide comprising or consisting of the amino acid sequence set forth in SEQ ID NO.:767 and a light chain polypeptide comprising or consisting of the amino acid sequence set forth in SEQ ID NO.:768.

It will be understood that, for example, production in a mammalian cell line can remove one or more C-terminal lysine of an antibody heavy chain (*see*, *e.g.*, Liu *et al. mAbs 6*(5):1145-1154 (2014)). Accordingly, an antibody or antigen-binding fragment of the present disclosure can comprise a heavy chain, a CH1-CH3, a CH3, or an Fc polypeptide wherein a C-terminal lysine residue is present or is absent; in other words, encompassed are embodiments where the C-terminal residue of a heavy chain, a CH1-CH3, or an Fc polypeptide is not a lysine due to removal of a C-terminal lysine, and

embodiments where a lysine is the C-terminal residue. In certain embodiments, a composition comprises a plurality of an antibody and/or an antigen-binding fragment of the present disclosure, wherein one or more antibody or antigen-binding fragment does not comprise a lysine residue at the C-terminal end of the heavy chain, CH1-CH3, or Fc polypeptide, and wherein one or more antibody or antigen-binding fragment comprises a lysine residue at the C-terminal end of the heavy chain, CH1-CH3, or Fc polypeptide. In other words, in certain embodiments, a heavy chain can comprise or consist of the amino acid sequence set forth in SEQ ID NO.:767 without the C-terminal lysine. In certain embodiments, a heavy chain or a CH1-CH3 can comprise of the amino acid sequence set forth in SEQ ID NO.:6 or SEQ ID ID NO.:7 without the C-terminal lysine.

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 an 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 originally were produced as pairs of Fab' fragments that have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

Fab fragments may be joined, *e.g.*, by a peptide linker, to form a single chain Fab, also referred to herein as "scFab." In these embodiments, an inter-chain disulfide bond that is present in a native Fab may not be present, and the linker serves in full or in part to link or connect the Fab fragments in a single polypeptide chain. A heavy chain-derived Fab fragment (*e.g.*, comprising, consisting of, or consisting essentially of VH + CH1, or "Fd") and a light chain-derived Fab fragment (*e.g.*, comprising, consisting of, or consisting essentially of VL + CL) may be linked in any arrangement to form a

scFab. For example, a scFab may be arranged, in N-terminal to C-terminal direction, according to (heavy chain Fab fragment – linker – light chain Fab fragment) or (light chain Fab fragment – linker – heavy chain Fab fragment). Peptide linkers and exemplary linker sequences for use in scFabs are discussed in further detail herein.

"Fv" is a small antibody fragment that contains a complete antigen-recognition and antigen-binding site. This fragment generally consists of a dimer of one heavy- and one light-chain variable region 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.

"Single-chain Fv" also abbreviated as "sFv" or "scFv", are antibody fragments that comprise the V_H and V_L antibody domains connected into a single polypeptide chain. In some embodiments, the scFv polypeptide comprises a polypeptide linker disposed between and linking the V_H and V_L domains that enables the scFv to retain or form the desired structure for antigen binding. Such a peptide linker can be incorporated into a fusion polypeptide using standard techniques well known in the art. For a review of scFv, 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*. In certain embodiments, the antibody or antigen-binding fragment comprises a scFv comprising a VH domain, a VL domain, and a peptide linker linking the VH domain to the VL domain. In particular embodiments, a scFv comprises a VH domain linked to a VL domain by a peptide linker, which can be in a VH-linker-VL orientation or in a VL-linker-VH orientation. Any scFv of the present disclosure may be engineered so that the C-terminal end of the VL domain is linked by a short peptide sequence to the N-terminal end of the VH domain, or vice versa (i.e., (N)VL(C)-linker-(N)VH(C) or (N)VH(C)-linker-(N)VL(C). Alternatively, in some embodiments, a linker may be linked to an N-terminal portion or end of the VH domain, the VL domain, or both.

Peptide linker sequences may be chosen, for example, based on: (1) their ability to adopt a flexible extended conformation; (2) their inability or lack of ability to adopt a

secondary structure that could interact with functional epitopes on the first and second polypeptides and/or on a target molecule; and/or (3) the lack or relative lack of hydrophobic or charged residues that might react with the polypeptides and/or target molecule. Other considerations regarding linker design (*e.g.*, length) can include the conformation or range of conformations in which the VH and VL can form a functional antigen-binding site. In certain embodiments, peptide linker sequences contain, for example, Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala, may also be included in a linker sequence. Other amino acid sequences which may be usefully employed as linker include those disclosed in Maratea et al., Gene 40:39 46 (1985); Murphy et al., Proc. Natl. Acad. Sci. USA 83:8258 8262 (1986); U.S. Pat. No. 4,935,233, and U.S. Pat. No. 4,751,180. Other illustrative and non-limiting examples of linkers may include, for example, Glu-Gly-Lys-Ser-Ser-Gly-Ser-Gly-Ser-Glu-Ser-Lys-Val-Asp (SEQ ID NO: 19) (Chaudhary et al., Proc. Natl. Acad. Sci. USA 87:1066-1070 (1990)) and Lys-Glu-Ser-Gly-Ser-Val-Ser-Ser-Glu-Gln-Leu-Ala-Gln-Phe-Arg-Ser-Leu-Asp (SEQ ID NO: 20) (Bird et al., Science 242:423-426 (1988)) and the pentamer Gly-Gly-Gly-Gly-Ser (SEQ ID NO: 21) when present in a single iteration or repeated 1 to 5 or more times, or more; see, e.g., SEQ ID NO: 17. Any suitable linker may be used, and in general can be about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 15 23, 24, 25, 26, 27, 28, 29, 30, 40, 50, 60, 70, 80, 90, 100 amino acids in length, or less than about 200 amino acids in length, and will preferably comprise a flexible structure (can provide flexibility and room for conformational movement between two regions, domains, motifs, fragments, or modules connected by the linker), and will preferably be biologically inert and/or have a low risk of immunogenicity in a human. Exemplary linkers include those comprising or consisting of the amino acid sequence set forth in any one or more of SEQ ID NOs: 10-21. In certain embodiments, the linker comprises or consists of an amino acid sequence having at least 75% (i.e., at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more) identity to the amino acid sequence set forth in any one of SEQ ID NOs: 10-21.

scFv can be constructed using any combination of the VH and VL sequences or any combination of the CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 sequences disclosed herein.

In some embodiments, linker sequences are not required; for example, when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

In certain embodiments, an antibody or antigen-binding fragment of the present disclosure is monospecific (*e.g.*, binds to a single epitope) or is multispecific (*e.g.*, binds to multiple epitopes and/or target molecules). Antibodies and antigen binding fragments may be constructed in various formats. Exemplary antibody formats disclosed in Spiess et al., Mol. Immunol. 67(2):95 (2015), and in Brinkmann and Kontermann, mAbs 9(2):182-212 (2017), which 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, κλ-bodies, orthogonal Fabs, DVD-Igs (*e.g.*, US Patent 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).

In certain embodiments, the antibody or antigen-binding fragment comprises two or more of VH domains, two or more VL domains, or both (*i.e.*, two or more VH

domains and two or more VL domains). In particular embodiments, an antigen-binding fragment comprises the format (N-terminal to C-terminal direction) VH-linker-VL-linker-VH-linker-VL, wherein the two VH sequences can be the same or different and the two VL sequences can be the same or different. Such linked scFvs can include any combination of VH and VL domains arranged to bind to a given target, and in formats comprising two or more VH and/or two or more VL, one, two, or more different eptiopes or antigens may be bound. It will be appreciated that formats incorporating multiple antigen-binding domains may include VH and/or VL sequences in any combination or orientation. For example, the antigen-binding fragment can comprise the format VL-linker-VH-linker-VL-linker-VH, VH-linker-VL-linker-VL-linker-VH, or VL-linker-VH-linker-VH-linker-VL.

Monospecific or multispecific antibodies or antigen-binding fragments of the present disclosure constructed comprise any combination of the VH and VL sequences and/or any combination of the CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 sequences disclosed herein. A bispecific or multispecific antibody or antigen-binding fragment may, in some embodiments, comprise one, two, or more antigen-binding domains (*e.g.*, a VH and a VL) of the instant disclosure. Two or more binding domains may be present that bind to the same or a different SARS-CoV-2 epitope, and a bispecific or multispecific antibody or antigen-binding fragment as provided herein can, in some embodiments, comprise a further SARS-CoV-2 binding domain, and/or can comprise a binding domain that binds to a different antigen or pathogen altogether.

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

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% (*e.g.*, having 85%, 86%,

87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%) dentity to the amino acid sequence set forth in any one of SEQ ID NOs.: 22, 32, 42, 52, 62, 72, 74, 84, 96, 106, 119, 129, 139, 150, 163, 173, 175, 178, 186, 189, 191, 198, 208, 218, 228, 240, 298, 312, 322, 332, 350, 351, 353, 359, 361, 363, 365, 367, 368, 369, 379, 389, 399, 409, 419, 429, 434, 444, 454, 464, 474, 484, 494, 504, 514, 524, 534, 544, 554, 564, 574, 584, 594, 604, 614, 624, 626, 628, 630, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, 684, 692, 740, 741, 742, 743, 748, 749, 750, 752, 754, 756, 758, 759, 761, 762, and 764, and wherein the first VL and the second VL are different and each independently comprise an amino acid sequence having at least 85% (*e.g.*, having 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.: 26, 36, 46, 56, 66, 78, 88, 94, 100, 110, 123, 133, 143, 154, 157, 168, 194, 196, 202, 212, 222, 232, 238, 244, 250, 252, 258, 268, 278, 288, 294, 296, 302, 308, 310, 316, 326, 336, 355, 357, 373, 383, 393, 403, 413, 423, 438, 448, 458, 468, 478, 488, 498, 508, 518, 528, 538, 548, 558, 568, 578, 588, 598, 608, 618, 686, 696, 738, 744, and 746, 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.

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 comprises an amino acid sequence having at least 85% (*e.g.*, having 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.: 139 and 342 and the first VL comprises an amino acid sequence having at least 85% (*e.g.*, having 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.:143 and 346 and wherein the second VH comprises an amino acid sequence having at least 85 (*e.g.*, having 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.: 399, 748, 749, 750, 752, 754, 756, 758, 759, and 761 and the second VL comprises an amino acid sequence having at least 85(*e.g.*, having 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.:403, 744, and 746.

In certain embodiments, the antibody or antigen-binding fragment comprises a 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 that, in general, are 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: C1q 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 Fc 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.

For example, to activate the complement cascade, the C1q 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.

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 FcεR, 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., *J Lab. Clin. Med.* 126 (1995) 330-341; and Gessner, J. E., et al., *Ann. Hematol.* 76 (1998) 231-248.

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 homologuous; 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.

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).

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.

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.

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).

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.

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).

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.

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).

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).

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) Fcγ 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.

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 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 Fc 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.

In some embodiments, an antibody or antigen-binding fragment includes a Fc moiety that comprises the substitution mtuations M428L/N434S. In some embodiments, an antibody or antigen-binding fragment includes a Fc polypeptide or fragment thereof that comprises the substitution mtuations 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 a 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. 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.

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)).

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.

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, a Fc polypeptide of the present disclosure comprises two CH2-CH3 polypeptides that associate to form a dimer.

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.

Antibodies and antigen-binding fragments of the present disclosure include "chimeric antibodies" in which a portion of the heavy and/or light chain is identical with or homologous to corresponding 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.

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 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 (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.

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 are typically 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.

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

In some embodiments, an antibody or antigen-binding fragment of the present disclosure is capable of binding to a SARS-CoV-2 surface glycoprotein with an EC50 of less than 500 ng/ml, less than 250 ng/ml, less than 100 ng/ml, less than 90 ng/ml, less than 80 ng/ml, less than 70 ng/ml, less than 60 ng/ml, less than 50 ng/ml, less than 40 ng/ml, less than 30 ng/ml, less than 25 ng/ml, less than 20 ng/ml, less than 16 ng/ml, less than 15 ng/ml, less than 14 ng/ml, less than 13 ng/ml, less than 12 ng/ml, less than 10 ng/ml, less than 9 ng/ml, less than 8 ng/ml, less than 7 ng/ml, less than 6 ng/ml, less than 5 ng/ml, less than 4 ng/ml, or less than 2 mg/ml, as measured by ELISA (optionally, indirect ELISA and/or sandwich ELISA) and/or by flow cytometry, wherein the SARS CoV-2 surface glycoprotein is expressed at a cell surface of a host cell.

In some embodiments, antibody or antigen-binding fragment of the present disclosure is capable of binding to a SARS-CoV-2 surface glycoprotein RBD with an EC50 of less than 500 ng/ml, less than 250 ng/ml, less than 100 ng/ml, less than 90 ng/ml, less than 80 ng/ml, less than 70 ng/ml, less than 60 ng/ml, less than 50 ng/ml, less than 40 ng/ml, less than 30 ng/ml, less than 25 ng/ml, less than 20 ng/ml, less than 16 ng/ml, less than 15 ng/ml, less than 14 ng/ml, less than 13 ng/ml, less than 12 ng/ml, less than 10 ng/ml, less than 9 ng/ml, less than 8 ng/ml, less than 7 ng/ml, less than 6

ng/ml, less than 5 ng/ml, less than 4 ng/ml, or less than 2 mg/ml, as measured by ELISA (optionally, indirect ELISA and/or sandwich ELISA) and/or by flow cytometry, wherein the SARS CoV-2 surface glycoprotein is expressed at a cell surface of a host cell.

In some embodiments, antibody or antigen-binding fragment of the present disclosure is capable of binding to a SARS-CoV-2 RBD with a KD of less than 5×10^{-8} M, less than 4×10^{-8} M, less than 3×10^{-8} M, less than 2×10^{-8} M, less than 1×10^{-8} M, less than 5×10^{-9} M, less than 1×10^{-9} M, less than 5×10^{-10} M, less than 1×10^{-10} M, less than 5×10^{-11} M, less than 1×10^{-11} M, less than 5×10^{-12} M, or less than 1×10^{-12} M, as determined using biolayer interferometry (BLI), optionally using an Octet instrument with antibody or antigen-binding fragment loaded on Protein A pins, optionally at 2.7 μg/ml, and SARS-CoV-2 RBD loaded for 5 minutes at 6 μg/ml, 1.5 μg/ml, or 0.4 μg/ml, further optionally with dissociation measured for 7 minutes.

In some embodiments, antibody or antigen-binding fragment of the present disclosure is capable of binding to a SARS-CoV-2 RBD with a KD of less than 6×10^{-8} M, less than 5×10^{-8} M, less than 4×10^{-8} M, less than 3×10^{-8} M, less than 2×10^{-8} M, less than 1×10^{-8} M, less than 5×10^{-9} M, less than 4×10^{-9} M, less than 3×10^{-9} M, less than 2×10^{-9} M, less than 1×10^{-9} M, or less than 8×10^{-10} M, as determined using surface plasmon resonance (SPR), optionally using a Biacore T200 instrument using a single-cycle kinetics approach.

In some embodiments, antibody or antigen-binding fragment of the present disclosure is capable of binding to a SARS-CoV-2 RBD and inhibiting an interaction between (i) the RBD and (ii) a human ACE2 and/or a human SIGLEC-1.

In some embodiments, antibody or antigen-binding fragment of the present disclosure is capable of neutralizing: (i) infection by a SARS-CoV-2 pseudovirus, optionally: (i)(a) with a neutralization IC50 of less than 100 ng/ml, less than 90 ng/ml, less than 80 ng/ml, less than 70 ng/ml, less than 60 ng/ml, less than 50 ng/ml, less than 40 ng/ml, less than 30 ng/ml, less than 25 ng/ml, less than 20 ng/ml, less than 15 ng/ml, less than 10 ng/ml, less than 9 ng/ml, less than 8 ng/ml, less than 7 ng/ml, less than 6 ng/ml, less than 5 ng/ml, less than 4 ng/ml, less than 3 ng/ml, less than 2 ng/ml, or less

than 1 ng/ml, preferably less than 10 ng/ml, less than 9 ng/ml, less than 8 ng/ml, less than 7 ng/ml, less than 6 ng/ml, less than 5 ng/ml, less than 4 ng/ml, less than 3 ng/ml, less than 2 ng/ml, or less than 1 ng/ml, and/or (i)(b) with a neutralization IC80 of less than 100 ng/ml, less than 90 ng/ml, less than 80 ng/ml, less than 70 ng/ml, less than 60 ng/ml, less than 50 ng/ml, less than 40 ng/ml, less than 30 ng/ml, or less than 25 ng/ml, preferably less than 50 ng/ml, less than 40 ng/ml, less than 30 ng/ml, or less than 25 ng/ml, and/or (i)(c) with a neutralization EC90 of less than 300 ng/ml, less than 200 ng/ml, less than 100 ng/ml, less than 90 ng/ml, less than 80 ng/ml, less than 70 ng/ml, less than 60 ng/ml 50 ng/ml, less than 40 ng/ml, less than 30 ng/ml, less than 25 ng/ml, less than 20 ng/ml, less than 15 ng/ml, or less than 10 ng/ml, wherein, further optionally, the SARS-CoV-2 pseudovirus comprises a VSV pseudovirus and/or a MLV pseudovirus, and/or (i)(d) the SARS-CoV-2 pseudovirus comprises a VSV pseudovirus and/or a MLV pseudovirus; and/or (ii) infection by live SARS-CoV-2, optionally (ii)(a) with a EC50 of less than 60 ng/ml, less than 50 ng/ml, less than 40 ng/ml, less than 30 ng/ml, less than 25 ng/ml, less than 20 ng/ml, less than 15 ng/ml, less than 12 ng/ml, less than 11 ng/ml, less than 10 ng/ml, less than 9 ng/ml, less than 8 ng/ml, less than 7 ng/ml, less 6 ng/ml, less than 5/ng ml, or less than 4 ng/ml, preferably less than 15 ng/ml, less than 12 ng/ml, less than 11 ng/ml, less than 10 ng/ml, less than 9 ng/ml, less than 8 ng/ml, less than 7 ng/ml, less 6 ng/ml, less than 5/ng ml, or less than 4 ng/ml, and/or (ii)(b) with a EC90 of less than 50 ng/ml, less than 40 ng/ml, less than 35 ng/ml, less than 30 ng/ml, less than 25 ng/ml, less than 20 ng/ml, less than 15 ng/ml, less than 12 ng/ml, less than 11 ng/ml, less than 10 ng/ml, less than 9 ng/ml, less than 8 ng/ml, less than 7 ng/ml, less 6 ng/ml, less than 5/ng ml, or less than 4 ng/ml, preferably less than 30 ng/ml, less than 25 ng/ml, less than 20 ng/ml, less than 15 ng/ml, or less than 12 ng/ml, and/or (ii)(c) over a 6-hour period, with a multiplicity of infection of 0.1; and/or (iii) infection by live SARS-CoV-2 in a host cell (*e.g.* a HEK293T cell) that expresses, optionally is engineered to overexpress, DC-SIGN, L-SIGN, SIGLEC, or ACE2; and/or (iv) infection by live SARS-CoV-2 in a host cell (*e.g.* a HEK293T cell) that expresses, optionally is engineered to overexpress, SIGLEC-1 or ACE2, wherein neutralizing infection comprises fully neutralizing infection.

In some embodiments, an antibody or antigen-binding fragment of the present disclosure is capable of neutralizing infection by a SARS-CoV-2 variant that comprises any one of the following mutations in the surface glycoprotein as compared to a SARS-CoV-2 surface glycoprotein comprising SEQ ID NO.:3: N501Y; S477N; N439K; L452R; E484K; K417N; T478K; S494P; A520S; N501T; A522S; Y453F; P384L.

In some embodiments, an antibody or antigen-binding fragment of the present disclosure is capable of neutralizing infection by the SARS-CoV-2 variant with a potency that is less than 3-fold lower than the potency with which the antibody or antigen-binding fragment neutralizes infection by a SARS-CoV-2 comprising the surface glycoprotein amino acid sequence set forth in SEQ ID NO.:3.

In some embodiments, an antibody or antigen-binding fragment of the present disclosure is capable of activating a FcγRIIa, a FcγRIIIa, or both, wherein, optionally:(i) the FcγRIIa comprises a H131 allele; and/or (ii) the FcγRIIIa comprises a V158 allele; and/or (iii) activation is determined using a SARS-CoV-2 S-expressing target cell, such as a CHO cell, and a reporter cell expressing a NFAT-driven reporter, such as luciferase.

In some embodiments, an antibody or antigen-binding fragment of the present disclosure has an *in vivo* half-life in a non-human primate of between 20 and 30 days, or between 22 and 28 days, or between 23 and 27 days, or between 24 and 26 days, or of about 25 days.

In some embodiments an antibody or antigen-binding fragment of the present disclosure is capable of neutralizing a SARS-CoV-2 infection and/or of neutralizing an infection of a target cell with an IC50 of about 20 to about 30 ng/ml.

In some embodiments, an antibody or antigen-binding fragment of the present disclosure is capable of neutralizing a SARS-CoV-2 infection and/or of neutralizing an infection of a target cell with an IC50 of about 10 to about 20 ng/ml.

In some embodiments, an antibody or antigen-binding fragment of the present disclosure is capable of neutralizing a SARS-CoV-2 infection and/or of neutralizing an infection of a target cell with an IC50 of about 5 to about 10 ng/ml.

In some embodiments, an antibody or antigen-binding fragment of the present disclosure is capable of neutralizing a SARS-CoV-2 infection and/or of neutralizing an infection of a target cell with an IC50 of about 1 to about 5 ng/ml.

In some embodiments, an antibody or antigen-binding fragment of the present disclosure is capable of neutralizing infection by SARS-CoV-2 and does not compete with a human ACE2 for binding to the SARS-CoV-2S protein, wherein, optionally, the neutralizing comprises neutralizing infection in an in vitro model of infection.

In some embodiments, an antibody or antigen-binding fragment of the present disclosure is provided that competes for binding to a SARS-CoV-2 surface glycoprotein with an antibody or antigen-binding fragment of the present disclosure.

Polynucleotides, Vectors, and Host cells

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.

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.

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.:30, 31, 40, 41, 50, 51, 60, 61, 70, 71, 73,

82, 83, 92, 93, 95, 104, 105, 114, 115, 116, 117, 118, 127, 128, 137, 138, 206, 207, 216, 217, 226, 227, 236, 237, 239, 248, 249, 251, 253, 262, 263, 272, 273, 282, 283, 292, 293, 295, 297, 306, 307, 309, 311, 320, 321, 330, 331, 340, 341, 377, 378, 387, 388, 397, 398, 407, 408, 417, 418, 427, 428, 433, 442, 443, 452, 453, 462, 463, 472, 473, 482, 483, 492, 493, 502, 503, 512, 513, 552, 523, 532, 533, 542, 543, 552, 553, 562, 563, 572, 573, 582, 583, 592, 593, 602, 603, 612, 613, 622, 623, 690, 691, 700-737, and 739.

In certain embodiments, a polynucleotide comprises (i) a polynucleotide having at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or at least 99% identity to, or that comprises or consists of, the nucleotide sequence set forth in SEQ ID NO.:407; and (ii) a polynucleotide having at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or at least 99% identity to, or that comprises or consists of, the nucleotide sequence set forth in SEQ ID NO.:408, 737, or 739.

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).

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 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). 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).

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.

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).

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.

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.

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.

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.*, glysocylation 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 a 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).

Insect cells useful expressing a binding protein 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 *Spodoptera frugiperda* cells.

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).

Plant cells can also be utilized as hosts for expressing a binding protein 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.

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.

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 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

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.

In certain embodiments, a composition comprises two or more different antibodies or antigen-binding fragments according to the present disclosure. In certain embodiments, antibodies or antigen-binding fragments to be used in a combination each independently have one or more of the following characteristics: neutralize naturally occurring SARS-CoV-2 variants; do not compete with one another for Spike protein binding; bind distinct Spike protein epitopes; have a reduced formation of resistance to SARS-CoV-2; when in a combination, have a reduced formation of resistance to SARS-CoV-2; potently neutralize live SARS-CoV-2 virus; exhibit additive or synergistic effects on neutralization of live SARS-CoV-2 virus when used in combination; exhibit effector functions; are protective in relevant animal model(s) of infection; are capable of being produced in sufficient quantities for large-scale production.

In certain embodiments, a composition comprises two or more different antibodies or antigen-binding fragments, which can be two or more presently disclosed antibodies or antigen-binding fragments. In any of the presently disclosed embodiments, an antibody or antigen-binding fragment thereof can be comprised in a composition that further comprises an antibody or antigen-binding fragment that comprises: (i) CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 amino acid sequences as set forth in SEQ ID NOs.:343-345 and 347-349, respectively; or (ii) CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 amino acid sequences as set forth in SEQ ID NOs.:140-142 and 144-146, respectively; or (iii) VH and VL amino acid sequences as set forth in SEQ ID NOs.:342 and 346, respectively; or (iv) VH and VL amino acid sequences as set forth in SEQ ID NOs.:139 and 143, respectively.

In certain embodiments, a composition comprises a first antibody or antigen-binding fragment, comprising a VH comprising or consisting of the amino acid sequence as set forth in SEQ ID NO: 32 and a VL comprising or consisting of the amino acid sequence as set forth in SEQ ID NO: 36; and a second antibody or antigen-

binding fragment comprising a VH comprising or consisting of the amino acid sequence as set forth in SEQ ID NO: 139, and a VL comprising or consisting of the amino acid sequence as set forth in SEQ ID NO: 143. In certain embodiments, a composition comprises a first antibody or antigen-binding fragment 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 CDRH1, CDRH2, and CDRH3 comprise or consist of the amino acid sequences set forth in SEQ ID NOs: 33-35, respectively, and the CDRL1, CDRL2, and CDRL3 comprise or consist of the amino acid sequences set forth in SEQ ID NOs: 37-39, respectively, and a second antibody or antigen-binding fragment 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 CDRH1, CDRH2, and CDRH3 comprise or consist of the amino acid sequences set forth in SEQ ID NOs: 140-142, respectively, and the CDRL1, CDRL2, and CDRL3 comprise or consist of the amino acid sequences set forth in SEQ ID NOs: 144-146, respectively.

In certain embodiments, a composition comprises a first antibody or antigen-binding fragment, comprising a VH comprising or consisting of the amino acid sequence as set forth in SEQ ID NO: 139 or 342 and a VL comprising or consisting of the amino acid sequence as set forth in SEQ ID NO: 143 or 346; and a second antibody or antigen-binding fragment comprising a VH comprising or consisting of the amino acid sequence as set forth in SEQ ID NO: 399, 748, 749, 750, 752, 754, 756, 758, 759, or 761, and a VL comprising or consisting of the amino acid sequence as set forth in SEQ ID NO: 403, 744, or 746. In certain embodiments, a composition comprises a first antibody or antigen-binding fragment 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 CDRH1, CDRH2, and CDRH3 comprise or consist of the amino acid sequences set forth in SEQ ID NOs: 140-142, respectively, or 343-345, respectively, and the CDRL1, CDRL2, and CDRL3 comprise or consist of the amino acid sequences set forth in SEQ ID NOs: 144-146,

respectively, and a second antibody or antigen-binding fragment 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 CDRH1, CDRH2, and CDRH3 comprise or consist of the amino acid sequences set forth in SEQ ID NOs: 400, 401, and any one of 751, 753, 755, 757, 760, respectively, and the CDRL1, CDRL2, and CDRL3 comprise or consist of the amino acid sequences set forth in SEQ ID NOs: 404, 405, and any one of 406, 745, and 747, respectively.

Also provided herein are compositions that comprise (i) a first antibody or antigen-binding fragment that is capable of binding to a SARS-CoV-2 surface glycoprotein and inhibiting an interaction between the SARS-CoV-2 surface glycoprotein and a first cell surface receptor selected from ACE2, DC-SIGN, L-SIGN, and SIGLEC-1; and (ii) a second antibody or antigen-binding fragment that is capable of binding to a SARS-CoV-2 surface glycoprotein and inhibiting an interaction between the SARS-CoV-2 surface glycoprotein and a second cell surface receptor selected from ACE2, DC-SIGN, L-SIGN, and SIGLEC-1, wherein the first cell surface receptor and the second cell surface receptor are different. As taught in the present disclosure, neutralization of infection can be achieved or improved by combingin antibodies or antigen-binding fragments, the binding of which to SARS-CoV-2 inhibits interactions between the SARS-CoV-2 and two or more cell surface receptors; *e.g.*, an attachment receptor and an entry receptor, two entry receptors, two attachment receptors, or the like. Methods of using such antibody combinations to treat or prevent a SARS-CoV-2 infection are also provided.

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. 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 and formulating mRNA-LNP and delivering the same are described in, for example, Pardi *et al.* (*J Control Release 217*345-351 (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

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 SARS-CoV-2 infection(*e.g.*, in a human subject, or in a sample obtained from a human subject).

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. Other detection methods include, but are not limited to, immunohistochemistry (IHC), flow cytometry (*e.g.*, FACS), Western blot, immunocytochemistry (ICC), enzyme-linked immunospot (ELISPOT), and immunoprecipitation (IP). Antibodies and antigen-binding fragments used in detection methods can be, for example, fluorescently or otherwise detectably labeled (*e.g.*, directly conjugated to a fluorophore or comprising a fluorophore-secondary conjugate).

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; survival; 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.

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.

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.

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.

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.

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 biologically male. In some embodiments, the human subject is biologically female.

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.

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 (*i.e.*, at least partially, or completely, ineffective), *e.g.*, by post-vaccine infection or symptoms in the subject, by clinical diagnosis or scientific or regulatory consensus.

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

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.

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.

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.

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.

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.

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.

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.

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

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.

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).

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.

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.

Compositions are administered in an effective amount (*e.g.*, to treat a coronavirus 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, tollowing 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.

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.

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.

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.

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.

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 compositions 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.

In certain embodiments, a combination therapy is provided that comprises one or more anti-SARS-CoV-2 antibody (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 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-γ, 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 nucelotide analog prodrugs such as, for example, remdesivir, sofosbuvir, acyclovir, and zidovudine. In particular embodiments, an anti-viral agent comprises lopinavir, ritonavir, favipiravir, or any combination thereof. In some embodiments, a combination therapy comprises leronlimab. Anti-inflammatory agents for use in a combination therapy of the present disclosure also include non-steroidal anti-inflammatory drugs (NSAIDS). It will be appreciated that in such a combination therapy, the one or more antibody (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.

In some embodiments, an antibody (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).

In certain embodiments, a combination therapy is provided that comprises two or more anti-SARS-CoV-2 antibodies, either or both of which can be 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 some embodiments, any presently disclosed antibody can be used in a method of treating or preventing a SARS-CoV-2 infection, wherein the method further comprises use of an antibody or antigen-binding fragment that comprises: (i) CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 amino acid sequences as set forth in SEQ ID NOs.:343-345 and 347-349, respectively; or (ii) CDRH1, CDRH2, CDRH3,

CDRL1, CDRL2, and CDRL3 amino acid sequences as set forth in SEQ ID NOs.:140-142 and 144-146, respectively; or (iii) VH and VL amino acid sequences as set forth in SEQ ID NOs.:342 and 346, respectively; or (iv) VH and VL amino acid sequences as set forth in SEQ ID NOs.:139 and 143, respectively.

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

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.

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.

The present disclosure also provides the following Embodiments:

Embodiment 1. 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.: 400, 23, 33, 43, 53, 63, 75, 85, 97, 107, 120, 130, 140, 147, 160, 170, 174, 183, 190, 199, 209, 219, 229, 241, 255, 265, 275, 285, 299, 313, 323, 333, 370, 380, 390, 410, 420, 430, 435, 445, 455, 465, 475, 485, 495, 505, 515, 525, 535, 545, 555, 565, 575, 585, 595, 605, 615, 631, and 693, 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.: 401, 24, 34, 44, 54, 64, 76, 86, 98, 108, 121, 131, 141, 148,

151, 161, 171, 184, 200, 210, 220, 230, 242, 256, 266, 276, 286, 300, 314, 324, 334, 352, 360, 362, 364, 366, 371, 381, 391, 411, 421, 431, 436, 446, 456, 466, 476, 486, 496, 506, 516, 526, 536, 546, 556, 566, 576, 586, 596, 606, 616, 625, 632, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 675, 677, 679, 681, 683, 685, and 694, 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.: 766, 25, 35, 45, 55, 65, 77, 87, 99, 109, 122, 132, 142, 149, 162, 164, 165, 172, 176, 177, 179, 180, 185, 187, 188, 201, 211, 221, 231, 243, 257, 267, 277, 287, 301, 315, 325, 335, 354, 372, 382, 392, 412, 422, 432, 437, 447, 457, 467, 477, 487, 497, 507, 517, 527, 537, 547, 557, 567, 577, 587, 597, 607, 617, 627, 633, 695, 751, 753, 755, 757, 760, 763, 765, and 402, 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.: 404, 27, 37, 47, 57, 67, 79, 89, 101, 111, 124, 134, 144, 152, 155, 156, 158, 159, 166, 181, 192, 203, 213, 223, 233, 245, 259, 269, 279, 289, 303, 317, 327, 337, 356, 374, 384, 394, 414, 424, 439, 449, 459, 469, 479, 489, 499, 509, 519, 529, 539, 549, 559, 569, 579, 589, 599, 609, 619, 687, and 697, 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.: 405, 28, 38, 48, 58, 68, 80, 90, 102, 112, 125, 135, 145, 153, 167, 182, 193, 204, 214, 224, 234, 246, 260, 270, 280, 290, 304, 318, 328, 338, 375, 385, 395, 415, 425, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 688, and 698, 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.: 406, 29, 39, 49, 59, 69, 81, 91, 103, 113, 126, 136, 146, 169, 195, 197, 205, 215, 225, 235, 247, 261, 271, 281, 291, 305, 319, 329, 339, 358, 376, 386, 396, 416, 426, 441, 451, 461, 471, 481, 491, 501, 511, 521, 531, 541, 551, 561, 571, 581, 591, 601, 611, 621, 689, 699, 745 and 747, 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.

Embodiment 2. The antibody or antigen-binding fragment of Embodiment1, 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.

Embodiment 3. The antibody or antigen-binding fragment of any one of Embodiments 1-2, comprising CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 amino acid sequences of SEQ ID NOs.: (i) 400, 401, 766, and 404-406, respectively; (ii)400-402 and 404-406, respectively; (iii) 43-45 and 47-49, respectively; (iv) 53-55 and 57-59, respectively; (v) 63-65 and 67-69, respectively; (vi) 75-77 and 79-81, respectively; (vii) 85-87 and 89-91, respectively; (viii) 97-99 and 101-103, respectively; (ix) 107-109 and 111-113, respectively; (x) 120-122 and 124-126, respectively; (xi) 130-132 and 134-136, respectively; (xii) 23 or 147, any one of 24, 148 or 151, 25 or 149, any one of 27, 152, 155, 156, 158, or 159, 28 or 153, and 29, respectively; (xiii) 43 or 160, 44 or 161, any one of 45, 162, 164, or 165, 47 or 166, 48 or 167, and 49 or 169, respectively; (xiv) any one of 130, 170, or 174, 130, 131, 132,

134 or 181, 135 or 182, and 136, respectively; (xv) any one of 53, 183, or 190, 54 or 184, any one of 55, 185, 187, or 188, 57 or 192, 58 or 193, and any one of 59, 195, or 197, respectively; (xvi) 199-201 and 203-205, respectively; (xvii) 209-211 and 213-215, respectively; (xviii) 219-221 and 223-225, respectively; (xix) 229-231 and 233-235, respectively; (xx) 241-243 and 245-247, respectively; (xxi) 255-257 and 259-261, respectively;(xxii) 265-267 and 269-271, respectively; (xxiii) 275-277 and 279-281, respectively; (xxiv) 285-287 and 289-291, respectively; (xxv) 299-301 and 303-305, respectively; (xxvi) 313-315 and 317-319, respectively; (xxvii) 323-325 and 327-329, respectively; (xxviii) 333-335 and 337-339, respectively; (xxix) 229, 230 or 352, 231 or 354, and 233 or 356, 234, and 235 or 358, respectively; (xxx) 313, any one of 314, 360, 362, 364, or 366, 315 and 317-319, respectively; (xxxi) 370-372 and 374-376, respectively; (xxxii) 380-382 and 384-386, respectively; (xxxiii) 390-392 and 394-396, respectively; (xxxiv)23-25 and 27-29, respectively; (xxxv) 410-412 and 414-416, respectively; (xxxvi) 420-422 and 424-426, respectively; (xxxvii) 435-437 and 439-441, respectively; (xxxviii) 445-447 and 449-451, respectively; (xxxix) 455-457 and 459-461, respectively; (xxxx) 465-467 and 469-471, respectively; (xxxxi) 475-477 and 479-481, respectively; (xxxxii) 485-487 and 489-491, respectively; (xxxxiii) 494-497 and 499-501, respectively; (xxxxiv) 505-507 and 509-511, respectively; (xxxxv) 515-517 and 519-521, respectively; (xxxxvi) 525-527 and 529-531, respectively; (xxxxvii) 535-537 and 539-541, respectively; (xxxxviii) 545-547 and 549-551, respectively; (xxxxix) 555-557 and 559-561, respectively; (xxxxx) 565-567 and 569-571, respectively; (xxxxxi) 575-577 and 579-581, respectively; (xxxxxii) 585, 586 or 625, 587 or 627, and 589-591, respectively; (xxxxxiii) 595-597 and 599-601, respectively; (xxxxxiv) 605-607 and 609-611, respectively; (xxxxxv) 615-617 and 619-621, respectively; (xxxxxvi) 631, 632 or 635 or 637 or 639 or 641 or 643 or 645 or 647 or 649 or 651 or 653 or 655 or 657 or 659 or 661 or 663 or 665 or 667 or 669 or 671 or 673 or 675 or 677 or 679 or 681 or 683 or 685, 633, and 697-699, respectively; (xxxxxvii) 693-695 and 697-699, respectively; (xxxxxviii) 400, 401 and any one of 751, 753, 755, 757, or 760 and 404, 405, and any one of 745 or 747, respectively; (xxxxxxix) 585, 586, and 762 or 764 and 589-591, respectively; (xxxxxxx) 33-35 and

37-39, respectively; or (xxxxxxxi) 400, 401, 766, 404, 405 or variant of 405 comprising one, two, or three amino acid substiutions, wherein each of the one, two, or three amino acid substitutions is optionally a conservative amino acid substitution, and 406, respectively.

Embodiment 4. An antibody, or antigen-binding fragment thereof, comprising the CDRH1, the CDRH2, and the CDRH3 of the VH amino acid sequence set forth in SEQ ID NO.:399, and the CDRL1, the CDRL2 or a variant of the CDRL2 comprising one, two, or three amino acid substiutions, wherein each of the one, two, or three amino acid substitutions is optionally a conservative amino acid substitution, and the CDRL3 of the VL amino acid sequence set forth in SEQ ID NO.:738, wherein the CDRs are according to IMGT,

and 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.

Embodiment 5. An antibody, or an antigen-binding fragment thereof, comprising a heavy chain variable domain (VH) comprising complementarity determining region (CDR)H1, CDRH2, and CDRH3, and a light chain variable domain (VL) comprising CDRL1, CDRL2, and CDRL3, wherein CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 comprise the amino acid sequences set forth in: (a) SEQ ID NOs.:400, 401, 766, 404, 405, and 406, respectively; (b) SEQ ID NOs.:400, 401, 769, 404, 405, and 406, respectively; (c) SEQ ID NOs.:400, 401, 770, 404, 405, and 406, respectively; (d) SEQ ID NOs.:400, 401, 771, 404, 405, and 406, respectively; (e) SEQ ID NOs.:400, 401, 772, 404, 405, and 406, respectively; (f) SEQ ID NOs.:400, 401, 773, 404, 405, and 406, respectively; (g) SEQ ID NOs.:400, 401, 766, 404, 405, and 745, respectively; (h) SEQ ID NOs.:400, 401, 769, 404, 405, and 745, respectively; (i) SEQ ID NOs.:400, 401, 770, 404, 405, and 745, respectively; (j) SEQ ID NOs.:400, 401, 771, 404, 405, and 745, respectively; (k) SEQ ID NOs.:400, 401, 772, 404, 405, and 745, respectively; (l) SEQ ID NOs.: 400, 401, 773, 405, 405, and 745, respectively;

(m) SEQ ID NOs.:400, 401, 766, 404, 405, and 747, respectively; (n) SEQ ID NOs.:400, 401, 769, 404, 405, and 747, respectively; (o) SEQ ID NOs.:400, 401, 770, 404, 405, and 747, respectively; (p) SEQ ID NOs.:400, 401, 771, 404, 405, and 747, respectively; (q) SEQ ID NOs.:400, 401, 772, 404, 405, and 747, respectively; or (r) SEQ ID NOs.:400, 401, 773, 404, 405, and 747, respectively,

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.

Embodiment 6. The antibody or antigen-binding fragment thereof of Embodiment 5, 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 CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 comprise the amino acid sequences set forth in: (a) SEQ ID NOs.:400, 401, 766, 404, 405, and 406, respectively.

Embodiment 7. The antibody or antigen-binding fragment of any one of Embodiments 4-6, comprising the amino acid sequences set forth in: (a) SEQ ID NOs.:400, 401, 402, 404, 405, and 406; (b) SEQ ID NOs.:400, 401, 751, 404, 405, and 406; (c) SEQ ID NOs.:400, 401, 753, 404, 405, and 406; (d) SEQ ID NOs.:400, 401, 755, 404, 405, and 406; (e) SEQ ID NOs.:400, 401, 757, 404, 405, and 406; (f) SEQ ID NOs.:400, 401, 760, 404, 405, and 406; (g) SEQ ID NOs.:400, 401, 402, 404, 405, and 745; (h) SEQ ID NOs.:400, 401, 751, 404, 405, and 745; (i) SEQ ID NOs.:400, 401, 753, 404, 405, and 745; (j) SEQ ID NOs.:400, 401, 755, 404, 405, and 745; (k) SEQ ID NOs.:400, 401, 757, 404, 405, and 745; (l) SEQ ID NOs.: 400, 401, 760, 404, 405, and 745; (m) SEQ ID NOs.:400, 401, 402, 404, 405, and 747; (n) SEQ ID NOs.:400, 401, 751, 404, 405, and 747; (o) SEQ ID NOs.:400, 401, 753, 404, 405, and 747; (p) SEQ ID NOs.:400, 401, 755, 404, 405, and 747; (q) SEQ ID NOs.:400, 401, 757, 404, 405, and 747; or (r) SEQ ID NOs.:400, 401, 760, 404, 405, and 747.

Embodiment 8. The antibody or antigen-binding fragment of any one of Embodiments 4-7, comprising, in VH, the amino acid sequence set forth in SEQ ID NO.: 400, the amino acid sequence set forth in SEQ ID NO.:401, and the amino acid sequence set forth in SEQ ID NO.:402, and in VL, the amino acid sequence set forth in SEQ ID NO.:404, the amino acid sequence set forth in SEQ ID NO.:405, and the amino acid sequence set forth in SEQ ID NO.:406.

Embodiment 9. An antibody, or an antigen-binding fragment thereof, comprising a heavy chain variable domain (VH) comprising complementarity determining region (CDR)H1, CDRH2, and CDRH3, and a light chain variable domain (VL) comprising CDRL1, CDRL2, and CDRL3, wherein CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 comprise the amino acid sequences set forth in SEQ ID NOs.:525, 526, 527, 529, 530, and 531, respectively,

and 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.

Embodiment 10. An antibody, or an antigen-binding fragment thereof, comprising a heavy chain variable domain (VH) comprising complementarity determining region (CDR)H1, CDRH2, and CDRH3, and a light chain variable domain (VL) comprising CDRL1, CDRL2, and CDRL3, wherein CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 comprise the amino acid sequences set forth in SEQ ID NOs.:585, 586 or 625, 587 or 627, 589, 590, and 591, respectively,

and 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.

Embodiment 11. An antibody, or an antigen-binding fragment thereof, comprising a heavy chain variable domain (VH) comprising complementarity determining region (CDR)H1, CDRH2, and CDRH3, and a light chain variable domain

(VL) comprising CDRL1, CDRL2, and CDRL3, wherein CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 comprise the amino acid sequences set forth in SEQ ID NOs.:229, 230, 231, 233, 234, and 235, respectively,

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.

Embodiment 12. The antibody or antigen-binding fragment of any one of Embodiments 1-11, wherein:

(i) the VH comprises or consists of an amino acid sequence having at least 85% (*e.g.,* 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.: 399, 22, 32, 42, 52, 62, 72, 74, 84, 96, 106, 119, 129, 139, 150, 163, 173, 175, 178, 186, 189, 191, 198, 208, 218, 228, 240, 254, 264, 274, 284, 298, 312, 322, 332, 350, 351, 353, 359, 361, 363, 365, 367, 368, 369, 379, 389, 409, 419, 429, 434, 444, 454, 464, 474, 484, 494, 504, 514, 524, 534, 544, 554, 564, 574, 584, 594, 604, 614, 624, 626, 628, 630, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, 684, 692, 740, 741, 742, 743, 748, 749, 750, 752, 754, 756, 758, 759, 761, 762, and 764, wherein the variation is optionally limited to one or more framework regions and/or the variation 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% (*e.g.,* 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.: 738, 26, 36, 46, 56, 66, 78, 88, 94, 100, 110, 123, 133, 143, 154, 157, 168, 194, 196, 202, 212, 222, 232, 238, 244, 250, 252, 258, 268, 278, 288, 294, 296, 302, 308, 310, 316, 326, 336, 355, 357, 373, 383, 393, 403, 413, 423, 438, 448, 458, 468, 478, 488, 498, 508, 518, 528, 538, 548, 558, 568, 578, 588, 598, 608, 618, 686, 696, 744, and 746, wherein the variation is optionally limited to one or more framework

regions and/or the variation comprises one or more substitution to a germline-encoded amino acid.

Embodiment 13. The antibody or antigen-binding fragment of any one of Embodiments 1-12, wherein the VH comprises or consists of an amino acid sequence having at least 85% identity to the amino acid sequence set forth in SEQ ID NO.:399 and the VL comprises or consists of an amino acid sequence having at least 85% identity to the amino acid sequence set forth in SEQ ID NO.:403 or SEQ ID NO.:738.

Embodiment 14. The antibody or antigen-binding fragment of any one of Embodiments 1-13, wherein the VH comprises or consists of an amino acid sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO.:399 and the VL comprises or consists of an amino acid sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO.:403 or SEQ ID NO.:738.

Embodiment 15. The antibody or antigen-binding fragment of any one of Embodiments 1-14, wherein the VH comprises or consists of an amino acid sequence having at least 95% identity to the amino acid sequence set forth in SEQ ID NO.:399 and the VL comprises or consists of an amino acid sequence having at least 95% identity to the amino acid sequence set forth in SEQ ID NO.:403 or SEQ ID NO.:738.

Embodiment 16. The antibody or antigen-binding fragment of any one of Embodiments 1-15, wherein the VH comprises or consists of an amino acid sequence having at least 97% identity to the amino acid sequence set forth in SEQ ID NO.:399 and the VL comprises or consists of an amino acid sequence having at least 97% identity to the amino acid sequence set forth in SEQ ID NO.:403 or SEQ ID NO.:738.

Embodiment 17. The antibody or antigen-binding fragment of any one of claims 1-16, wherein the VH comprises or consists of an amino acid sequence having at least 99% identity to the amino acid sequence set forth in SEQ ID NO.:399 and the VL comprises or consists of an amino acid sequence having at least 99% identity to the amino acid sequence set forth in SEQ ID NO.:403 or SEQ ID NO.:738.

Embodiment 18. The antibody or antigen-binding fragment of any one of Embodiments 1-12, wherein the VH and the VL have at least 85% identity (*e.g.,* 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%) to the amino acid sequences set forth in:

(i) SEQ ID NOs.:524 and 528, respectively;

(ii) SEQ ID NOs.:584 or 624 or 626 or 628 and 588, respectively;

(iii) SEQ ID NOs.:228 or 740 or 741 or 742 or 743 and 232, respectively; or

(iv) SEQ ID NOs.:228 or 740 or 741 or 742 or 743 and 238, respectively.

Embodiment 19. The antibody or antigen-binding fragment of any one of Embodiments 1-18, wherein the VH comprises or consists of any VH amino acid sequence set forth in Table 2, and wherein the VL comprises or consists of any VL amino acid sequence set forth in Table 2, wherein, optionally, the VH and the VL comprise or consist of the amino acid sequences according to SEQ ID NOs.: (i) 399 and 403 or 738, respectively; (ii) 32 and 36, respectively; (iii) 42 and 46, respectively; (iv) 52 and 56, respectively; (v) 62 and 66, respectively; (vi) 72 and 66, respectively; (vii) 74 and 78, respectively; (viii) 84 and 88, respectively; (ix) 84 and 88, respectively; (x) 96 and 100, respectively; (xi) 106 and 110, respectively; (xii) 119 and 123, respectively; or (xiii) 129 and 133, respectively; (xiv) 22 or 150 and 26, 154, or 157, respectively; (xv) 42 or 163 and 46 or 168, respectively; (xvi) any one of 129, 173, 175, or 178 and 133, respectively; (xvii) any one of 52, 186, 189, or 191 and any one of 56, 194, or 196, respectively; (xviii) 198 and 202, respectively; (xix) 208 and 212, respectively; (xx) 218 and 222, respectively; (xxi) 228 and 232 or 238, respectively;

(xxii) 240 and any one of 244, 250, or 252, respectively; (xxiii) 254 and 258, respectively; (xxiv) 264 and 268, respectively; (xxv) 274 and 278, respectively; or (xxvi) 284 and any one of 288, 294, or 296, respectively; (xxvii) 298 and any one of 302, 308, or 310, respectively; (xxviii) 312 and 316, respectively; (xxix) 322 and 326, respectively; (xxx) 332 and 336, respectively; (xxxi) any one of 228, 350, 351, or 353 and 232, 238, 355, or 357, respectively; (xxxii) any one of 312, 359, 361, 363, 365, 367, or 368 and 316, respectively; (xxxiii) 369 and 373, respectively; (xxxiv) 379 and 383, respectively; (xxxv) 389 and 393, respectively; (xxxvi) 22 and 26, respectively; (xxxvii) 409 and 413, respectively; (xxxviii) 419 and 423, respectively; (xxxix) 434 and 438, respectively; (xxxx) 444 and 448, respectively; (xxxxi) 454 and 458, respectively; (xxxxii) 464 and 468, respectively; (xxxxiii) 474 and 478, respectively; (xxxxiv) 484 and 488, respectively; (xxxxv) 494 and 498, respectively; (xxxxvi) 504 and 508, respectively; (xxxxvii) 514 and 518, respectively; (xxxxviii) 524 and 528, respectively; (xxxxix) 534 and 538, respectively; (xxxxx) 544 and 548, respectively; (xxxxxi) 554 and 558, respectively; (xxxxxii) 564 and 568, respectively; (xxxxxiii) 574 and 578, respectively; (xxxxxiv) 584 and 588, respectively; (xxxxxv) 594 and 598, respectively; (xxxxxvi) 604 and 608, respectively; (xxxxxvii) 614 and 618, respectively; (xxxxxviii) 624, 626, or 628 and 588, respectively; (xxxxxix) 630, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, or 684, and 686, respectively; (xxxxxx) 692 and 696, respectively; (xxxxxxi) any one of 740-743 and 238, respectively; (xxxxxxii) any one of 399, 748, 749, 750, 752, 754, 756, 758, 759, and 761 and any one of 403, 744, and 746, respectively; or (xxxxxxiii) 762 or 764 and 588, respectively.

Embodiment 20. An antibody, or an antigen-binding fragment thereof, comprising a heavy chain variable domain (VH) and a light chain variable domain (VL), wherein the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO:399 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO:738,

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.

Embodiment 21. An antibody, or an antigen-binding fragment thereof, comprising a heavy chain variable domain (VH) and a light chain variable domain (VL), wherein the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO:399 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO:403,

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.

Embodiment 22. An antibody, or an antigen-binding fragment thereof, comprising a heavy chain variable domain (VH) and a light chain variable domain (VL), wherein the VH comprises or consists of the amino acid sequence set forth in any one of SEQ ID NOs:399, 748, 749, 750, 752, 754, 756, 758, 759, and 761, the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO:403,

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.

Embodiment 23. An antibody, or an antigen-binding fragment thereof, comprising a heavy chain variable domain (VH) and a light chain variable domain (VL), wherein the VH comprises or consists of the amino acid sequence set forth in any one of SEQ ID NOs:399, 748, 749, 750, 752, 754, 756, 758, 759, and 761, the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO:738,

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.

Embodiment 24. An antibody, or an antigen-binding fragment thereof, comprising a heavy chain variable domain (VH) and a light chain variable domain (VL), wherein the VH comprises or consists of the amino acid sequence set forth in any one of SEQ ID NOs:399, 748, 749, 750, 752, 754, 756, 758, 759, and 761, the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO:744,

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.

Embodiment 25. An antibody, or an antigen-binding fragment thereof, comprising a heavy chain variable domain (VH) and a light chain variable domain (VL), wherein the VH comprises or consists of the amino acid sequence set forth in any one of SEQ ID NOs:399, 748, 749, 750, 752, 754, 756, 758, 759, and 761, the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO:746,

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.

Embodiment 26. An antibody, or an antigen-binding fragment thereof, comprising a heavy chain variable domain (VH) and a light chain variable domain (VL), wherein the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO:524 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO:528,

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.

Embodiment 27. An antibody, or an antigen-binding fragment thereof, comprising a heavy chain variable domain (VH) and a light chain variable domain (VL), wherein the VH comprises or consists of the amino acid sequence set forth in any

one of SEQ ID NOs.:584, 624, 626, and 628 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO:588,

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.

Embodiment 28. An antibody, or an antigen-binding fragment thereof, comprising a heavy chain variable domain (VH) and a light chain variable domain (VL), wherein the VH comprises or consists of the amino acid sequence set forth in any one of SEQ ID NOs.:228, 740, 741, 742, and 743, and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO:232,

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.

Embodiment 29. An antibody, or an antigen-binding fragment thereof, comprising a heavy chain variable domain (VH) and a light chain variable domain (VL), wherein the VH comprises or consists of the amino acid sequence set forth in any one of SEQ ID NOs.:228, 740, 741, 742, and 743, and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO:238,

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.

Embodiment 30. An antibody, or an antigen-binding fragment thereof, comprising a heavy chain variable domain (VH) and a light chain variable domain (VL), wherein the VH comprises or consists of the amino acid sequence as set forth in SEQ ID NO: 32 and the VL comprises or consists of the amino acid sequence as set forth in SEQ ID NO: 36.

Embodiment 31. 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 CDRH1, CDRH2, and CDRH3 comprise or consist of the amino acid sequences set forth in SEQ ID NOs: 33-35, respectively, and the CDRL1, CDRL2, and CDRL3 comprise or consist of the amino acid sequences set forth in SEQ ID NOs: 37-39, respectively.

Embodiment 32. The antibody or antigen-binding fragment of any one of Embodiments 3-31, 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.

Embodiment 33. The antibody or antigen-binding fragment of any one of Embodiments 1-32, which:

(i) recognizes an epitope in the ACE2 receptor binding motif (RBM, SEQ ID NO.:5) of SARS-CoV-2;

(ii) is capable of blocking an interaction between SARS-CoV-2 (*e.g.*, SARS-CoV-2 RBM) and human ACE2;

(iii) is capable of binding to SARS-CoV-2S protein;

(iv) recognizes an epitope that is conserved in the ACE2 RBM of SARS-CoV-2 and in an ACE2 RBM of SARS-CoV-1;

(v) is cross-reactive against SARS-CoV-2 and SARS-CoV-1 coronavirus;

(vii) recognizes an epitope in the SARS-CoV-2 surface glycoprotein that is not in the ACE2 RBM;

(viii) is capable of binding to a SARS-CoV-2 S protein trimer in a prefusion conformation;

or

(ix) any combination of (i)-(viii).

Embodiment 34. The antibody or antigen-binding fragment of any one of Embodiments 1-33, which is a IgG, IgA, IgM, IgE, or IgD isotype.

Embodiment 35. The antibody or antigen-binding fragment of any one of Embodiments 1-34, which is an IgG isotype selected from IgG1, IgG2, IgG3, and IgG4.

Embodiment 36. The antibody or antigen-binding fragment of any one of Embodiments 1-35, which is human, humanized, or chimeric.

Embodiment 37. The antibody or antigen-binding fragment of any one of Embodiments 1-36, 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, a scFv, or a scFab.

Embodiment 38. The antibody or antigen-binding fragment of Embodiment 37, wherein the scFv comprises more than one VH domain and more than one VL domain.

Embodiment 39. The antibody or antigen-binding fragment of any one of Embodiments 1-38, wherein the antibody or antigen-binding fragment is a multi-specific antibody or antigen binding fragment.

Embodiment 40. The antibody or antigen-binding fragment of Embodiment 39, wherein the antibody or antigen binding fragment is a bispecific antibody or antigen-binding fragment.

Embodiment 41. The antibody or antigen-binding fragment of Embodiment 39 or 40, 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% (*e.g.,* 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.: 22, 32, 42, 52, 62, 72, 74, 84, 96, 106, 119, 129, 139, 150, 163, 173, 175, 178, 186, 189, 191, 198, 208, 218, 228, 240, 254, 264, 274, 284, 298, 312, 322, 332, 350, 351, 353, 359, 361, 363, 365, 367, 368, 369, 379, 389, 399, 409, 419, 429, 434, 444, 454, 464, 474, 484, 494, 504, 514, 524, 534, 544, 554, 564, 574, 584, 594, 604, 614, 624, 626, 628, 630, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, 684, 692, 740, 741, 742, 743, 748, 749, 750, 752, 754, 756, 758, 759, 761, 762, and 764, and

wherein the first VL and the second VL are different and each independently comprise an amino acid sequence having at least 85% (*e.g.,* 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.: 26, 36, 46, 56, 66, 78, 88, 94, 100, 110, 123, 133, 143, 154, 157, 168, 194, 196, 202, 212, 222, 232, 238, 244, 250, 252, 258, 268, 278, 288, 294, 296, 302, 308, 310, 316, 326, 336, 355, 357, 373, 383, 393, 403, 413, 423, 438, 448, 458, 468, 478, 488, 498, 508, 518, 528, 538, 548, 558, 568, 578, 588, 598, 608, 618, 686, 696 738, 744, and 746;

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.

Embodiment 42. The antibody or antigen-binding fragment of Embodiment 40 or 41, comprising:

(i) a first VH and a first VL; and

(ii) a second VH and a second VL,

wherein the first VH comprises an amino acid sequence having at least 85% (*e.g.,* 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.: 139 and 342 and the first VL comprises 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.:143 and 346 and wherein the second VH comprises an amino acid sequence having at least 85% (*e.g.,* 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.: 399, 748, 749, 750, 752, 754, 756, 758, 759, and 761 and the second VL comprises 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.:403, 744, and 746.

Embodiment 43. The antibody or antigen-binding fragment of Embodiment 39 or 40, comprising a first antigen-binding portion having a first specificity and a second antigen-binding portion having a second specificity, wherein the first antigen-binding portion comprises a VH that comprises or consists of the amino acid sequence set forth in SEQ ID NO:399 and a VL that comprises or consists of the amino acid sequence set forth in SEQ ID NO.:738 or SEQ ID NO.:403.

Embodiment 44. The antibody or antigen-binding fragment of Embodiment 43, wherein the second antigen-binding portion comprises a VH that comprises or consists of the amino acid sequence set forth in SEQ ID NO.:139 and a VL that comprises or consists of the amino acid sequence set forth in SEQ ID NO.:143.

Embodiment 45. The antibody or antigen-binding fragment of Embodiment 43, wherein the second antigen-binding portion comprises a VH that comprises or consists of the amino acid sequence set forth in SEQ ID NO.:342 and a VL that comprises or consists of the amino acid sequence set forth in SEQ ID NO.:346.

Embodiment 46. The antibody or antigen-binding fragment of any one of Embodiments 1-45, wherein the antibody or antigen-binding fragment further comprises a Fc polypeptide or a fragment thereof.

Embodiment 47. The antibody or antigen-binding fragment of Embodiment 46, 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.

Embodiment 48. The antibody or antigen-binding fragment of Embodiment 47, 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.

Embodiment 49. The antibody or antigen-binding fragment of Embodiment 47 or 48, wherein the mutation that enhances binding to FcRn comprises: (i) M428L/N434S; (ii) M252Y/S254T/T256E; (iii) T250Q/M428L; (iv) 257I/Q311I; (v) P257I/N434H; (vi) D376V/N434H; (vii) T307A/E380A/N434A; or (viii) any combination of (i)-(vii).

Embodiment 50. The antibody or antigen-binding fragment of any one of Embodiments 47-49, wherein the mutation that enhances binding to FcRn comprises M428L/N434S.

Embodiment 51. The antibody or antigen-binding fragment of any one of Embodiments 47-50, wherein the mutation that enhances binding to a FcγR comprises S239D; I332E; A330L; G236A; or any combination thereof.

Embodiment 52. The antibody or antigen-binding fragment of any one of Embodiments 47-51, 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.

Embodiment 53. The antibody or antigen-binding fragment of any one of Embodiments 47-52, wherein the Fc polypeptide comprises a L234A mutation and a L235A mutation.

Embodiment 54. The antibody or antigen-binding fragment of any one of Embodiments 1-53, 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.

Embodiment 55. The antibody or antigen-binding fragment of any one of Embodiments 1-54, which is capable of binding to a SARS-CoV-2 surface glycoprotein with an EC50 of less than 500 ng/ml, less than 250 ng/ml, less than 100 ng/ml, less than 90 ng/ml, less than 80 ng/ml, less than 70 ng/ml, less than 60 ng/ml, less than 50 ng/ml, less than 40 ng/ml, less than 30 ng/ml, less than 25 ng/ml, less than 20 ng/ml, less than 16 ng/ml, less than 15 ng/ml, less than 14 ng/ml, less than 13 ng/ml, less than 12 ng/ml, less than 10 ng/ml, less than 9 ng/ml, less than 8 ng/ml, less than 7 ng/ml, less than 6 ng/ml, less than 5 ng/ml, less than 4 ng/ml, or less than 2 mg/ml, as measured by ELISA (optionally, indirect ELISA and/or sandwich ELISA) and/or by flow cytometry, wherein the SARS CoV-2 surface glycoprotein is expressed at a cell surface of a host cell.

Embodiment 56. The antibody or antigen-binding fragment of any one of Embodiments 1-55, which is capable of binding to a SARS-CoV-2 surface glycoprotein RBD with an EC50 of less than 500 ng/ml, less than 250 ng/ml, less than 100 ng/ml, less than 90 ng/ml, less than 80 ng/ml, less than 70 ng/ml, less than 60 ng/ml, less than

50 ng/ml, less than 40 ng/ml, less than 30 ng/ml, less than 25 ng/ml, less than 20 ng/ml, less than 16 ng/ml, less than 15 ng/ml, less than 14 ng/ml, less than 13 ng/ml, less than 12 ng/ml, less than 10 ng/ml, less than 9 ng/ml, less than 8 ng/ml, less than 7 ng/ml, less than 6 ng/ml, less than 5 ng/ml, less than 4 ng/ml, or less than 2 mg/ml, as measured by ELISA (optionally, indirect ELISA and/or sandwich ELISA) and/or by flow cytometry, wherein the SARS CoV-2 surface glycoprotein is expressed at a cell surface of a host cell.

Embodiment 57. The antibody or antigen-binding fragment of any one of Embodiments 1-56, which is capable of binding to a SARS-CoV-2 RBD with a KD of less than 5×10^{-8} M, less than 4×10^{-8} M, less than 3×10^{-8} M, less than 2×10^{-8} M, less than 1×10^{-8} M, less than 5×10^{-9} M, less than 1×10^{-9} M, less than 5×10^{-10} M, less than 1×10^{-10} M, less than 5×10^{-11} M, less than 1×10^{-11} M, less than 5×10^{-12} M, or less than 1×10^{-12} M, as determined using biolayer interferometry (BLI), optionally using an Octet instrument with antibody or antigen-binding fragment loaded on Protein A pins, optionally at 2.7 μg/ml, and SARS-CoV-2 RBD loaded for 5 minutes at 6 μg/ml, 1.5 μg/ml, or 0.4 μg/ml, further optionally with dissociation measured for 7 minutes.

Embodiment 58. The antibody or antigen-binding fragment of any one of Embodiments 1-57, which is capable of binding to a SARS-CoV-2 RBD with a KD of less than 6×10^{-8} M, less than 5×10^{-8} M, less than 4×10^{-8} M, less than 3×10^{-8} M, less than 2×10^{-8} M, less than 1×10^{-8} M, less than 5×10^{-9} M, less than 4×10^{-9} M, less than 3×10^{-9} M, less than 2×10^{-9} M, less than 1×10^{-9} M, or less than 8×10^{-10} M, as determined using surface plasmon resonance (SPR), optionally using a Biacore T200 instrument using a single-cycle kinetics approach.

Embodiment 59. The antibody or antigen-binding fragment of any one of claims 1-58, which is capable of binding to a SARS-CoV-2 RBD and inhibiting an interaction between (i) the RBD and (ii) a human ACE2 and/or a human SIGLEC-1.

Embodiment 60. The antibody or antigen-binding fragment of any one of Embodiments 1-59, which is capable of neutralizing:

(i) infection by a SARS-CoV-2 pseudovirus, optionally:

(i)(a) with a neutralization IC50 of less than 100 ng/ml, less than 90 ng/ml, less than 80 ng/ml, less than 70 ng/ml, less than 60 ng/ml, less than 50 ng/ml, less than 40 ng/ml, less than 30 ng/ml, less than 25 ng/ml, less than 20 ng/ml, less than 15 ng/ml, less than 10 ng/ml, less than 9 ng/ml, less than 8 ng/ml, less than 7 ng/ml, less than 6 ng/ml, less than 5 ng/ml, less than 4 ng/ml, less than 3 ng/ml, less than 2 ng/ml, or less than 1 ng/ml, preferably less than 10 ng/ml, less than 9 ng/ml, less than 8 ng/ml, less than 7 ng/ml, less than 6 ng/ml, less than 5 ng/ml, less than 4 ng/ml, less than 3 ng/ml, less than 2 ng/ml, or less than 1 ng/ml, and/or

(i)(b) with a neutralization IC80 of less than 100 ng/ml, less than 90 ng/ml, less than 80 ng/ml, less than 70 ng/ml, less than 60 ng/ml, less than 50 ng/ml, less than 40 ng/ml, less than 30 ng/ml, or less than 25 ng/ml, preferably less than 50 ng/ml, less than 40 ng/ml, less than 30 ng/ml, or less than 25 ng/ml, and/or

(i)(c) with a neutralization EC90 of less than 300 ng/ml, less than 200 ng/ml, less than 100 ng/ml, less than 90 ng/ml, less than 80 ng/ml, less than 70 ng/ml, less than 60 ng/ml 50 ng/ml, less than 40 ng/ml, less than 30 ng/ml, less than 25 ng/ml, less than 20 ng/ml, less than 15 ng/ml, or less than 10 ng/ml, wherein, further optionally, the SARS-CoV-2 pseudovirus comprises a VSV pseudovirus and/or a MLV pseudovirus, and/or

(i)(d) the SARS-CoV-2 pseudovirus comprises a VSV pseudovirus and/or a MLV pseudovirus; and/or

(ii) infection by live SARS-CoV-2, optionally

(ii)(a) with a EC50 of less than 60 ng/ml, less than 50 ng/ml, less than 40 ng/ml, less than 30 ng/ml, less than 25 ng/ml, less than 20 ng/ml, less than 15 ng/ml, less than 12 ng/ml, less than 11 ng/ml, less than 10 ng/ml, less than 9 ng/ml, less than 8 ng/ml, less than 7 ng/ml, less 6 ng/ml, less than 5/ng ml, or

less than 4 ng/ml, preferably less than 15 ng/ml, less than 12 ng/ml, less than 11 ng/ml, less than 10 ng/ml, less than 9 ng/ml, less than 8 ng/ml, less than 7 ng/ml, less 6 ng/ml, less than 5/ng ml, or less than 4 ng/ml, and/or

(ii)(b) with a EC90 of less than 50 ng/ml, less than 40 ng/ml, less than 35 ng/ml, less than 30 ng/ml, less than 25 ng/ml, less than 20 ng/ml, less than 15 ng/ml, less than 12 ng/ml, less than 11 ng/ml, less than 10 ng/ml, less than 9 ng/ml, less than 8 ng/ml, less than 7 ng/ml, less 6 ng/ml, less than 5/ng ml, or less than 4 ng/ml, preferably less than 30 ng/ml, less than 25 ng/ml, less than 20 ng/ml, less than 15 ng/ml, or less than 12 ng/ml, and/or

(ii)(c) over a 6-hour period, with a multiplicity of infection of 0.1; and/or

(iii) infection by live SARS-CoV-2 in a host cell (*e.g.* a HEK293T cell) that expresses, optionally is engineered to overexpress, DC-SIGN, L-SIGN, SIGLEC, or ACE2; and/or

(iv) infection by live SARS-CoV-2 in a host cell (*e.g.* a HEK293T cell) that expresses, optionally is engineered to overexpress, SIGLEC-1 or ACE2, wherein neutralizing infection comprises fully neutralizing infection.

Embodiment 61. The antibody or antigen-binding fragment of any one of Embodiments 1-60, which is capable of neutralizing infection by a SARS-CoV-2 variant that comprises any one of the following mutations in the surface glycoprotein as compared to a SARS-CoV-2 surface glycoprotein comprising SEQ ID NO.:3: N501Y; S477N; N439K; L452R; E484K; K417N; T478K; S494P; A520S; N501T; A522S; Y453F; P384L.

Embodiment 62. The antibody or antigen-binding fragment of Embodiment 61, which is capable of neutralizing infection by the SARS-CoV-2 variant with a potency that is less than 3-fold lower than the potency with which the antibody or antigen-binding fragment neutralizes infection by a SARS-CoV-2 comprising the surface glycoprotein amino acid sequence set forth in SEQ ID NO.:3.

Embodiment 63. The antibody or antigen-binding fragment of any one of Embodiments 1-62, which is capable of activating a FcγRIIa, a FcγRIIIa, or both, wherein, optionally:(i)the FcγRIIa comprises a H131 allele; and/or

(ii) the FcγRIIIa comprises a V158 allele; and/or

(iii) activation is determined using a SARS-CoV-2 S-expressing target cell, such as a CHO cell, and a reporter cell expressing a NFAT-driven reporter, such as luciferase.

Embodiment 64. The antibody or antigen-binding fragment of any one of Embodiments 1-63, comprising:

(a) the CH1-CH3 amino acid sequence set forth in SEQ ID NO.:6 and the CL amino acid sequence set forth in SEQ ID NO.:8;

(b) The CH1-CH3 amino acid sequence set forth in SEQ ID NO.:6 and the CL amino acid sequence set forth in SEQ ID NO.:9;

(c) the CH1-CH3 amino acid sequence set forth in SEQ ID NO.:7 and the CL amino acid sequence set forth in SEQ ID NO.:8; or

(d) The CH1-CH3 amino acid sequence set forth in SEQ ID NO.:7 and the CL amino acid sequence set forth in SEQ ID NO.:9.

Embodiment 65. An isolated antibody comprising:

(i) the heavy chain amino acid sequence set forth in SEQ ID NO.:767; and

(ii) the light chain amino acid sequence set forth in SEQ ID NO.:768.

Embodiment 66. The antibody or antigen-binding fragment of any one of Embodiments 1-65, which has an *in vivo* half-life in a non-human primate of between 20 and 30 days, or between 22 and 28 days, or between 23 and 27 days, or between 24 and 26 days, or of about 25 days.

Embodiment 67. The antibody or antigen-binding fragment of any one of Embodiments 1-66, wherein the antibody or antigen-binding fragment is capable of

neutralizing a SARS-CoV-2 infection and/or of neutralizing an infection of a target cell with an IC50 of about 20 to about 30 ng/ml.

Embodiment 68. The antibody or antigen-binding fragment of any one of Embodiments 1-66, wherein the antibody or antigen-binding fragment is capable of neutralizing a SARS-CoV-2 infection and/or of neutralizing an infection of a target cell with an IC50 of about 10 to about 20 ng/ml.

Embodiment 69. The antibody or antigen-binding fragment of any one of Embodiments 1-66, wherein the antibody or antigen-binding fragment is capable of neutralizing a SARS-CoV-2 infection and/or of neutralizing an infection of a target cell with an IC50 of about 5 to about 10 ng/ml.

Embodiment 70. The antibody or antigen-binding fragment of any one of Embodiments 1-66, wherein the antibody or antigen-binding fragment is capable of neutralizing a SARS-CoV-2 infection and/or of neutralizing an infection of a target cell with an IC50 of about 1 to about 5 ng/ml.

Embodiment 71. The antibody or antigen-binding fragment of any one of Embodiments 1-70, wherein the antibody or antigen-binding fragment is capable of neutralizing infection by SARS-CoV-2 and does not compete with a human ACE2 for binding to the SARS-CoV-2S protein,

wherein, optionally, the neutralizing comprises neutralizing infection in an in vitro model of infection.

Embodiment 72. An antibody, or an antigen-binding fragment thereof, that competes for binding to a SARS-CoV-2 surface glycoprotein with the antibody or antigen-binding fragment of any one of Embodiments 1-71.

Embodiment 73. An isolated polynucleotide encoding the antibody or antigen-binding fragment of any one of Embodiments 1-72, or encoding a VH, a heavy chain, a VL, and/or a light chain of the antibody or the antigen-binding fragment.

Embodiment 74. The polynucleotide of Embodiment73, wherein the polynucleotide comprises deoxyribonucleic acid (DNA) or ribonucleic acid (RNA), wherein the RNA optionally comprises messenger RNA (mRNA).

Embodiment 75. The polynucleotide of Embodiment73 or 74, which is codon-optimized for expression in a host cell.

Embodiment 76. The polynucleotide of any one of Embodiments 73-75, comprising a polynucleotide having at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or at least 99% identity to, or comprises or consists of, the polynucleotide sequence according to any one or more of SEQ ID NOs.: 30, 31, 40, 41, 50, 51, 60, 61, 70, 71, 73, 82, 83, 92, 93, 95, 104, 105, 114, 115, 116, 117, 118, 127, 128, 137, 138, 206, 207, 216, 217, 226, 227, 236, 237, 239, 248, 249, 251, 253, 262, 263, 272, 273, 282, 283, 292, 293, 295, 297, 306, 307, 309, 311, 320, 321, 330, 331, 340, 341, 377, 378, 387, 388, 397, 398, 407, 408, 417, 418, 427, 428, 433, 442, 443, 452, 453, 462, 463, 472, 473, 482, 483, 492, 493, 502, 503, 512, 513, 552, 523, 532, 533, 542, 543, 552, 553, 562, 563, 572, 573, 582, 583, 592, 593, 602, 603, 612, 613, 622, 623, 690, 691, 700-737 and 739.

Embodiment 77. The polynucleotide of any one of Embodiments 73-76, comprising:

(i) a polynucleotide having at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or at least 99% identity to, or that comprises or consists of, the nucleotide sequence set forth in SEQ ID NO.:407; and

(ii) a polynucleotide having at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or at least 99% identity to, or that comprises or consists of, the nucleotide sequence set forth in SEQ ID NO.:408, 737, or 739.

Embodiment 78. A recombinant vector comprising the polynucleotide of any one of Embodiments 73-77.

Embodiment 79. A host cell comprising the polynucleotide of any one of Embodiments 77 and/or the vector of Embodiment78, wherein the polynucleotide is heterologous to the host cell.

Embodiment 80. A human B cell comprising the polynucleotide of any one of Embodiments 73-77, wherein polynucleotide is heterologous to the human B cell and/or wherein the human B cell is immortalized.

Embodiment 81. A composition comprising: (i) the antibody or antigen-binding fragment of any one of Embodiments 1-72; (ii) the polynucleotide of any one of Embodiments 73-77; (iii) the recombinant vector of Embodiment 78; (iv) the host cell of Embodiment 79; and/or (v)the human B cell of Embodiment 80, and a pharmaceutically acceptable excipient, carrier, or diluent.

Embodiment 82. The composition of Embodiment 81, comprising two or more antibodies or antigen-binding fragments of any of Embodiments 1-72.

Embodiment 83. The composition of Embodiment 82, comprising:

(i) a first antibody or antigen-binding fragment, comprising a VH comprising or consisting of the amino acid sequence as set forth in SEQ ID NO: 32 and a VL comprising or consisting of the amino acid sequence as set forth in SEQ ID NO: 36; and

(ii) a second antibody or antigen-binding fragment comprising, a VH comprising or consisting of the amino acid sequence as set forth in SEQ ID NO: 139 and a VL comprising of consisting of the amino acid sequence as set forth in SEQ ID NO: 143.

Embodiment 84. The composition of Embodiment 82, comprising:

(i) a first antibody or antigen-binding fragment 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 CDRH1, CDRH2, and CDRH3 comprise or consist of the amino acid sequences set forth in SEQ ID NOs: 33-35, respectively, and the CDRL1, CDRL2, and CDRL3 comprise or consist of the amino acid sequences set forth in SEQ ID NOs: 37-39, respectively; and

(ii) a second antibody or antigen-binding fragment 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 CDRH1, CDRH2, and CDRH3 comprise or consist of the amino acid sequences set forth in SEQ ID NOs: 140-142, respectively, and the CDRL1, CDRL2, and CDRL3 comprise or consist of the amino acid sequences set forth in SEQ ID NOs: 144-146, respectively.

Embodiment 85. The composition of Embodiment 82, comprising:

(i) a first antibody or antigen-binding fragment, comprising a VH comprising or consisting of the amino acid sequence as set forth in SEQ ID NO: 139 or 342 and a VL comprising or consisting of the amino acid sequence as set forth in SEQ ID NO: 143 or 346; and

(ii) a second antibody or antigen-binding fragment comprising a VH comprising or consisting of the amino acid sequence as set forth in SEQ ID NO: 399, 748, 749, 750, 752, 754, 756, 758, 759, or 761, and a VL comprising or consisting of the amino acid sequence as set forth in SEQ ID NO: 403, 744, or 746.

Embodiment 86. The composition of Embodiment 82, comprising:

(i) a first antibody or antigen-binding fragment 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 CDRH1, CDRH2, and CDRH3 comprise or consist of the amino acid sequences set forth in SEQ ID NOs: 140-142, respectively, or 343-345, respectively, and the CDRL1, CDRL2, and CDRL3 comprise or consist of the amino acid sequences set forth in SEQ ID NOs: 144-146, respectively; and

(ii) a second antibody or antigen-binding fragment 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 CDRH1, CDRH2, and CDRH3 comprise or consist of the amino acid sequences set forth in SEQ ID NOs: 400, 401, and any one of 751, 753, 755, 757, 760, respectively, and the CDRL1, CDRL2, and CDRL3 comprise or consist of the amino acid sequences set forth in SEQ ID NOs: 404, 405, and any one of 406, 745, and 747, respectively.

Embodiment 87. A composition comprising:

(i) a first antibody or antigen-binding fragment, comprising

(i)(a) a VH comprising or consisting of the amino acid sequence as set forth in SEQ ID NO: 32, and

(i)(b) a VL comprising or consisting of the amino acid sequence as set forth in SEQ ID NO: 36; and

(ii) a second antibody or antigen-binding fragment comprising

(ii)(a) a VH comprising or consisting of the amino acid sequence as set forth in SEQ ID NO: 139 and

(ii)(b) a VL comprising of consisting of the amino acid sequence as set forth in SEQ ID NO: 143.

Embodiment 88. A composition comprising:

(i) a first antibody or antigen-binding fragment that is capable of binding to a SARS-CoV-2 surface glycoprotein and comprises

(i)(a) a VH comprising the CDRH1, CDRH2, and CDRH3 amino acid sequences set forth in SEQ ID NOs.:400, 402, and 766, respectively, and

(i)(b) a VL comprising the CDRL1, CDRL2, and CDRL3 amino acid sequences set forth in SEQ ID NOs.:404, 405, and 406, respectively; and

(ii) a second antibody or antigen-binding fragment that is capable of binding to a SARS-CoV-2 surface glycoprotein and comprises

(ii)(a) a VH comprising the CDRH1, CDRH2, and CDRH3 amino acid sequences set forth in SEQ ID NOs.:140, 141 or 344, and 142, respectively, and

(ii)(b) a VL comprising CDRL1, CDRL2, and CDRL3 amino acid sequences as set forth in SEQ ID NOs.:144, 145, and 146, respectively.

Embodiment 89. A composition comprising:

(i) a first antibody or antigen-binding fragment that is capable of binding to a SARS-CoV-2 surface glycoprotein and comprises

(i)(a) a VH comprising the amino acid sequence set forth in SEQ ID NO.:399 and

(i)(b) a VL comprising the amino acid sequence set forth in SEQ ID NOs.:403 or SEQ ID NO.:738; and

(ii) a second antibody or antigen-binding fragment that is capable of binding to a SARS-CoV-2 surface glycoprotein and comprises

(ii)(a) a VH comprising the amino acid sequence set forth in SEQ ID NOs.:139 or 342, and

(ii)(b) a VL comprising the amino acid sequence set forth in SEQ ID NO.:143.

Embodiment 90. The composition of any one of Embodiments 82-89, wherein the first antibody or antigen-binding fragment and the second antibody or antigen-binding fragment each comprise an IgG1 Fc polypeptide comprising a M428L mutation and a N434S mutation.

Embodiment 91. The composition of any one of Embodiments 82-90, wherein the first antibody or antigen-binding fragment and the second antibody or antigen-binding fragment each comprise an IgG1 Fc polypeptide comprising a G236A mutation, a A330L mutation, and a I332E mutation.

Embodiment 92. A composition comprising the polynucleotide of any one of Embodiments 73-77 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.

Embodiment 93. A composition comprising:

(i) a first antibody or antigen-binding fragment that is capable of binding to a SARS-CoV-2 surface glycoprotein and inhibiting an interaction between the SARS-CoV-2 surface glycoprotein and a first cell surface receptor selected from ACE2, DC-SIGN, L-SIGN, and SIGLEC-1; and

(ii) a second antibody or antigen-binding fragment that is capable of binding to a SARS-CoV-2 surface glycoprotein and inhibiting an interaction between the SARS-CoV-2 surface glycoprotein and a second cell surface receptor selected from ACE2, DC-SIGN, L-SIGN, and SIGLEC-1,

wherein the first cell surface receptor and the second cell surface receptor are different.

Embodiment 94. A method of treating a coronavirus infection, *e.g.* a SARS-CoV-2 infection, in a subject, the method comprising administering to the subject an effective amount of: (i) the antibody or antigen-binding fragment of any one of Embodiments 1-72; (ii) the polynucleotide of any one of Embodiments 73-77; (iii) the recombinant vector of Embodiment 78; (iv) the host cell of Embodiment 79; (v) the human B cell of Embodiment 80; and/or (vi) the composition of any one of Embodiments 81-93.

Embodiment 95. A method of treating a coronavirus infection, *e.g.* a SARS-CoV-2 infection, in a subject, the method comprising administering to the subject:

(i) a first antibody or antigen-binding fragment that is capable of binding to a SARS-CoV-2 surface glycoprotein and comprises

(i)(a) a VH comprising the CDRH1, CDRH2, and CDRH3 amino acid sequences set forth in SEQ ID NOs.:400, 402, and 766, respectively, and

(i)(b) a VL comprising the CDRL1, CDRL2, and CDRL3 amino acid sequences set forth in SEQ ID NOs.:404, 405, and 406, respectively; and

(ii) a second antibody or antigen-binding fragment that is capable of binding to a SARS-CoV-2 surface glycoprotein and comprises

(ii)(a) a VH comprising the CDRH1, CDRH2, and CDRH3 amino acid sequences set forth in SEQ ID NOs.:140, 141 or 344, and 142, respectively, and

(ii)(b) a VL comprising CDRL1, CDRL2, and CDRL3 amino acid sequences as set forth in SEQ ID NOs.:144, 145, and 146, respectively.

Embodiment 96. A method of treating a coronavirus infection, *e.g.* a SARS-CoV-2 infection, in a subject, the method comprising administering to the subject:

(i) a first antibody or antigen-binding fragment that is capable of binding to a SARS-CoV-2 surface glycoprotein and comprises

(i)(a) a VH comprising the amino acid sequence set forth in SEQ ID NO.:399 and

(i)(b) a VL comprising the amino acid sequence set forth in SEQ ID NOs.:403 or SEQ ID NO.:738; and

(ii) a second antibody or antigen-binding fragment that is capable of binding to a SARS-CoV-2 surface glycoprotein and comprises

(ii)(a) a VH comprising the amino acid sequence set forth in SEQ ID NOs.:139 or 342, and

(ii)(b) a VL comprising the amino acid sequence set forth in SEQ ID NO.:143.

Embodiment 97. A method of preventing or treating or neutralizing a coronavirus infection in a subject, the method comprising administering to a subject who has received a first antibody or antigen binding fragment comprising:

(i)(a) VH and VL amino acid sequences according to SEQ ID NOs.:32 and 36 respectively; or

(i)(b) CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 amino acid sequences according to SEQ ID NOS.:33-35 and 37-39, respectively;

a second antibody or antigen binding fragment comprising:

(ii)(a) a VH amino acid sequence according to SEQ ID NO.: 139, and a VL amino acid sequence according to SEQ ID NO: 143; or

(ii)(b) CDRH1, CDRH2, and CDRH3 amino acids according to SEQ ID NOs: 140-142, respectively, and CDRL1, CDRL2, and CDRL3 amino acid sequences according to SEQ ID NOs: 144-146.

Embodiment 98. A method of preventing or treating or neutralizing a coronavirus infection in a subject, the method comprising administering to a subject who has received a first antibody or antigen binding fragment comprising:

(i)(a) a VH amino acid sequence according to SEQ ID NO.: 139, and a VL amino acid sequence according to SEQ ID NO: 143; or

(i)(b) CDRH1, CDRH2, and CDRH3 amino acid sequences according to SEQ ID NOs: 140-142, respectively; and CDRL1, CDRL2, and CDRL3 amino acid sequences according to SEQ ID NOs: 144-146, respectively;

a second antibody or antigen binding fragment comprising:

(ii)(a) VH and VL amino acid sequences according to SEQ ID NOs.:32 and 36 respectively; or

(ii)(b) CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 amino acid sequences according to SEQ ID NOS.:33-35 and 37-39, respectively.

Embodiment 99. A method of preventing or treating or neutralizing a coronavirus infection in a subject, the method comprising administering to a subject who has received a first antibody or antigen binding fragment comprising:

(i)(a) a VH amino acid sequence according to SEQ ID NO.: 139 or 342 and a VL amino acid sequence according to SEQ ID NO: 143 or 346; or

(i)(b) CDRH1, CDRH2, and CDRH3 amino acid sequences according to SEQ ID NOs: 140-142, respectively, or 343-345, respectively and CDRL1, CDRL2, and CDRL3 amino acid sequences according to SEQ ID NOs: 144-146, respectively;

a second antibody or antigen binding fragment comprising:

(ii)(a) a VH amino acid sequence according to SEQ ID NO: 399, 748, 749, 750, 752, 754, 756, 758, 759, or 761 and a VL amino acid sequence according to SEQ ID NO: 403, 744, or 746; or

(ii)(b) CDRH1, CDRH2, and CDRH3 amino acid sequences according to SEQ ID NOs: 400, 401, and any one of 751, 753, 755, 757, 760, respectively and CDRL1, CDRL2, and CDRL3 amino acid sequences according to SEQ ID NOs: 404, 405, and any one of 406, 745, and 747, respectively.

Embodiment 100. A method of preventing or treating or neutralizing a coronavirus infection in a subject, the method comprising administering to a subject who has received a first antibody or antigen binding fragment comprising:

(i)(a) a VH amino acid sequence according to SEQ ID NO: 399, 748, 749, 750, 752, 754, 756, 758, 759, or 761 and a VL amino acid sequence according to SEQ ID NO: 403, 744, or 746; or

(i)(b) CDRH1, CDRH2, and CDRH3 amino acid sequences according to SEQ ID NOs: 400, 401, and any one of 751, 753, 755, 757, 760, respectively and CDRL1, CDRL2, and CDRL3 amino acid sequences according to SEQ ID NOs: 404, 405, and any one of 406, 745, and 747, respectively;

a second antibody or antigen binding fragment comprising:

(ii)(a) a VH amino acid sequence according to SEQ ID NO.: 139 or 342 and a VL amino acid sequence according to SEQ ID NO: 143 or 346; or

(ii)(b) CDRH1, CDRH2, and CDRH3 amino acid sequences according to SEQ ID NOs: 140-142, respectively, or 343-345, respectively and CDRL1, CDRL2, and CDRL3 amino acid sequences according to SEQ ID NOs: 144-146, respectively.

Embodiment 101. The method of any one of Embodiments 95-100, wherein the first antibody or antigen-binding fragment and the second antibody or antigen-binding fragment each comprise an IgG1 Fc polypeptide comprising a M428L mutation and a N434S mutation.

Embodiment 102. The method of any one of Embodiments 95-101, wherein the first antibody or antigen-binding fragment and the second antibody or antigen-binding fragment each comprise an IgG1 Fc polypeptide comprising a G236A mutation, a A330L mutation, and a I332E mutation.

Embodiment 103. A method of treating a coronavirus (*e.g.* SARS-CoV-2) infection in a subject, the method comprising administering to the subject:

(i) a first antibody or antigen-binding fragment that is capable of binding to a SARS-CoV-2 surface glycoprotein and inhibiting an interaction between the SARS-CoV-2 surface glycoprotein and a first cell surface receptor selected from ACE2, DC-SIGN, L-SIGN, and SIGLEC-1; and

(ii) a second antibody or antigen-binding fragment that is capable of binding to a SARS-CoV-2 surface glycoprotein and inhibiting an interaction between the SARS-CoV-2 surface glycoprotein and a second cell surface receptor selected from ACE2, DC-SIGN, L-SIGN, and SIGLEC-1,

wherein the first cell surface receptor and the second cell surface receptor are different.

Embodiment 104. The antibody or antigen-binding fragment of any one of claims 1-72, the polynucleotide of any one of Embodiments 73-77, the recombinant vector of Embodiment 78, the host cell of Embodiment 79, the human B cell of Embodiment 80, and/or the composition of any one of Embodiments 81-93 for use in a method of treating a coronavirus (*e.g.* SARS-CoV-2) infection in a subject.

Embodiment 105. The antibody or antigen-binding fragment of any one of claims 1-72, the polynucleotide of any one of Embodiments 73-77, the recombinant vector of Embodiment78, the host cell of Embodiment 79, the human B cell of Embodiment 80, and/or the composition of any one of Embodiments 81-93 for use in the preparation of a medicament for the treatment of a coronavirus (*e.g.* SARS-CoV-2) infection in a subject.

Embodiment 106. A method for *in vitro* diagnosis of a coronavirus (*e.g.* SARS-CoV-2) infection, the method comprising:

(i) contacting a sample from a subject with an antibody or antigen-binding fragment of any one of Embodiments 1-72; and

(ii) detecting a complex comprising an antigen and the antibody, or comprising an antigen and the antigen-binding fragment.

Embodiment 107. The method of Embodiment 106, wherein the sample comprises blood isolated from the subject.

Table 2. Sequences

Sequence Description	SEQ ID NO.	Sequence
SARS-CoV-2 Wuhan seafood market pneumonia virus isolate Wuhan-Hu-1 genomic sequence (GenBank: MN908947.3;January 23, 2020)	1	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

Sequence Description	SEQ ID NO.	Sequence
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Sequence Description	SEQ ID NO.	Sequence
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Sequence Description	SEQ ID NO.	Sequence
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Sequence Description	SEQ ID NO.	Sequence
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Sequence Description	SEQ ID NO.	Sequence
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Sequence Description	SEQ ID NO.	Sequence
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Sequence Description	SEQ ID NO.	Sequence
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Sequence Description	SEQ ID NO.	Sequence
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Sequence Description	SEQ ID NO.	Sequence
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Sequence Description	SEQ ID NO.	Sequence
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Sequence Description	SEQ ID NO.	Sequence
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Sequence Description	SEQ ID NO.	Sequence
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Sequence Description	SEQ ID NO.	Sequence
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Sequence Description	SEQ ID NO.	Sequence
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Sequence Description	SEQ ID NO.	Sequence
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Sequence Description	SEQ ID NO.	Sequence
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Sequence Description	SEQ ID NO.	Sequence
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SARS-CoV-2 Wuhan seafood market pneumonia virus isolate Wuhan-Hu-1 genomic sequence (GenBank: MN908947.3;January 23, 2020) – amino acid translation	2	MESLVPGFNEKTHVQLSLPVLQVRDVLVRGF GDSVEEVLSEARQHLKDGTCGLVEVEKGVLP QLEQPYVFIKRSDARTAPHGHVMVELVAELE GIQYGRSGETLGVLVPHVGEIPVAYRKVLLR KNGNKGAGGHSYGADLKSFDLGDELGTDPY EDFQEN WNTKHSSGVTRELMRELNGGAYTRYVDNNF CGPDGYPLECIKDLLARAGKASCTLSEQLDFI DTKRGVYCCREHEHEIAWYTERSEKSYELQT PFEIKLAKKFDTFNGECPNFVFPLNSIIKTIQPR VEKKKLDGFMGRIRSVYPVASPNECNQMCLS TLMKCDHCGETSWQTGDFVKATCEFCGTEN LTKEGATTCGYLPQNAVVKIYCPACHNSEVG

Sequence Description	SEQ ID NO.	Sequence
		PEHSLAEYHNESGLKTILRKGGRTIAFGGCVF SYVGCHNKCAYWVPRASANIGCNHTGVVGE GSEGLNDNL LEILQKEKVNINIVGDFKLNEEIAIILASFSAST SAFVETVKGLDYKAFKQIVESCGNFKVTKGK AKKGAWNIGEQKSILSPLYAFASEAARVVRSI FSRTLETAQNSVRVLQKAAITILDGISQYSLRL IDAMMFTSDLATNNLVVMAYITGGVVQLTSQ WLTNIFGTVYEKLKPVLDWLEEKFKEGVEFL RDGWEIVKFISTCACEIVGGQIVTCAKEIKESV QTFFKLVNKFLALCADSIIIGGAKLKALNLGE TFVTHSKGLYRKCVKSREETGLLMPLKAPKEI IFLEGETLPTEVLTEEVVLKTGDLQPLEQPTSE AVEAPLVGTPVCINGLMLLEIKDTEKYCALAP NMMVTNNTFTLKGGAPTKVTFGDDTVIEVQ GYKSVNITFELDERIDKVLNEKCSAYTVELGT EVNEFACVVADAVIKTLQPVSELLTPLGIDLD EWSMATYYLFDESGEFKLASHMYCSFYPPDE DEEEGDCEEEEFEPSTQYEYGTEDDYQGKPLE FGATSAALQPEEEQEEDWLDDDSQQTVGQQ DGSEDNQTTTIQTIVEVQPQLEMELTPVVQTI EVNSFSGYLKLTDNVYIKNADIVEEAKKVKP TVVVNAANVYLKHGGGVAGALNKATNNAM QVESDDYIATNGPLKVGGSCVLSGHNLAKHC LHVVGPNVNKGEDIQLLKSAYENFNQHEVLL APLLSAGIFGADPIHSLRVCVDTVRTNVYLAV FDKNLYDKLVSSFLEMKSEKQVEQKIAEIPKE EVKPFITESKPSVEQRKQDDKKIKACVEEVTT TLEETKFLTENLLLYIDINGNLHPDSATLVSDI DITFLKKDAPYIVGDVVQEGVLTAVVIPTKKA GGTTEMLAKALRKVPTDNYITTYPGQGLNGY TVEEAKTVLKKCKSAFYILPSIISNEKQEILGT VSWNLREMLAHAEETRKLMPVCVETKAIVST IQRKYKGIKIQEGVVDYGARFYFYTSKTTVAS LINTLNDLNETLVTMPLGYVTHGLNLEEAAR YMRSLKVPATVSVSSPDAVTAYNGYLTSSSK TPEEHFIETISLAGSYKDWSYSGQSTQLGIEFL KRGDKSVYYTSNPTTFHLDGEVITFDNLKTLL SLREVRTIKVFTTVDNINLHTQVVDMSMTYG QQFGPTYLDGADVTKIKPHNSHEGKTFYVLP NDDTLRVEAFEYYHTTDPSFLGRYMSALNHT KKWKYPQVNGLTSIKWADNNCYLATALLTL QQIELKFNPPALQDAYYRARAGEAANFCALIL AYCNKTVGELGDVRETMSYLFQHANLDSCK RVLNVVCKTCGQQQTTLKGVEAVMYMGTLS

Sequence Description	SEQ ID NO.	Sequence
		YEQFKKGVQIPCTCGKQATKYLVQQESPFVM MSAPPAQYELKHGTFTCASEYTGNYQCGHY KHITSKETLYCIDGALLTKSSEYKGPITDVFYK ENSYTTTIKPVTYKLDGVVCTEIDPKLDNYYK KDNSYFTEQPIDLVPNQPYPNASFDNFKFVCD NIKFADDLNQLTGYKKPASRELKVTFFPDLN GDVVAIDYKHYTPSFKKGAKLLHKPIVWHVN NATNKATYKPNTWCIRCLWSTKPVETSNSFD VLKSEDAQGMDNLACEDLKPVSEEVVENPTI QKDVLECNVKTTEVVGDIILKPANNSLKITEE VGHTDLMAAYVDNSSLTIKKPNELSRVLGLK TLATHGLAAVNSVPWDTIANYAKPFLNKVVS TTTNIVTRCLNRVCTNYMPYFFTLLLQLCTFT RSTNSRIKASMPTTIAKNTVKSVGKFCLEASF NYLKSPNFSKLINIIIWFLLLSVCLGSLIYSTAA LGVLMSNLGMPSYCTGYREGYLNSTNVTIAT YCTGSIPCSVCLSGLDSLDTYPSLETIQITISSF KWDLTAFGLVAEWFLAYILFTRFFYVLGLAA IMQLFFSYFAVHFISNSWLMWLIINLVQMAPI SAMVRMYIFFASFYYVWKSYVHVVDGCNSS TCMMCYKRNRATRVECTTIVNGVRRSFYVY ANGGKGFCKLHNWNCVNCDTFCAGSTFISDE VARDLSLQFKRPINPTDQSSYIVDSVTVKNGSI HLYFDKAGQKTYERHSLSHFVNLDNLRANNT KGSLPINVIVFDGKSKCEESSAKSASVYYSQL MCQPILLLDQALVSDVGDSAEVAVKMFDAY VNTFSSTFNVPMEKLKTLVATAEAELAKNVS LDNVLSTFISAARQGFVDSDVETKDVVECLK LSHQSDIEVTGDSCNNYMLTYNKVENMTPRD LGACIDCSARHINAQVAKSHNIALIWNVKDF MSLSEQLRKQIRSAAKKNNLPFKLTCATTRQ VVNVVTTKIALKGGKIVNNWLKQLIKVTLVF LFVAAIFYLITPVHVMSKHTDFSSEIIGYKAID GGVTRDIASTDTCFANKHADFDTWFSQRGGS YTNDKACPLIAAVITREVGFVVPGLPGTILRTT NGDFLHFLPRVFSAVGNICYTPSKLIEYTDFAT SACVLAAECTIFKDASGKPVPYCYDTNVLEG SVAYESLRPDTRYVLMDGSIIQFPNTYLEGSV RVVTTFDSEYCRHGTCERSEAGVCVSTSGRW VLNNDYYRSLPGVFCGVDAVNLLTNMFTPLI QPIGALDISASIVAGGIVAIVVTCLAYYFMRFR RAFGEYSHVVAFNTLLFLMSFTVLCLTPVYSF LPGVYSVIYLYLTFYLTNDVSFLAHIQWMVM FTPLVPFWITIAYIICISTKHFYWFFSNYLKRRV VFNGVSFSTFEEAALCTFLLNKEMYLKLRSD

Sequence Description	SEQ ID NO.	Sequence
		VLLPLTQYNRYLALYNKYKYFSGAMDTTSY REAACCHLAKALNDFSNSGSDVLYQPPQTSIT SAVLQSGFRKMAFPSGKVEGCMVQVTCGTT TLNGLWLDDVVYCPRHVICTSEDMLNPNYED LLIRKSNHNFLVQAGNVQLRVIGHSMQNCVL KLKVDTANPKTPKYKFVRIQPGQTFSVLACY NGSPSGVYQCAMRPNFTIKGSFLNGSCGSVGF NIDYDCVSFCYMHHMELPTGVHAGTDLEGN FYGPFVDRQTAQAAGTDTTITVNVLAWLYA AVINGDRWFLNRFTTTLNDFNLVAMKYNYEP LTQDHVDILGPLSAQTGIAVLDMCASLKELLQ NGMNGRTILGSALLEDEFTPFDVVRQCSGVTF QSAVKRTIKGTHHWLLLTILTSLLVLVQSTQ WSLFFFLYENAFLPFAMGIIAMSAFAMMFVK HKHAFLCLFLLPSLATVAYFNMVYMPASWV MRIMTWLDMVDTSLSGFKLKDCVMYASAVV LLILMTARTVYDDGARRVWTLMNVLTLVYK VYYGNALDQAISMWALIISVTSNYSGVVTTV MFLARGIVFMCVEYCPIFFITGNTLQCIMLVY CFLGYFCTCYFGLFCLLNRYFRLTLGVYDYL VSTQEFRYMNSQGLLPPKNSIDAFKLNIKLLG VGGKPCIKVATVQSKMSDVKCTSVVLLSVLQ QLRVESSSKLWAQCVQLHNDILLAKDTTEAF EKMVSLLSVLLSMQGAVDINKLCEEMLDNR ATLQAIASEFSSLPSYAAFATAQEAYEQAVAN GDSEVVLKKLKKSLNVAKSEFDRDAAMQRK LEKMADQAMTQMYKQARSEDKRAKVTSAM QTMLFTMLRKLDNDALNNIINNARDGCVPLN IIPLTTAAKLMVVIPDYNTYKNTCDGTTFTYA SALWEIQQVVDADSKIVQLSEISMDNSPNLA WPLIVTALRANSAVKLQNNELSPVALRQMSC AAGTTQTACTDDNALAYYNTTKGGRFVLAL LSDLQDLKWARFPKSDGTGTIYTELEPPCRFV TDTPKGPKVKYLYFIKGLNNLNRGMVLGSLA ATVRLQAGNATEVPANSTVLSFCAFAVDAAK AYKDYLASGGQPITNCVKMLCTHTGTGQAIT VTPEANMDQESFGGASCCLYCRCHIDHPNPK GFCDLKGKYVQIPTTCANDPVGFTLKNTVCT VCGMWKGYGCSCDQLREPMLQSADAQSFLN RVCGVSAARLTPCGTGTSTDVVYRAFDIYND KVAGFAKFLKTNCCRFQEKDEDDNLIDSYFV VKRHTFSNYQHEETIYNLLKDCPAVAKHDFF KFRIDGDMVPHISRQRLTKYTMADLVYALRH FDEGNCDTLKEILVTYNCCDDDYFNKKDWY DFVENPDILRVYANLGERVRQALLKTVQFCD

Sequence Description	SEQ ID NO.	Sequence
		AMRNAGIVGVLTLDNQDLNGNWYDFGDFIQ TTPGSGVPVV DSYYSLLMPILTLTRALTAESHVDTDLTKPYI KWDLLKYDFTEERLKLFDRYFKYWDQTYHP NCVNCLDDRCILHCANFNVLFSTVFPPTSFGP LVRKIFVDGVPFVVSTGYHFRELGVVHNQDV NLHSSRLSFKELLVYAADPAMHAASGNLLLD KRTTCFSVAALTNNVAFQTVKPGNFNKDFYD FAVSKGFFKEGSSVELKHFFFAQDGNAAISDY DYYRYNLPTMCDIRQLLFVVEVVDKYFDCY DGGCINANQVIVNNLDKSAGFPFNKWGKARL YYDSMSYEDQDALFAYTKRNVIPTITQMNLK YAISAKNRARTVAGVSICSTMTNRQFHQKLL KSIAATRGATVVIGTSKFYGGWHNMLKTVYS DVENPHLMGWDYPKCDRAMPNMLRIMASL VLARKHTTCCSLSHRFYRLANECAQVLSEMV MCGGSLYVKPGGTSSGDATTAYANSVFNICQ AVTANVNALLSTDGNKIADKYVRNLQHRLY ECLYRNRDVDTDFVNEFYAYLRKHFSMMILS DDAVVCFNSTYASQGLVASIKNFKSVLYYQN NVFMSEAKCWTETDLTKGPHEFCSQHTMLV KQGDDYVYLPYPDPSRILGAGCFVDDIVKTD GTLMIERFVSLAIDAYPLTKHPNQEYADVFHL YLQYIRKLHDELTGHMLDMYSVMLTNDNTS RYWEPEFYEAMYTPHTVLQAVGACVLCNSQ TSLRCGACIRRPFLCCKCCYDHVISTSHKLVL SVNPYVCNAPGCDVTDVTQLYLGGMSYYCK SHKPPISFPLCANGQVFGLYKNTCVGSDNVTD FNAIATCDWTNAGDYILANTCTERLKLFAAE TLKATEETFKLSYGIATVREVLSDRELHLSWE VGKPRPPLNRNYVFTGYRVTKNSKVQIGEYT FEKGDYGDAVVYRGTTTYKLNVGDYFVLTS HTVMPLSAPTLVPQEHYVRITGLYPTLNISDE FSSNVANYQKVGMQKYSTLQGPPGTGKSHF AIGLALYYPSARIVYTACSHAAVDALCEKAL KYLPIDKCSRIIPARARVECFDKFKVNSTLEQY VFCTVNALPETTADIVVFDEISMATNYDLSVV NARLRAKHYVYIGDPAQLPAPRTLLTKGTLE PEYFNSVCRLMKTIGPDMFLGTCRRCPAEIVD TVSALVYDNKLKAHKDKSAQCFKMFYKGVI THDVSSAINRPQIGVVREFLTRNPAWRKAVFI SPYNSQNAVASKILGLPTQTVDSSQGSEYDYV IFTQTTETAHSCNVNRFNVAITRAKVGILCIMS DRDLYDKLQFTSLEIPRRNVATLQAENVTGLF KDCSKVITGLHPTQAPTHLSVDTKFKTEGLCV

Sequence Description	SEQ ID NO.	Sequence
		DIPGIPKDMTYRRLISMMGFKMNYQVNGYPN MFITREEAIRHVRAWIGFDVEGCHATREAVG TNLPLQLGFSTGVNLVAVPTGYVDTPNNTDF SRVSAKPPPGDQFKHLIPLMYKGLPWNVVRI KIVQMLSDTLKNLSDRVVFVLWAHGFELTSM KYFVKIGPERTCCLCDRRATCFSTASDTYAC WHHSIGFDYVYNPFMIDVQQWGFTGNLQSN HDLYCQVHGNAHVASCDAIMTRCLAVHECF VKRVDWTIEYPIIGDELKINAACRKVQHMVV KAALLADKFPVLHDIGNPKAIKCVPQADVEW KFYDAQPCSDKAYKIEELFYSYATHSDKFTD GVCLFWNCNVDRYPANSIVCRFDTRVLSNLN LPGCDGGSLYVNKHAFHTPAFDKSAFVNLKQ LPFFYYSDSPCESHGKQVVSDIDYVPLKSATCI TRCNLGGAVCRHHANEYRLYLDAYNMMISA GFSLWVYKQFDTYNLWNTFTRLQSLENVAF NVVNKGHFDGQQGEVPVSIINNTVYTKVDGV DVELFENKTTLPVNVAFELWAKRNIKPVPEV KILNNLGVDIAANTVIWDYKRDAPAHISTIGV CSMTDIAKKPTETICAPLTVFFDGRVDGQVDL FRNARNGVLITEGSVKGLQPSVGPKQASLNG VTLIGEAVKTQFNYYKKVDGVVQQLPETYFT QSRNLQEFKPRSQMEIDFLELAMDEFIERYKL EGYAFEHIVYGDFSHSQLGGLHLLIGLAKRFK ESPFELEDFIPMDSTVKNYFITDAQTGSSKCVC SVIDLLLDDFVEIIKSQDLSVVSKVVKVTIDYT EISFMLWCKDGHVETFYPKLQSSQAWQPGVA MPNLYKMQRMLLEKCDLQNYGDSATLPKGI MMNVAKYTQLCQYLNTLTLAVPYNMRVIHF GAGSDKGVAPGTAVLRQWLPTGTLLVDSDL NDFVSDADSTLIGDCATVHTANKWDLIISDM YDPKTKNVTKENDSKEGFFTYICGFIQQKLAL GGSVAIKITEHSWNADLYKLMGHFAWWTAF VTNVNASSSEAFLIGCNYLGKPREQIDGYVM HANYIFWRNTNPIQLSSYSLFDMSKFPLKLRG TAVMSLKEGQINDMILSLLSKGRLIIRENNRV VISSDVLVNN
surface glycoprotein [SARS-CoV-2 Wuhan seafood market pneumonia virus];	3	mfvflvllpl vssqcvnltt rtqlppaytn sftrgvyypd kvfrssvlhs tqdlflpffs 61 nvtwfhaihv sgtngtkrfd npvlpfndgv yfasteksni irgwifgttl dsktqslliv 121 nnatnvvikv cefqfcndpf lgvyyhknnk swmesefrvy ssannctfey vsqpflmdle181 gkqgnfknlr efvfknidgy fkiyskhtpi nlvrdlpqgf saleplvdlp iginitrfqt 241 llalhrsylt pgdsssgwta gaaayyvgyl qprtfllkyn

Sequence Description	SEQ ID NO.	Sequence
GenBank: QHD43416.1; January 23, 2020		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
surface glycoprotein RBD [SARS-CoV-2 Wuhan seafood market pneumonia virus]; GenBank: QHD43416.1; January 23, 2020	4	nitnlcpfgevfnatrfasvyawnrkrisncvadysvlynsasfstfkc ygvsptklndlcftnvyadsfvirgdevrqiapgqtgkiadynyklpd dftgcviawnsnnldskvggnynylyrlfrksnlkpferdisteiyqa gstpcngvegfncyfplqsygfqptngvgyqpyrvvvlsfellhapa tvcgpkkstnlvknkcvnfnfngltgtg
Receptor Binding Motif (RBM) in surface glycoprotein RBD [SARS-CoV-2 Wuhan	5	Nsnnldskvggnynylyrlfrksnlkpferdisteiyqagstpcngve gfncyfplqsygfqptngvgyqpy

Sequence Description	SEQ ID NO.	Sequence
seafood market pneumonia virus]; GenBank: QHD43416.1; January 23, 2020		
SARS-CoV-2 CH1-CH3 LS G1m17 IgHG1*01 (aa)	6	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSRDELTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVLHE ALHSHYTQKSLSLSPGK
SARS-CoV-2 CH1-CH3 LS, ALE G1m17 IgHG1*01 (aa)	7	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLAGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNKALPLPEEKTIS KAKGQPREPQVYTLPPSRDELTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVLHE ALHSHYTQKSLSLSPGK
SARS-CoV-2 CL IgLC*01 (aa)	8	GQPKAAPSVTLFPPSSEELQANKATLVCLISDF YPGAVTVAWKADSSPVKAGVETTTPSKQSN NKYAASSYLSLTPEQWKSHRSYSCQVTHEGS TVEKTVAPTECS
SARS-CoV-2 CL (CK) k1m3 IgKC*01 (aa)	9	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQG LSSPVTKSFNRGEC
Linker (aa)	10	GSTSGSGKPGSGEGSTKG
Linker (aa)	11	GSGKPGSGEG

Sequence Description	SEQ ID NO.	Sequence
Linker (aa)	12	GKPGSGEG
Linker (aa)	13	SGKPGSGE
Linker (aa)	14	BPXXXZ, wherein each X is independently a glycine (G) or serine (S), B is a positively charged amino acid and Z is glycine (G) or a negatively charged amino acid
Linker (aa)	15	(GxS)y, wherein x is 1-10 and y is 1-10
Linker (aa)	16	GGGGSGGGGSGGGGS
Linker (aa)	17	GGGGSGGGGSGGGGSGGGGSGGGGS GGGGSGGGGSGGGGSGGGGSGGGGS
Linker (aa)	18	GSTSGGGSGGGSGGGGSS
Linker (aa)	19	EGKSSGSGSESKVD
Linker (aa)	20	KESGSVSSEQLAQFRSLD
Linker (aa)	21	GGGGS
SARS-CoV-2 S2X16-v1 mAb VH (aa)	22	EVQLVQSGAEVKKPGASVKVSCKAS**GYIFTD HY**MHWVRQAPGQGLEWMGW**INPNSGGT**N YAQKFQGRVTMTRDTSINTAYMELSRLRSDD TAVHYC**ARDRSRFRFFSPDFDY**WGQGTLVT VSS
SARS-CoV-2 S2X16-v1 mAb CDRH1 (aa)	23	**GYIFTDHY**
SARS-CoV-2 S2X16-v1 mAb CDRH2 (aa)	24	**INPNSGGT**
SARS-CoV-2 S2X16-v1 mAb CDRH3 (aa)	25	**ARDRSRFRFFSPDFDY**
SARS-CoV-2 S2X16-v1 mAb VL (aa)	26	EIVLTQSPLSLPVTPGEPASISCRSS**QSLLHSN GYNY**LDWYLQKPGQSPQLLIY**LGS**NRASGVP DRFSGSGSGTDFTLKISRVEAEDVGVYYC**MQ ALQTPPT**FGQGTKVEIK
SARS-CoV-2	27	**QSLLHSNGYNY**

Sequence Description	SEQ ID NO.	Sequence
S2X16-v1 mAb CDRL1 (aa)		
SARS-CoV-2 S2X16-v1 mAb CDRL2 (aa)	28	**LGS**
SARS-CoV-2 S2X16-v1 mAb CDRL3 (aa)	29	**MQALQTPPT**
SARS-CoV-2 S2X16-v1 mAb VH (nt)	30	GAGGTGCAGCTGGTGCAGTCTGGGGCTGAG GTGAAGAAGCCTGGGGCCTCAGTGAAGGTC TCCTGCAAGGCTTCT**GGATACATCTTCACC GACCACTAT**ATGCACTGGGTGCGACAGGC CCCTGGACAAGGGCTTGAGTGGATGGGATG G**ATCAACCCTAACAGTGGTGGCACA**AACT ATGCACAGAAGTTTCAGGGCAGGGTCACCA TGACCAGGGACACGTCCATCAACACAGCCT ACATGGAGCTGAGCAGGCTGAGATCTGACG ACACGGCCGTGCATTACTGT**GCGAGAGAT CGGTCACGATTTCGATTTTTCTCCCCCGA CTTTGACTAC**TGGGGCCAGGGAACCCTGG TCACCGTCTCCTCAG
SARS-CoV-2 S2X16-v1 mAb VL (nt)	31	GAAATTGTGCTGACTCAGTCTCCACTCTCCC TGCCCGTCACCCCTGGAGAGCCGGCCTCCA TCTCCTGCAGGTCTAGT**CAGAGCCTCCTGC ATAGTAATGGATACAACTAT**TTGGATTGG TACCTGCAGAAGCCAGGGCAGTCTCCACAG CTCCTGATCTAT**TTGGGTTCT**AATCGGGCC TCCGGGGTCCCTGACAGGTTCAGTGGCAGT GGCTCAGGCACAGATTTCACACTGAAAATC AGCAGAGTGGAGGCTGAGGATGTTGGGGTT TATTACTGC**ATGCAAGCTCTACAAACTCC TCCAACG**TTCGGCCAAGGGACCAAGGTGG AAATCAAAC
SARS-CoV-2 S2X28-v1 mAb VH (aa)	32	EVQLVESGGGVVQPGRSLRLSCAAS**GFTFST YA**MHWVRQAPGKGLEWVAV**ILSDGSNK**YY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDT AVYYC**ARDRSPLVGFGDNYGMDV**WGQGTT VTVSS

Sequence Description	SEQ ID NO.	Sequence
SARS-CoV-2 S2X28-v1 mAb CDRH1 (aa)	33	**GFTFSTYA**
SARS-CoV-2 S2X28-v1 mAb CDRH2 (aa)	34	**ILSDGSNK**
SARS-CoV-2 S2X28-v1 mAb CDRH3 (aa)	35	**ARDRSPLVGFGDNYGMDV**
SARS-CoV-2 S2X28-v1 mAb VL (aa)	36	SYELTQPPSVSVSPGQTARITCSGD**ALPKKY**A YWYQQKSGQAPVLVIY**EDS**KRPSGIPERFSGS SSGTMATLTISGAQVEDEADYYC**SSTDSSGN QGV**FGGGTKLTVL
SARS-CoV-2 S2X28-v1 mAb CDRL1 (aa)	37	**ALPKKY**
SARS-CoV-2 S2X28-v1 mAb CDRL2 (aa)	38	**EDS**
SARS-CoV-2 S2X28-v1 mAb CDRL3 (aa)	39	**SSTDSSGNQGV**
SARS-CoV-2 S2X28-v1 mAb VH (nt)	40	GAGGTGCAGCTGGTGGAGTCTGGGGGAGG CGTGGTCCAGCCTGGGAGGTCCCTGAGACT CTCCTGTGCAGCCTCT**GGATTCACCTTCAG TACCTATGCT**ATGCACTGGGTCCGCCAGGC TCCAGGCAAGGGGCTAGAGTGGGTGGCAGT T**ATATTATCTGATGGAAGTAATAAA**TATT ACGCAGACTCTGTGAAGGGCCGATTCACCA TCTCCAGAGACAATTCCAAGAACACGCTGT ATCTGCAAATGAACAGCCTGAGAGCTGAGG ACACGGCTGTGTATTACTGT**GCGAGAGATC GAAGTCCCCTCGTGGGATTCGGGGACAA CTATGGTATGGACGTC**TGGGGCCAAGGGA

Sequence Description	SEQ ID NO.	Sequence
		CCACGGTCACCGTCTCCTCA
SARS-CoV-2 S2X28-v1 mAb VL (nt)	41	TCCTATGAGCTGACACAGCCACCCTCGGTG TCAGTGTCCCCAGGACAAACGGCCAGGATC ACCTGCTCTGGAGAT**GCATTGCCAAAAAA ATAT**GCTTATTGGTACCAGCAGAAGTCAGG CCAGGCCCCTGTGCTGGTCATCTAT**GAGGA CAGC**AAACGACCCTCCGGGATCCCTGAGA GATTCTCTGGCTCCAGCTCAGGGACAATGG CCACCTTGACTATCAGTGGGGCCCAGGTGG AGGATGAAGCTGACTACTACTGT**TCCTCAA CAGACAGCAGTGGTAATCAAGGGGTA**TT CGGCGGAGGGACCAAGCTGACCGTCCTAG
SARS-CoV-2 S2X30-v1 mAb VH (aa)	42	EVQLVQSGAEVKKPGSSVKVSCKAS**GGTFGS YT**ISWVRQAPGQGLEWMGR**IIPILSIP**NYAQK FQGRVTFTADKSTSTAYMELSSLRSEDTAVY YC**ARGGGGTHAVPHYYFDS**WGQGTLVTVS S
SARS-CoV-2 S2X30-v1 mAb CDRH1 (aa)	43	**GGTFGSYT**
SARS-CoV-2 S2X30-v1 mAb CDRH2 (aa)	44	**IIPILSIP**
SARS-CoV-2 S2X30-v1 mAb CDRH3 (aa)	45	**ARGGGGTHAVPHYYFDS**
SARS-CoV-2 S2X30-v1 mAb VL (aa)	46	EIVMMQSPATLSVSPGERATLSCRAS**QSVSSN** LAWYQHKPGQAPRLLIY**GAS**TRATGIPARFS GSGSGTEFTLTISSMQSEDFAVYYC**QQYNNW PFT**FGGGTKVEIK
SARS-CoV-2 S2X30-v1 mAb CDRL1 (aa)	47	**QSVSSN**
SARS-CoV-2 S2X30-v1	48	**GAS**

Sequence Description	SEQ ID NO.	Sequence
mAb CDRL2 (aa)		
SARS-CoV-2 S2X30-v1 mAb CDRL3 (aa)	49	**QQYNNWPFT**
SARS-CoV-2 S2X30-v1 mAb VH (nt)	50	GAGGTGCAGCTGGTGCAATCTGGGGCTGAG GTGAAGAAGCCTGGGTCCTCGGTGAAGGTC TCCTGCAAGGCTTCT**GGAGGCACCTTCGG CAGCTATACT**ATCAGCTGGGTGCGACAGG CCCCTGGACAAGGGCTTGAGTGGATGGGAA GG**ATCATCCCTATCCTTAGTATACCA**AAC TACGCACAGAAGTTCCAGGGCAGAGTCACG TTTACCGCGGACAAATCCACGAGCACAGCC TACATGGAGCTGAGCAGCCTGAGATCTGAG GACACGGCCGTGTATTACTGT**GCGAGAGG AGGGGGTGGGACCCACGCAGTTCCCCAC TACTACTTTGACTCC**TGGGGCCAGGGAAC CCTGGTCACCGTCTCCTCAG
SARS-CoV-2 S2X30-v1 mAb VL (nt)	51	GAAATAGTGATGATGCAGTCTCCAGCCACC CTGTCTGTGTCTCCAGGGGAAAGAGCCACC CTCTCCTGCAGGGCCAGT**CAGAGTGTTAG CAGCAAC**TTAGCCTGGTACCAGCATAAACC TGGCCAGGCTCCCAGGCTCCTCATCTAT**GG TGCATCC**ACCAGGGCCACTGGTATCCCAGC CAGGTTCAGTGGCAGTGGGTCTGGGACAGA GTTCACTCTCACCATCAGCAGCATGCAGTC TGAAGATTTTGCAGTTTATTACTGT**CAGCA GTATAATAACTGGCCTTTCACT**TTCGGCG GAGGGACCAAGGTGGAGATCAAAC
SARS-CoV-2 S2X47-v1 mAb VH (aa)	52	QVQLQESGPGLVKPSQTLSLTCTVS**GGSISS**R **SYY**WSWIRQPAGKGLEWIGR**IYTSG**N**T**NYNP SLRSRVTISVDTSKNQFSLKLGSVTAADTAVY YC**ARERIIGTAHVGGWFDP**WGQGTLVTVSS
SARS-CoV-2 S2X47-v1 mAb CDRH1 (aa)	53	**GGSISSRSYY**
SARS-CoV-2 S2X47-v1 mAb CDRH2	54	**IYTSGNT**

Sequence Description	SEQ ID NO.	Sequence
(aa)		
SARS-CoV-2 S2X47-v1 mAb CDRH3 (aa)	55	**ARERIIGTAHVGGWFDP**
SARS-CoV-2 S2X47-v1 mAb VL (aa)	56	QTVVTQPPSASGTPGQRVTISCSGS**SSNIGSDT** VNWYLQLPGTAPKLLIY**TNN**QRPSGVPDRFS GSKSGTSASLAISGLQSEDEANYYC**AAWDDS LNGWV**FGGGTKLTVL
SARS-CoV-2 S2X47-v1 mAb CDRL1 (aa)	57	**SSNIGSDT**
SARS-CoV-2 S2X47-v1 mAb CDRL2 (aa)	58	**TNN**
SARS-CoV-2 S2X47-v1 mAb CDRL3 (aa)	59	**AAWDDSLNGWV**
SARS-CoV-2 S2X47-v1 mAb VH (nt)	60	CAGGTGCAGCTACAGGAGTCGGGCCCAGG ACTGGTGAAGCCTTCACAGACCCTGTCCCT CACCTGCACTGTCTCT**GGTGGCTCCATCAG CAGTCGAAGTTACTAC**TGGAGCTGGATCC GGCAGCCCGCCGGGAAGGGACTGGAGTGG ATTGGGCGT**ATCTATACCAGTGGCAACAC C**AACTACAACCCCTCCCTCAGGAGTCGAGT CACCATATCAGTGGACACGTCCAAGAACCA GTTCTCCCTGAAGCTGGGCTCTGTGACCGC CGCAGACACGGCCGTGTATTATTGT**GCGAG AGAGCGTATAATTGGAACCGCGCACGTG GGTGGGTGGTTCGACCCC**TGGGGCCAGG GAACCCTGGTCACCGTCTCCTCAG
SARS-CoV-2 S2X47-v1 mAb VL (nt)	61	CAGACTGTGGTGACTCAGCCACCCTCAGCG TCTGGGACCCCCGGGCAGAGGGTCACCATC TCTTGTTCTGGAAGC**AGCTCCAACATCGG AAGTGATACT**GTAAACTGGTACCTGCAGCT CCCAGGAACGGCCCCCAAACTCCTCATCTA T**ACTAATAAT**CAGCGGCCCTCAGGGGTCCC

Sequence Description	SEQ ID NO.	Sequence
		TGACCGATTCTCTGGCTCCAAGTCTGGCAC CTCAGCCTCCCTGGCCATCAGTGGGCTCCA GTCTGAGGATGAGGCTAATTATTACTGT**GC AGCATGGGATGACAGCCTGAATGGTTGG GTG**TTCGGCGGAGGGACCAAGCTGACCGTC CTAG
SARS-CoV-2 S2X55-v1 mAb VH (aa)	62	EVQLVQSGAEVKKPGASVKVSCKAS**GYTFT GYY**MHWVRQAPGQGLEWMGW**INPNSGAT** NFAQKFQGRVTMTRDRSISTAYMELRSLRSD DTAVYYC**ARDLGDSRLSGWFDP**WGQGTLV TVSS
SARS-CoV-2 S2X55-v1 mAb CDRH1 (aa)	63	**GYTFTGYY**
SARS-CoV-2 S2X55-v1 mAb CDRH2 (aa)	64	**INPNSGAT**
SARS-CoV-2 S2X55-v1 mAb CDRH3 (aa)	65	**ARDLGDSRLSGWFDP**
SARS-CoV-2 S2X55-v1 mAb VL (aa)	66	QSALTQPASVSGSPGQSITISCTGT**SSDVGSYN L**VSWYQQHPGKAPKLMIY**EGS**KRPSGVSYRF SGSKSGNTASLTISGLQAEDEADYYC**CSYAG SSTWV**FGGGTKLTVL
SARS-CoV-2 S2X55-v1 mAb CDRL1 (aa)	67	**SSDVGSYNL**
SARS-CoV-2 S2X55-v1 mAb CDRL2 (aa)	68	**EGS**
SARS-CoV-2 S2X55-v1 mAb CDRL3	69	**CSYAGSSTWV**

Sequence Description	SEQ ID NO.	Sequence
(aa)		
SARS-CoV-2 S2X55-v1 mAb VH (nt)	70	GAGGTGCAGCTGGTGCAGTCTGGGGCTGAG GTGAAGAAGCCTGGGGCCTCAGTGAAGGTC TCCTGCAAGGCTTCT**GGATACACCTTCACC GGCTACTAT**ATGCACTGGGTGCGACAGGC CCCTGGACAAGGGCTTGAGTGGATGGGATG G**ATCAACCCTAACAGTGGTGCCACA**AACT TTGCACAGAAGTTTCAGGGCAGGGTCACCA TGACCAGGGACAGGTCCATCAGCACAGCCT ACATGGAGTTGAGAAGCCTGAGATCTGACG ACACGGCCGTTTATTACTGT**GCGAGAGATC TCGGGGATAGCAGGTTGAGTGGCTGGTT CGACCCC**TGGGGCCAGGGAACCCTGGTCA CCGTCTCCTCAG
SARS-CoV-2 S2X55-v1 mAb VL (nt)	71	CAGTCTGCCCTGACTCAGCCTGCCTCCGTGT CTGGGTCTCCTGGACAGTCGATCACCATCT CCTGCACTGGAACC**AGCAGTGATGTTGGG AGTTATAACCTT**GTCTCCTGGTACCAACAG CACCCAGGCAAAGCCCCCAAACTCATGATT TAT**GAGGGCAGT**AAGCGGCCCTCAGGGGT TTCTTATCGCTTCTCTGGCTCCAAGTCTGGC AACACGGCCTCCCTGACAATCTCTGGGCTC CAGGCTGAGGACGAGGCTGATTATTACTGC **TGCTCATATGCAGGTAGTAGCACTTGGG TG**TTCGGCGGAGGGACCAAGCTGACCGTCC TAG
SARS-CoV-2 S2X55-v2 mAb VH (aa)	72	QVQLVQSGAEVKKPGASVKVSCKAS**GYTFT GYY**MHWVRQAPGQGLEWMGW**INPNSGAT** NFAQKFQGRVTMTRDRSISTAYMELRSLRSD DTAVYYC**ARDLGDSRLSGWFDP**WGQGTLV TVSS
SARS-CoV-2 S2X55-v2 mAb VH (nt)	73	CAGGTCCAGCTGGTGCAGTCTGGGGCTGAG GTGAAGAAGCCTGGGGCCTCAGTGAAGGTC TCCTGCAAGGCTTCT**GGATACACCTTCACC GGCTACTAT**ATGCACTGGGTGCGACAGGC CCCTGGACAAGGGCTTGAGTGGATGGGATG G**ATCAACCCTAACAGTGGTGCCACA**AACT TTGCACAGAAGTTTCAGGGCAGGGTCACCA TGACCAGGGACAGGTCCATCAGCACAGCCT ACATGGAGTTGAGAAGCCTGAGATCTGACG ACACGGCCGTTTATTACTGT**GCGAGAGATC TCGGGGATAGCAGGTTGAGTGGCTGGTT**

Sequence Description	SEQ ID NO.	Sequence
		CGACCCCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
SARS-CoV-2 S2X56-v1 mAb VH (aa)	74	QVQLVQSGAEVKKPGSSVKVSCKAS**GGTFGSYT**ISWVRQAPGQGLEWMGR**IIPILSIP**NYAQKFQGRVTFTADKSTSTAYMELSSLRSEDTAVYYC**ARGGGGTHAVPHYYFDS**WGQGTLVTVSS
SARS-CoV-2 S2X56-v1 mAb CDRH1 (aa)	75	**GGTFGSYT**
SARS-CoV-2 S2X56-v1 mAb CDRH2 (aa)	76	**IIPILSIP**
SARS-CoV-2 S2X56-v1 mAb CDRH3 (aa)	77	**ARGGGGTHAVPHYYFDS**
SARS-CoV-2 S2X56-v1 mAb VL (aa)	78	QTVLTQPASVSGSPGQSITISCTGT**SSDVGSYNL**VSWYQQHPGKAPKLMIY**EGS**KRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYC**CSYAGSSTHV**FGTGTKVIVL
SARS-CoV-2 S2X56-v1 mAb CDRL1 (aa)	79	**SSDVGSYNL**
SARS-CoV-2 S2X56-v1 mAb CDRL2 (aa)	80	**EGS**
SARS-CoV-2 S2X56-v1 mAb CDRL3 (aa)	81	**CSYAGSSTHV**
SARS-CoV-2 S2X56-v1	82	CAGGTCCAGCTGGTGCAATCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCTTCT**GGAGGCACCTTCGG**

Sequence Description	SEQ ID NO.	Sequence
mAb VH (nt)		**CAGCTATACT**ATCAGCTGGGTGCGACAGG CCCCTGGACAAGGGCTTGAGTGGATGGGAA GG**ATCATCCCTATCCTTAGTATACCA**AAC TACGCACAGAAGTTCCAGGGCAGAGTCACG TTTACCGCGGACAAATCCACGAGCACAGCC TACATGGAGCTGAGCAGCCTGAGATCTGAG GACACGGCCGTGTATTACTGT**GCGAGAGG AGGGGGTGGGACCCACGCAGTTCCCCAC TACTACTTTGACTCC**TGGGGCCAGGGAAC CCTGGTCACCGTCTCCTCAG
SARS-CoV-2 S2X56-v1 mAb VL (nt)	83	CAGACTGTGCTGACTCAGCCTGCCTCCGTG TCTGGGTCTCCTGGACAGTCGATCACCATCT CCTGCACTGGAACC**AGCAGTGATGTTGGG AGTTATAACCTT**GTCTCCTGGTACCAACAG CACCCAGGCAAAGCCCCCAAACTCATGATT TAT**GAGGGCAGT**AAGCGGCCCTCAGGGGT TTCTAATCGCTTCTCTGGCTCCAAGTCTGGC AACACGGCCTCCCTGACAATCTCTGGGCTC CAGGCTGAGGACGAGGCTGATTATTACTGC **TGCTCATATGCAGGTAGTAGCACCCATG TC**TTCGGAACTGGGACCAAGGTCATCGTCC TAG
SARS-CoV-2 S2X58-v1 mAb VH (aa)	84	QVQLVQSGAEVKKPGASVKVSCKAS**GYTFT SYY**MHWVRQAPGQGLEWMGI**INRSGGST**SY AQKFQGRVTMTRDTSTSTVYMDLSSLRSEDT AVYYC**ARDSGIAARVVY**WGQGTLVTVSS
SARS-CoV-2 S2X58-v1 mAb CDRH1 (aa)	85	**GYTFTSYY**
SARS-CoV-2 S2X58-v1 mAb CDRH2 (aa)	86	**INRSGGST**
SARS-CoV-2 S2X58-v1 mAb CDRH3 (aa)	87	**ARDSGIAARVVY**
SARS-CoV-2 S2X58-v1	88	NIQMTQSPSSLSASVGDRVTITCQAS**QDISNY** LNWYQQKPGKVPKLLIY**DAS**NLETGVPSRFS

Sequence Description	SEQ ID NO.	Sequence
mAb VL (aa)		GSGSGTDFTFTISSLQPEDIATYYC**QQHDNLF** **T**FGPGTKVDIK
SARS-CoV-2 S2X58-v1 mAb CDRL1 (aa)	89	**QDISNY**
SARS-CoV-2 S2X58-v1 mAb CDRL2 (aa)	90	**DAS**
SARS-CoV-2 S2X58-v1 mAb CDRL3 (aa)	91	**QQHDNLFT**
SARS-CoV-2 S2X58-v1 mAb VH (nt)	92	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAG GTGAAGAAGCCTGGGGCCTCAGTGAAGGTT TCCTGCAAGGCATCT**GGATACACCTTCAC** **CAGCTACTAT**ATGCACTGGGTGCGACAGG CCCCTGGACAAGGGCTTGAGTGGATGGGAA TA**ATCAACCGTAGTGGTGGTAGCACA**AG CTACGCACAGAAGTTCCAGGGCAGAGTCAC CATGACCAGGGACACGTCCACGAGCACAGT CTACATGGACCTGAGCAGCCTGAGATCTGA GGACACGGCCGTCTATTACTGT**GCGAGAG** **ATTCGGGGATAGCAGCCAGGGTTGTCTA** **C**TGGGGCCAGGGAACCCTGGTCACCGTCTC CTCAG
SARS-CoV-2 S2X58-v1 mAb VL (nt)	93	AACATCCAGATGACCCAGTCTCCATCCTCC CTGTCTGCATCTGTAGGAGACAGAGTCACC ATCACTTGCCAGGCGAGT**CAGGACATTAG** **CAACTAT**TTAAATTGGTATCAGCAGAAACC AGGGAAAGTCCCTAAGCTCCTGATCTAC**GA** **TGCATCC**AATTTGGAAACAGGGGTCCCATC AAGGTTCAGTGGAAGTGGATCTGGGACAGA TTTTACTTTCACCATCAGCAGCCTGCAGCCT GAAGATATTGCAACATATTACTGT**CAACAG** **CATGATAATCTTTTCACT**TTCGGCCCTGGG ACCAAAGTGGATATCAAAC
SARS-CoV-2 S2X58-v2	94	DIVMTQSPSSLSASVGDRVTITCQAS**QDISNY** LNWYQQKPGKVPKLLIY**DAS**NLETGVPSRFS

Sequence Description	SEQ ID NO.	Sequence
mAb VL (aa)		GSGSGTDFTFTISSLQPEDIATYYC**QQHDNLF** **T**FGPGTKVDIK
SARS-CoV-2 S2X58-v2 mAb VL (nt)	95	GACATCGTGATGACCCAGTCTCCATCCTCC CTGTCTGCATCTGTAGGAGACAGAGTCACC ATCACTTGCCAGGCGAGT**CAGGACATTAG** **CAACTAT**TTAAATTGGTATCAGCAGAAACC AGGGAAAGTCCCTAAGCTCCTGATCTAC**GA** **TGCATCC**AATTTGGAAACAGGGGTCCCATC AAGGTTCAGTGGAAGTGGATCTGGGACAGA TTTTACTTTCACCATCAGCAGCCTGCAGCCT GAAGATATTGCAACATATTACTGT**CAACAG** **CATGATAATCTTTTCACT**TTCGGCCCTGGG ACCAAAGTGGATATCAAAC
SARS-CoV-2 S2X71-v1 mAb VH (aa)	96	EVQLVESGGGLIQPGGSLRLSCAAS**GFTVSAN** **Y**MSWVRQTPGKGLEWVSV**IYSGGST**YYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVY YC**ARDLAAAAGP**WGQGTLVTVSS
SARS-CoV-2 S2X71-v1 mAb CDRH1 (aa)	97	**GFTVSANY**
SARS-CoV-2 S2X71-v1 mAb CDRH2 (aa)	98	**IYSGGST**
SARS-CoV-2 S2X71-v1 mAb CDRH3 (aa)	99	**ARDLAAAAGP**
SARS-CoV-2 S2X71-v1 mAb VL (aa)	100	DIQMTQSPSSLSASVGDRVTITCRAS**QGIRND** LGWFQQKPGKAPKLLIY**AAS**SLQSGVPSRFSG SGSGTDFTLTISSLQPEDFATYYC**LQDYNYPR** **T**FGQGTKLEIK
SARS-CoV-2 S2X71-v1 mAb CDRL1 (aa)	101	**QGIRND**
SARS-CoV-2	102	**AAS**

Sequence Description	SEQ ID NO.	Sequence
S2X71-v1 mAb CDRL2 (aa)		
SARS-CoV-2 S2X71-v1 mAb CDRL3 (aa)	103	**LQDYNYPRT**
SARS-CoV-2 S2X71-v1 mAb VH (nt)	104	GAGGTGCAGCTGGTGGAGTCTGGAGGAGG CTTGATCCAGCCTGGGGGGTCCCTGAGACT CTCCTGTGCAGCCTCT**GGGTTCACCGTCAG TGCCAACTAC**ATGAGCTGGGTCCGCCAGA CTCCAGGGAAGGGGCTGGAGTGGGTCTCAG TT**ATTTATAGCGGTGGTAGCACA**TACTAC GCAGACTCCGTGAAGGGCCGATTCACCATC TCCAGAGACAATTCCAAGAACACGCTGTAC CTTCAAATGAACAGCCTGAGAGCCGAGGAC ACGGCCGTGTATTACTGT**GCGAGAGATTTA GCTGCAGCTGCTGGGCCC**TGGGGCCAGG GAACCCTGGTCACCGTCTCCTCAG
SARS-CoV-2 S2X71-v1 mAb VL (nt)	105	GACATCCAGATGACCCAGTCTCCATCCTCC CTGTCTGCATCTGTAGGAGACAGAGTCACC ATCACTTGCCGGGCAAGT**CAGGGCATTAG AAATGAT**TTAGGCTGGTTTCAGCAGAAACC AGGGAAAGCCCCTAAGCTCCTGATCTAT**GC TGCATCC**AGTTTACAAAGTGGGGTCCCATC AAGGTTCAGCGGCAGTGGATCTGGCACAGA TTTCACTCTCACCATCAGCAGCCTGCAGCCT GAAGATTTTGCAACTTATTACTGT**CTACAA GATTACAATTACCCTCGGACT**TTTGGCCA GGGGACCAAGCTGGAGATCAAAC
SARS-CoV-2 S2X76-v1 mAb VH (aa)	106	QVQLVQSGAEVKKPGASVKVSCKAS**GYSFT NYY**MHWVRQAPGQGLEWMGI**INASGGST**R YAQKFQGRVTMTRDTSTSTVYMELSSLRSED TAVYYC**ARDSGIAARVVY**WGQGTLVTVSS
SARS-CoV-2 S2X76-v1 mAb CDRH1 (aa)	107	**GYSFTNYY**
SARS-CoV-2 S2X76-v1	108	**INASGGST**

Sequence Description	SEQ ID NO.	Sequence
mAb CDRH2 (aa)		
SARS-CoV-2 S2X76-v1 mAb CDRH3 (aa)	109	**ARDSGIAARVVY**
SARS-CoV-2 S2X76-v1 mAb VL (aa)	110	AIRMTQSPSSLSASVGDRVTITCQAS**QDISNY** LNWYQQKPGKAPKLLIY**DAS**NLETGVPSRFS GSGSGTDFTFTISSLQPEDIATYYC**QQHDDLF T**FGPGTKVDIK
SARS-CoV-2 S2X76-v1 mAb CDRL1 (aa)	111	**QDISNY**
SARS-CoV-2 S2X76-v1 mAb CDRL2 (aa)	112	**DAS**
SARS-CoV-2 S2X76-v1 mAb CDRL3 (aa)	113	**QQHDDLFT**
SARS-CoV-2 S2X76-v1 mAb VH (nt)	114	caggtccagctggtgcagtctggggctgaggtgaagaagcctggggc ctcagtgaaggtttcctgcaaggcatct**gggtacagcttcaccaacta ctat**atgcactgggtgcgacaggcccctggacaagggcttgagtggat gggaata**atcaacgctagtggtggtagcaca**aggtacgcacagaag ttccagggcagagtcaccatgaccagggacacgtccacgagcacagt ctacatggagttgagcagcctgagatctgaggacacggccgtgtattac tgt**gcgagagattcggggatagcagccagggttgtctac**tggggcc agggaaccctggtcaccgtctcctcag
SARS-CoV-2 S2X76-v1 mAb VL (nt)	115	GCCATCCGGATGACCCAGTCTCCATCCTCC CTGTCTGCATCTGTAGGAGACAGAGTCACC ATCACTTGCCAGGCGAGT**CAGGACATTAG CAACTAT**TTAAATTGGTATCAGCAGAAACC AGGGAAAGCCCCTAAGCTCCTGATCTAC**GA TGCATCC**AATTTGGAAACAGGGGTCCCATC AAGGTTCAGTGGAAGTGGATCTGGGACAGA TTTTACTTTCACCATCAGCAGCCTGCAGCCT GAAGATATTGCGACATATTACTGT**CAACAA CATGATGATCTTTTCACT**TTCGGCCCTGGG

Sequence Description	SEQ ID NO.	Sequence
		ACCAAAGTGGATATCAAAC
SARS-CoV-2 S2X76-v2 mAb VH (nt)	116	caggtccagcttgtgcagtctggggctgaggtgaagaagcctggggc ctcagtgaaggtttcctgcaaggcatct**gggtacagcttcaccaacta ctat**atgcactgggtgcgacaggcccctggacaagggcttgagtggat gggaata**atcaacgctagtggtggtagcaca**aggtacgcacagaag ttccagggcagagtcaccatgaccagggacacgtccacgagcacagt ctacatggagttgagcagcctgagatctgaggacacggccgtgtattac tgt**gcgagagattcggggatagcagccagggttgtctac**tggggcc agggaaccctggtcaccgtctcctcag
SARS-CoV-2 S2X76-v3 mAb VH (nt)	117	caggtacagctggtgcagtctggggctgaggtgaagaagcctggggc ctcagtgaaggtttcctgcaaggcatct**gggtacagcttcaccaacta ctat**atgcactgggtgcgacaggcccctggacaagggcttgagtggat gggaata**atcaacgctagtggtggtagcaca**aggtacgcacagaag ttccagggcagagtcaccatgaccagggacacgtccacgagcacagt ctacatggagttgagcagcctgagatctgaggacacggccgtgtattac tgt**gcgagagattcggggatagcagccagggttgtctac**tggggcc agggaaccctggtcaccgtctcctcag
SARS-CoV-2 S2X76-v4 mAb VH (nt)	118	caggtacagcttgtgcagtctggggctgaggtgaagaagcctggggc ctcagtgaaggtttcctgcaaggcatct**gggtacagcttcaccaacta ctat**atgcactgggtgcgacaggcccctggacaagggcttgagtggat gggaata**atcaacgctagtggtggtagcaca**aggtacgcacagaag ttccagggcagagtcaccatgaccagggacacgtccacgagcacagt ctacatggagttgagcagcctgagatctgaggacacggccgtgtattac tgt**gcgagagattcggggatagcagccagggttgtctac**tggggcc agggaaccctggtcaccgtctcctcag
SARS-CoV-2 S2X11-v1 mAb VH (aa)	119	EVQLVESGGGLVQPGGSLRLSCAVS**GFIVSSN Y**MTWVRQAPGKGLEWVSV**IYSGGST**FYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVY YC**ARDFPVRRGVNI**WGQGTLVTVSS
SARS-CoV-2 S2X11-v1 mAb CDRH1 (aa)	120	**GFIVSSNY**
SARS-CoV-2 S2X11-v1 mAb CDRH2 (aa)	121	**IYSGGST**
SARS-CoV-2	122	**ARDFPVRRGVNI**

Sequence Description	SEQ ID NO.	Sequence
S2X11-v1 mAb CDRH3 (aa)		
SARS-CoV-2 S2X11-v1 mAb VL (aa)	123	DIQLTQSPSSLSASVGDRVTITCQAS**QDIVNY**L NWYQQKPGKAPKLLIY**DAS**NLETGVPSRFSG SGSGTDFTFTISSLQPEDIATYYC**HQYDNLPP A**FGGGTKVEIK
SARS-CoV-2 S2X11-v1 mAb CDRL1 (aa)	124	**QDIVNY**
SARS-CoV-2 S2X11-v1 mAb CDRL2 (aa)	125	**DAS**
SARS-CoV-2 S2X11-v1 mAb CDRL3 (aa)	126	**HQYDNLPPA**
SARS-CoV-2 S2X11-v1 mAb VH (nt)	127	GAGGTGCAACTGGTGGAGTCTGGGGGAGG CTTGGTCCAGCCTGGGGGGTCCCTGAGACT CTCCTGTGCAGTCTCT**GGATTCATCGTCAG TAGCAACTAC**ATGACTTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGGAGTGGGTCTCAGT T**ATTTATAGCGGTGGTAGCACA**TTCTACG CAGACTCCGTGAAGGGCCGATTCACCATTT CCAGAGACAATTCCAAGAACACGCTGTATC TTCAAATGAACAGCCTGAGAGCTGAGGACA CGGCTGTGTATTATTGT**GCGAGAGATTTCC CCGTACGTCGGGGAGTTAATATC**TGGGGC CAGGGAACCCTGGTCACCGTCTCCTCAG
SARS-CoV-2 S2X11-v1 mAb VL (nt)	128	GACATCCAGTTGACCCAGTCTCCATCCTCCC TGTCTGCATCTGTAGGAGACAGAGTCACCA TCACTTGCCAGGCGAGT**CAGGACATTGTC AACTAT**TTAAATTGGTATCAACAGAAACCA GGGAAAGCCCCTAAGCTCCTGATCTAC**GAT GCATCC**AATTTGGAAACAGGGGTCCCATCA AGGTTCAGTGGAAGTGGATCTGGGACAGAT TTTACTTTCACCATCAGCAGCCTGCAGCCTG AAGATATTGCAACATATTACTGT**CACCAGT ATGATAATCTCCCTCCGGCT**TTCGGCGGA

Sequence Description	SEQ ID NO.	Sequence
		GGGACCAAGGTGGAGATCAAAC
SARS-CoV-2 S2X35-v1 mAb VH (aa)	129	QVQLVQSGAEVKKPGASVKVSCKAS**GYTFT NYGI**SWVRQAPGQGLEWMGW**ISAYKGNT**N YAQKLQGRVTMTTDTSTSTAYMELRSLRSDD TAVYYC**ARPDYQVLGYDFWIGYYGMDV**W GQGTTVIVSS
SARS-CoV-2 S2X35-v1 mAb CDRH1 (aa)	130	**GYTFTNYG**
SARS-CoV-2 S2X35-v1 mAb CDRH2 (aa)	131	**ISAYKGNT**
SARS-CoV-2 S2X35-v1 mAb CDRH3 (aa)	132	**ARPDYQVLGYDFWIGYYGMDV**
SARS-CoV-2 S2X35-v1 mAb VL (aa)	133	QSVLTQPPSVSGAPGQRVTISCTGS**SSNIGAG YD**VHWYQQLPGTAPKLLIY**GNT**NRPSGVPDR FSGSKSGTSASLAITGLQAEDEADYYC**QSYDS SLSGSEVV**FGGGTKLTVL
SARS-CoV-2 S2X35-v1 mAb CDRL1 (aa)	134	**SSNIGAGYD**
SARS-CoV-2 S2X35-v1 mAb CDRL2 (aa)	135	**GNT**
SARS-CoV-2 S2X35-v1 mAb CDRL3 (aa)	136	**QSYDSSLSGSEVV**
SARS-CoV-2 S2X35-v1 mAb VH (nt)	137	CAGGTCCAGCTGGTGCAGTCTGGAGCTGAG GTGAAGAAGCCTGGGGCCTCAGTGAAGGTC TCCTGCAAGGCTTCT**GGTTACACCTTTACC AACTATGGT**ATCAGCTGGGTGCGACAGGC

Sequence Description	SEQ ID NO.	Sequence
		CCCTGGACAAGGGCTTGAGTGGATGGGATG G**ATCAGCGCTTACAAGGGTAACACA**AACT ATGCACAGAAACTCCAGGGCAGAGTCACCA TGACCACAGACACATCCACGAGCACAGCCT ACATGGAGCTGAGGAGCCTGAGATCTGACG ACACGGCCGTGTATTACTGT**GCGAGACCC GATTATCAGGTCCTGGGGTACGATTTTTG GATTGGGTACTACGGTATGGACGTC**TGG GGCCAAGGGACCACGGTCATCGTCTCCTCA
SARS-CoV-2 S2X35-v1 mAb VL (nt)	138	CAGTCTGTGTTGACGCAGCCGCCCTCAGTG TCTGGGGCCCCAGGGCAGAGGGTCACCATC TCCTGCACTGGGAGC**AGCTCCAACATCGG GGCAGGTTATGAT**GTACACTGGTACCAGC AGCTTCCAGGAACAGCCCCCAAACTCCTCA TCTAT**GGTAACACC**AATCGGCCCTCAGGGG TCCCTGACCGATTCTCTGGCTCCAAGTCTGG CACCTCAGCCTCCCTGGCCATCACTGGGCT CCAGGCTGAGGATGAGGCTGATTATTACTG C**CAGTCTTATGACAGCAGCCTGAGTGGT TCGGAGGTGGTG**TTCGGCGGAGGGACCAA GCTGACCGTCCTAG
SARS-CoV-2 S309 mAb VH (aa)	139	QVQLVQSGAEVKKPGASVKVSCKAS**GYPFT SYG**ISWVRQAPGQGLEWMGW**ISTYNGNT**NY AQKFQGRVTMTTDTSTTGYMELRRLRSDDT AVYYC**ARDYTRGAWFGESLIGGFDN**WGQG TLVTVSS
SARS-CoV-2 S309 mAb CDRH1 (aa)	140	GYPFTSYG
SARS-CoV-2 S309 mAb CDRH2 (aa)	141	ISTYNGNT
SARS-CoV-2 S309 mAb CDRH3 (aa)	142	ARDYTRGAWFGESLIGGFDN
SARS-CoV-2 S309 mAb VL (aa)	143	EIVLTQSPGTLSLSPGERATLSCRAS**QTVSSTS** LAWYQQKPGQAPRLLIY**GAS**SRATGIPDRFSG SGSGTDFTLTISRLEPEDFAVYYC**QQHDTSLT** FGGGTKVEIK
SARS-CoV-2 S309 mAb	144	QTVSSTS

Sequence Description	SEQ ID NO.	Sequence
CDRL1 (aa)		
SARS-CoV-2 S309 mAb CDRL2 (aa)	145	GAS
SARS-CoV-2 S309 mAb CDRL3 (aa)	146	QQHDTSLT
SARS-CoV-2 S2X16-v2 mAb CDRH1 (aa)	147	**GYIFTDHYMH**
SARS-CoV-2 S2X16-v2 mAb CDRH2 (aa)	148	**WINPNSGGTNYAQKFQG**
SARS-CoV-2 S2X16-v2 mAb CDRH3 (aa)	149	**DRSRFRFFSPDFDY**
SARS-CoV-2 S2X16-v3 mAb VH (aa)	150	EVQLVQSGAEVKKPGASVKVSCKAS**GYIFTD HY**MHWVRQAPGQGLEWMGF**INPNSGGT**NY AQKFQGRVTMTRDTSINTAYMELSRLRSDDT AVHYC**ARDRSRFRFFSPDFDY**WGQGTLVTV SS
SARS-CoV-2 S2X16-v3 mAb CDRH2 (aa)	151	**FINPNSGGTNYAQKFQG**
SARS-CoV-2 S2X16-v4 mAb CDRL1 (aa)	152	**RSSQSLLHSNGYNYLD**
SARS-CoV-2 S2X16-v4 mAb CDRL2 (aa)	153	**LGSNRAS**
SARS-CoV-2 S2X16-v5 mAb VL (aa)	154	EIVLTQSPLSLPVTPGEPASISCRSS**QSLLHSQ GYNY**LDWYLQKPGQSPQLLIY**LGS**NRASGVP DRFSGSGSGTDFTLKISRVEAEDVGVYYC**MQ ALQTPPT**FGQGTKVEIK

Sequence Description	SEQ ID NO.	Sequence
SARS-CoV-2 S2X16-v5 mAb CDRL1 (aa)	155	**RSSQSLLHSQGYNYLD**
SARS-CoV-2 S2X16-v6 mAb CDRL1 (aa)	156	**QSLLHSQGYNY**
SARS-CoV-2 S2X16-v7 mAb VL (aa)	157	EIVLTQSPLSLPVTPGEPASISCRSS**QSLLHSN AYNY**LDWYLQKPGQSPQLLIY**LGS**NRASGVP DRFSGSGSGTDFTLKISRVEAEDVGVYYC**MQ ALQTPPT**FGQGTKVEIK
SARS-CoV-2 S2X16-v7 mAb CDRL1 (aa)	158	**RSSQSLLHSNAYNYLD**
SARS-CoV-2 S2X16-v8 mAb CDRL1 (aa)	159	**QSLLHSNAYNY**
SARS-CoV-2 S2X30-v2 mAb CDRH1 (aa)	160	**GGTFGSYTIS**
SARS-CoV-2 S2X30-v2 mAb CDRH2 (aa)	161	**RIIPILSIPNYAQKFQG**
SARS-CoV-2 S2X30-v2 mAb CDRH3 (aa)	162	**GGGGTHAVPHYYFDS**
SARS-CoV-2 S2X30-v3 mAb VH (aa)	163	EVQLVQSGAEVKKPGSSVKVSCKAS**GGTFGS YT**ISWVRQAPGQGLEWMGR**IIPILSIP**NYAQK FQGRVTFTADKSTSTAYMELSSLRSEDTAVY YC**ARGGGGTHAVPHYYFES**WGQGTLVTVS S
SARS-CoV-2	164	**ARGGGGTHAVPHYYFES**

Sequence Description	SEQ ID NO.	Sequence
S2X30-v3 mAb CDRH3 (aa)		
SARS-CoV-2 S2X30-v4 mAb CDRH3 (aa)	165	**GGGGTHAVPHYYFES**
SARS-CoV-2 S2X30-v5 mAb CDRL1 (aa)	166	**RASQSVSSNLA**
SARS-CoV-2 S2X30-v5 mAb CDRL2 (aa)	167	**GASTRAT**
SARS-CoV-2 S2X30-v6 mAb VH (aa)	168	EIVMMQSPATLSVSPGERATLSCRAS**QSVSSN** LAWYQHKPGQAPRLLIY**GAS**TRATGIPARFS GSGSGTEFTLTISSMQSEDFAVYYC**QQYNNF PFT**FGGGTKVEIK
SARS-CoV-2 S2X30-v6 mAb CDRL3 (aa)	169	**QQYNNFPFT**
SARS-CoV-2 S2X35-v2 mAb CDRH1 (aa)	170	**GYTFTNYGIS**
SARS-CoV-2 S2X35-v2 mAb CDRH2 (aa)	171	**WISAYKGNTNYAQKLQG**
SARS-CoV-2 S2X35-v2 mAb CDRH3 (aa)	172	**PDYQVLGYDFWIGYYGMDV**
SARS-CoV-2 S2X35-v3 mAb VH (aa)	173	QVQLVQSGAEVKKPGASVKVSCKAS**GYTFT NYG**ISWVRQAPGQGLEWMGF**ISAYKGNT**NY AQKLQGRVTMTTDTSTSTAYMELRSLRSDDT AVYYC**ARPDYQVLGYDFWIGYYGMDV**WG QGTTVIVSS

Sequence Description	SEQ ID NO.	Sequence
SARS-CoV-2 S2X35-v3 mAb CDRH1 (aa)	174	**FISAYKGNTNYAQKLQG**
SARS-CoV-2 S2X35-v4 mAb VH (aa)	175	QVQLVQSGAEVKKPGASVKVSCKAS**GYTFT NYGI**SWVRQAPGQGLEWMGW**ISAYKGNT**N YAQKLQGRVTMTTDTSTSTAYMELRSLRSDD TAVYYC**ARPDYQVLGYDFFIGYYGMDV**WG QGTTVIVSS
SARS-CoV-2 S2X35-v4 mAb CDRH3 (aa)	176	**ARPDYQVLGYDFFIGYYGMDV**
SARS-CoV-2 S2X35-v5 mAb CDRH3 (aa)	177	**PDYQVLGYDFFIGYYGMDV**
SARS-CoV-2 S2X35-v6 mAb VH (aa)	178	QVQLVQSGAEVKKPGASVKVSCKAS**GYTFT NYGI**SWVRQAPGQGLEWMGF**ISAYKGNT**NY AQKLQGRVTMTTDTSTSTAYMELRSLRSDDT AVYYC**ARPDYQVLGYDFFAGYYGMDV**WG QGTTVIVSS
SARS-CoV-2 S2X35-v6 mAb CDRH3 (aa)	179	**ARPDYQVLGYDFFAGYYGMDV**
SARS-CoV-2 S2X35-v7 mAb CDRH3 (aa)	180	**PDYQVLGYDFFAGYYGMDV**
SARS-CoV-2 S2X35-v8 mAb CDRL1 (aa)	181	**TGSSSNIGAGYDVH**
SARS-CoV-2 S2X35-v8 mAb CDRL2 (aa)	182	**GNTNRPS**

Sequence Description	SEQ ID NO.	Sequence
SARS-CoV-2 S2X47-v2 mAb CDRH1 (aa)	183	**GGSISSRSYYWS**
SARS-CoV-2 S2X47-v2 mAb CDRH2 (aa)	184	**RIYTSGNTNYNPSLRS**
SARS-CoV-2 S2X47-v2 mAb CDRH3 (aa)	185	**ERIIGTAHVGGWFDP**
SARS-CoV-2 S2X47-v3 mAb VH (aa)	186	QVQLQESGPGLVKPSQTLSLTCTVS**GGSISSR SYY**WSWIRQPAGKGLEWIGR**IYTSGNT**NYNP SLRSRVTISVDTSKNQFSLKLGSVTAADTAVY YC**ARERIIGTAHVGGFFDP**WGQGTLVTVSS
SARS-CoV-2 S2X47-v3 mAb CDRH3 (aa)	187	**ARERIIGTAHVGGFFDP**
SARS-CoV-2 S2X47-v4 mAb CDRH3 (aa)	188	**ERIIGTAHVGGFFDP**
SARS-CoV-2 S2X47-v5 mAb VH (aa)	189	QVQLQESGPGLVKPSQTLSLTCTVS**GGSISSR SYY**FSWIRQPAGKGLEWIGR**IYTSGNT**NYNP SLRSRVTISVDTSKNQFSLKLGSVTAADTAVY YC**ARERIIGTAHVGGWFDP**WGQGTLVTVSS
SARS-CoV-2 S2X47-v5 mAb CDRH1 (aa)	190	**GGSISSRSYYFS**
SARS-CoV-2 S2X47-v6 mAb VH (aa)	191	QVQLQESGPGLVKPSQTLSLTCTVS**GGSISSR SYY**FSWIRQPAGKGLEWIGR**IYTSGNT**NYNP SLRSRVTISVDTSKNQFSLKLGSVTAADTAVY YC**ARERIIGTAHVGGFFDP**WGQGTLVTVSS
SARS-CoV-2 S2X47-v7 mAb CDRL1	192	**SGSSSNIGSDTVN**

Sequence Description	SEQ ID NO.	Sequence
(aa)		
SARS-CoV-2 S2X47-v7 mAb CDRL2 (aa)	193	**TNNQRPS**
SARS-CoV-2 S2X47-v8 mAb VL (aa)	194	QTVVTQPPSASGTPGQRVTISCSGS**SSNIGSDT** VNWYLQLPGTAPKLLIY**TNN**QRPSGVPDRFS GSKSGTSASLAISGLQSEDEANYYC**AAFDDSL NGFV**FGGGTKLTVL
SARS-CoV-2 S2X47-v8 mAb CDRL3 (aa)	195	**AAFDDSLNGFV**
SARS-CoV-2 S2X47-v9 mAb VL (aa)	196	QTVVTQPPSASGTPGQRVTISCSGS**SSNIGSDT** VNWYLQLPGTAPKLLIY**TNN**QRPSGVPDRFS GSKSGTSASLAISGLQSEDEANYYC**AAFDDSL NGWV**FGGGTKLTVL
SARS-CoV-2 S2X47-v9 mAb CDRL3 (aa)	197	**AAFDDSLNGWV**
SARS-CoV-2 S2H30-v1 mAb VH (aa)	198	EVHLVESGGGLVQPGGSLRLSCAAS**GFIVSSN Y**MSWVRQAPGKGLEWVSV**IYSGGST**FYADS VKGRFTISRDNSKNTVYLQMNSLRVEDTAVY YC**ARDMGGQPGGYFDY**WGQGTLVTVSS
SARS-CoV-2 S2H30-v1 mAb CDRH1 (aa)	199	**GFIVSSNY**
SARS-CoV-2 S2H30-v1 mAb CDRH2 (aa)	200	**IYSGGST**
SARS-CoV-2 S2H30-v1 mAb CDRH3 (aa)	201	**ARDMGGQPGGYFDY**
SARS-CoV-2	202	DIVMTQSPSTLSASVGDRVTITCRAS**QSFSSW**

Sequence Description	SEQ ID NO.	Sequence
S2H30-v1 mAb VL (aa)		LAWYQQKPGKAPKLLIY**KAS**NLESGVPSRFS GSGSGTEFTLTISSLQPDDFATYYC**QQYNTYA T**FGQGTKVEIK
SARS-CoV-2 S2H30-v1 mAb CDRL1 (aa)	203	**QSFSSW**
SARS-CoV-2 S2H30-v1 mAb CDRL2 (aa)	204	**KAS**
SARS-CoV-2 S2H30-v1 mAb CDRL3 (aa)	205	**QQYNTYAT**
SARS-CoV-2 S2H30-v1 mAb VH (nt)	206	GAGGTGCATCTGGTGGAGTCTGGGGGAGGC TTGGTCCAGCCTGGGGGGTCCCTGAGACTC TCCTGTGCAGCCTCT**GGATTCATCGTCAGT AGCAACTAC**ATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGGAGTGGGTCTCAGT T**ATTTATAGCGGTGGTAGTACA**TTCTACG CAGACTCCGTGAAGGGCAGATTCACCATCT CCAGAGACAATTCCAAGAACACGGTGTATC TTCAAATGAACAGCCTGAGAGTCGAGGACA CGGCTGTGTATTACTGT**GCGCGGGACATG GGGGGGCAGCCTGGAGGCTACTTTGACT AC**TGGGGCCAGGGAACCCTGGTCACCGTCT CCTCAG
SARS-CoV-2 S2H30-v1 mAb VL (nt)	207	GACATCGTGATGACCCAGTCTCCTTCCACC CTGTCTGCATCTGTAGGAGACAGAGTCACC ATCACTTGCCGGGCCAGT**CAGAGTTTTAGT AGCTGG**TTGGCCTGGTATCAGCAGAAACC AGGGAAGGCCCCTAAGCTCCTGATCTAT**AA GGCATCT**AATTTAGAAAGTGGGGTCCCATC AAGGTTCAGCGGCAGTGGATCTGGGACAGA ATTCACTCTCACTATCAGCAGCCTGCAGCCT GATGATTTTGCAACTTATTACTGC**CAACAG TATAATACTTATGCGACG**TTCGGCCAAGG GACCAAGGTGGAAATCAAGC

Sequence Description	SEQ ID NO.	Sequence
SARS-CoV-2 S2H37-v1 mAb VH (aa)	208	EVQLVESGGGLVQPGGSLRLSCAAS**GLTVSS NY**MSWVRQAPGKGLEWVSL**IYSGGTT**YYA DSVKGRFTISRDNSKNTLYLQMNSLRTEDTA VYYC**ARDPPHRSGGV**WGQGTLVTVSS
SARS-CoV-2 S2H37-v1 mAb CDRH1 (aa)	209	**GLTVSSNY**
SARS-CoV-2 S2H37-v1 mAb CDRH2 (aa)	210	**IYSGGTT**
SARS-CoV-2 S2H37-v1 mAb CDRH3 (aa)	211	**ARDPPHRSGGV**
SARS-CoV-2 S2H37-v1 mAb VL (aa)	212	AIWMTQSPSSLSASVGDRVTITCQAS**QDINNY** LNWYQQKPGKAPKLLIY**DAS**NLETGVPSRFS GSGSGTYFTFTISSLQPEDIATYYC**QQSDNLPI T**FGQGTRLEIK
SARS-CoV-2 S2H37-v1 mAb CDRL1 (aa)	213	**QDINNY**
SARS-CoV-2 S2H37-v1 mAb CDRL2 (aa)	214	**DAS**
SARS-CoV-2 S2H37-v1 mAb CDRL3 (aa)	215	**QQSDNLPIT**
SARS-CoV-2 S2H37-v1 mAb VH (nt)	216	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGT TTGGTCCAGCCTGGGGGGTCCCTGAGACTC TCCTGTGCAGCCTCT**GGATTGACCGTCAGT AGCAACTAC**ATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGGAGTGGGTCTCACT T**ATTTATAGCGGTGGTACCACA**TACTACG CAGACTCCGTGAAGGGCCGATTCACCATCT

Sequence Description	SEQ ID NO.	Sequence
		CCAGAGACAATTCCAAGAACACACTATATC TTCAAATGAACAGCCTGAGAACTGAGGACA CGGCTGTGTATTACTGT**GCGAGAGACCCT CCCCACCGCAGTGGCGGGGTC**TGGGGCC AGGGAACCCTGGTCACCGTCTCCTCAG
SARS-CoV-2 S2H37-v1 mAb VL (nt)	217	GCCATCTGGATGACCCAGTCTCCATCCTCCC TGTCTGCATCTGTAGGAGACAGAGTCACCA TCACTTGCCAGGCGAGT**CAGGACATTAAC AACTAT**TTAAATTGGTATCAGCAGAAACCA GGGAAAGCCCCTAAACTCCTGATCTAC**GAT GCATCC**AATTTGGAAACAGGGGTCCCATCA AGGTTCAGTGGAAGTGGATCTGGGACATAT TTTACTTTCACCATCAGCAGCCTGCAGCCTG AAGATATTGCAACATATTACTGT**CAACAGT CTGATAATCTCCCGATCACA**TTCGGCCAA GGGACACGACTGGAGATTAAAC
SARS-CoV-2 S2H40-v1 mAb VH (aa)	218	EVQLVQSGAEVKKPGASVKVSCKAS**GYTFT GYY**MHWVRQAPGQGLEWMGW**INPISGAT**N YAQKFQGRVTMTRDTSISTAYMELSRLRSDD TAVYYC**ARVASSGWYELEILYGVDV**WGQG TTVTVSS
SARS-CoV-2 S2H40-v1 mAb CDRH1 (aa)	219	**GYTFTGYY**
SARS-CoV-2 S2H40-v1 mAb CDRH2 (aa)	220	**INPISGAT**
SARS-CoV-2 S2H40-v1 mAb CDRH3 (aa)	221	**ARVASSGWYELEILYGVDV**
SARS-CoV-2 S2H40-v1 mAb VL (aa)	222	QSVLTQPASVSGSPGQSITISCTGT**SSDVGGY NY**VSWYQQHPGKAPKLMIY**EVS**NRPSGVSN RFSGSKSGNTASLTISGLQAEDEADYYC**SSYT SSTQV**FGTGTKVTVL
SARS-CoV-2 S2H40-v1	223	**SSDVGGYNY**

Sequence Description	SEQ ID NO.	Sequence
mAb CDRL1 (aa)		
SARS-CoV-2 S2H40-v1 mAb CDRL2 (aa)	224	**EVS**
SARS-CoV-2 S2H40-v1 mAb CDRL3 (aa)	225	**SSYTSSSTQV**
SARS-CoV-2 S2H40-v1 mAb VH (nt)	226	GAGGTGCAGCTGGTGCAGTCTGGGGCTGAG GTGAAGAAGCCTGGGGCCTCAGTGAAGGTC TCCTGCAAGGCTTCT**GGATACACCTTCACC GGCTACTAT**ATGCACTGGGTGCGACAGGC CCCTGGACAGGGGCTTGAGTGGATGGGATG G**ATCAACCCTATCAGTGGTGCCACA**AACT ATGCACAGAAGTTTCAGGGCAGGGTCACCA TGACCAGGGACACGTCCATCAGCACAGCCT ACATGGAGCTGAGCAGGCTGAGATCTGACG ACACGGCCGTGTATTACTGT**GCGAGAGTA GCTAGCAGTGGCTGGTATGAACTGGAAA TTCTCTACGGTGTGGACGTC**TGGGGCCAA GGGACCACGGTCACCGTCTCCTCA
SARS-CoV-2 S2H40-v1 mAb VL (nt)	227	CAGTCTGTGCTGACTCAGCCTGCCTCCGTGT CTGGGTCTCCTGGACAGTCGATCACCATCT CCTGCACTGGAACC**AGCAGTGACGTTGGT GGTTATAACTAT**GTCTCCTGGTACCAACAG CACCCAGGCAAAGCCCCCAAACTCATGATT TAT**GAGGTCAGT**AATCGGCCCTCAGGGGTT TCTAATCGCTTCTCTGGCTCCAAGTCTGGCA ACACGGCCTCCCTGACCATCTCTGGGCTCC AGGCTGAGGACGAGGCTGATTATTACTGC**A GCTCATATACAAGCAGCAGCACTCAGGT C**TTCGGAACTGGGACCAAGGTCACCGTCCT AG
SARS-CoV-2 S2H58-v1 mAb VH (aa)	228	EVQLVQSGAEVKKPGASVKVSCKAS**GYTFT GYY**IHWVRQAPGQGLEWMGW**INPNSGGT**N FAQKFQGRVTMTRATSFSTAYMELSSLRSDD TAVYYC**ASSGYLGYYYYGMDV**WGQGTTVT VSS

Sequence Description	SEQ ID NO.	Sequence
SARS-CoV-2 S2H58-v1 mAb CDRH1 (aa)	229	**GYTFTGYY**
SARS-CoV-2 S2H58-v1 mAb CDRH2 (aa)	230	**INPNSGGT**
SARS-CoV-2 S2H58-v1 mAb CDRH3 (aa)	231	**ASSGYLGYYYYGMDV**
SARS-CoV-2 S2H58-v1 mAb VL (aa)	232	AIWMTQSPLSLPVTPGEPASISCRSS**QSLLHSN VYNY**LDWYLQKPGQSPQLLIY**LGS**NRASGVP DRFSGSGSGTDFTLKISRVEAEDVGVYYC**MQ ALQTPHT**FGQGTKLEIK
SARS-CoV-2 S2H58-v1 mAb CDRL1 (aa)	233	**QSLLHSNVYNY**
SARS-CoV-2 S2H58-v1 mAb CDRL2 (aa)	234	**LGS**
SARS-CoV-2 S2H58-v1 mAb CDRL3 (aa)	235	**MQALQTPHT**
SARS-CoV-2 S2H58-v1 mAb VH (nt)	236	GAGGTGCAGCTGGTGCAGTCTGGGGCTGAG GTGAAGAAGCCTGGGGCCTCAGTGAAGGTC TCCTGCAAGGCTTCT**GGATACACCTTCACC GGCTACTAT**ATACACTGGGTGCGACAGGC CCCTGGACAAGGGCTTGAGTGGATGGGATG G**ATCAACCCTAACAGTGGTGGCACA**AACT TTGCACAGAAGTTTCAGGGCAGGGTCACCA TGACCAGGGCCACGTCCTTCAGCACAGCCT ACATGGAGCTGAGCAGTCTGAGATCTGACG ACACGGCCGTGTATTACTGT**GCGAGTAGT GGTTACCTCGGTTATTACTACTACGGTAT GGACGTC**TGGGGCCAAGGGACCACGGTCA CCGTCTCCTCA

Sequence Description	SEQ ID NO.	Sequence
SARS-CoV-2 S2H58-v1 mAb VL (nt)	237	GCCATCTGGATGACCCAGTCTCCACTCTCCC TGCCCGTCACCCCTGGAGAGCCGGCCTCCA TCTCCTGCAGGTCTAGT**CAGAGCCTCCTGC ATAGTAATGTATACAACTAT**TTGGATTGGT ACCTGCAGAAGCCAGGGCAGTCTCCACAGC TCCTGATCTAT**TTGGGTTCT**AATCGGGCCT CCGGGGTCCCTGACAGGTTCAGTGGCAGTG GATCAGGCACAGATTTTACACTGAAAATCA GCAGAGTGGAGGCTGAGGATGTTGGGGTTT ATTACTGC**ATGCAAGCTCTACAAACTCCT CACACT**TTTGGCCAGGGGACCAAGCTGGA GATCAAAC
SARS-CoV-2 S2H58-v2 mAb VL (aa)	238	DIVMTQTPLSLPVTPGEPASISCRSS**QSLLHSN VYNY**LDWYLQKPGQSPQLLIY**LGS**NRASGVP DRFSGSGSGTDFTLKISRVEAEDVGVYYC**MQ ALQTPHT**FGQGTKLEIK
SARS-CoV-2 S2H58-v2 mAb VL (nt)	239	GATATTGTGATGACCCAGACTCCACTCTCC CTGCCCGTCACCCCTGGAGAGCCGGCCTCC ATCTCCTGCAGGTCTAGT**CAGAGCCTCCTG CATAGTAATGTATACAACTAT**TTGGATTG GTACCTGCAGAAGCCAGGGCAGTCTCCACA GCTCCTGATCTAT**TTGGGTTCT**AATCGGGC CTCCGGGGTCCCTGACAGGTTCAGTGGCAG TGGATCAGGCACAGATTTTACACTGAAAAT CAGCAGAGTGGAGGCTGAGGATGTTGGGGT TTATTACTGC**ATGCAAGCTCTACAAACTC CTCACACT**TTTGGCCAGGGGACCAAGCTGG AGATCAAAC
SARS-CoV-2 S2H62-v1 mAb VH (aa)	240	EVHLVESGGGLVQPGGSLRLSCAAS**VITVSSN Y**MSWVRQAPGKGLEWVSL**IYSGGST**YYADS VKGRFTISRDNFKNTLYLQMNSLRAEDTAVY YC**ARDLDIAGGMDV**WGQGTTVTVSS
SARS-CoV-2 S2H62-v1 mAb CDRH1 (aa)	241	**VITVSSNY**
SARS-CoV-2 S2H62-v1 mAb CDRH2	242	**IYSGGST**

Sequence Description	SEQ ID NO.	Sequence
(aa)		
SARS-CoV-2 S2H62-v1 mAb CDRH3 (aa)	243	**ARDLDIAGGMDV**
SARS-CoV-2 S2H62-v1 mAb VL (aa)	244	DIVMTQTPSSLSASVGDRVTITCRAG**QTISNY** LNWYQQKPGKAPKLLIY**AAS**SLQSGVPSRFS GSGSGTDFTLTISSLQPEDFATYYC**QQSYSTP YT**FGQGTKLEIK
SARS-CoV-2 S2H62-v1 mAb CDRL1 (aa)	245	**QTISNY**
SARS-CoV-2 S2H62-v1 mAb CDRL2 (aa)	246	**AAS**
SARS-CoV-2 S2H62-v1 mAb CDRL3 (aa)	247	**QQSYSTPYT**
SARS-CoV-2 S2H62-v1 mAb VH (nt)	248	GAGGTGCATCTGGTGGAGTCTGGGGGAGGC TTGGTCCAGCCTGGGGGGTCCCTGAGACTC TCCTGTGCAGCCTCT**GTAATCACCGTCAGT AGCAACTAC**ATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGGAGTGGGTCTCACT T**ATTTATAGCGGTGGTAGCACA**TACTACG CAGACTCCGTGAAGGGCCGATTCACCATCT CCAGAGACAATTTCAAGAACACGCTGTATC TTCAAATGAACAGCCTGAGAGCTGAGGACA CGGCTGTGTATTACTGT**GCGAGAGATCTG GATATAGCAGGCGGTATGGACGTC**TGGG GCCAAGGGACCACGGTCACCGTCTCCTCA
SARS-CoV-2 S2H62-v1 mAb VL (nt)	249	gatattgtgatgacccagactccatcctccctgtctgcatctgtaggaga cagagtcaccatcacttgccgggcaggt**cagaccattagcaactat**tt aaattggtatcagcagaaaccagggaaagcccctaagctcctgatctat **gctgcatcc**agtttgcaaagtggggtcccatcaaggttcagtggcagtg gatctgggacagatttcactctcaccatcagcagtctgcaacctgaagat tttgcaacttactactgt**caacagagttacagtaccccgtacact**tttgg ccaggggaccaagctggagatcaaac

Sequence Description	SEQ ID NO.	Sequence
SARS-CoV-2 S2H62-v2 mAb VL (aa)	250	DIGMTQTPSSLSASVGDRVTITCRAG**QTISNY** LNWYQQKPGKAPKLLIY**AAS**SLQSGVPSRFS GSGSGTDFTLTISSLQPEDFATYYC**QQSYSTP YT**FGQGTKLEIK
SARS-CoV-2 S2H62-v2 mAb VL (nt)	251	gatattgggatgacccagactccatcctccctgtctgcatctgtaggaga cagagtcaccatcacttgccgggcaggtcagaccattagcaactattta aattggtatcagcagaaaccagggaaagcccctaagctcctgatctatg ctgcatccagtttgcaaagtggggtcccatcaaggttcagtggcagtgg atctgggacagatttcactctcaccatcagcagtctgcaacctgaagattt tgcaacttactactgtcaacagagttacagtaccccgtacacttttggcca ggggaccaagctggagatcaaac
SARS-CoV-2 S2H62-v3 mAb VL (aa)	252	DIQLTQSPSSLSASVGDRVTITCRAG**QTISNY**L NWYQQKPGKAPKLLIY**AAS**SLQSGVPSRFSG SGSGTDFTLTISSLQPEDFATYYC**QQSYSTPY TF**GQGTKLEIK
SARS-CoV-2 S2H62-v3 mAb VL (nt)	253	gacatccagttgacccagtctccatcctccctgtctgcatctgtaggaga cagagtcaccatcacttgccgggcaggt**cagaccattagcaactat**tt aaattggtatcagcagaaaccagggaaagcccctaagctcctgatctat **gctgcatcc**agtttgcaaagtggggtcccatcaaggttcagtggcagtg gatctgggacagatttcactctcaccatcagcagtctgcaacctgaagat tttgcaacttactactgt**caacagagttacagtaccccgtacact**tttgg ccaggggaccaagctggagatcaaa
SARS-CoV-2 S2H66-v1 mAb VH (aa)	254	EVQLQESGPGLVKPSETLSLTCSVS**GGSISSY YW**SWIRQPPGKALEWIGY**IYYSGST**NYNSSL KSRVTISLDTSKNQFSLKLSSVAAADTAVYYC **ARHDPFRAVTGHFDY**WGQGTLVTVSS
SARS-CoV-2 S2H66-v1 mAb CDRH1 (aa)	255	**GGSISSYY**
SARS-CoV-2 S2H66-v1 mAb CDRH2 (aa)	256	**IYYSGST**
SARS-CoV-2 S2H66-v1 mAb CDRH3 (aa)	257	**ARHDPFRAVTGHFDY**
SARS-CoV-2	258	QTVLTQPHSVSESPGKTVTISCTRS**SGSIASNY**

Sequence Description	SEQ ID NO.	Sequence
S2H66-v1 mAb VL (aa)		VQWYQQRPGSSPTIVIY**EDS**RRPSGVPDRFSG SIDSSSNSASLSISRLKTEDEADYYC**QSYYRN TVV**FGGGTKLTVL
SARS-CoV-2 S2H66-v1 mAb CDRL1 (aa)	259	**SGSIASNY**
SARS-CoV-2 S2H66-v1 mAb CDRL2 (aa)	260	**EDS**
SARS-CoV-2 S2H66-v1 mAb CDRL3 (aa)	261	**QSYYRNTVV**
SARS-CoV-2 S2H66-v1 mAb VH (nt)	262	GAGGTGCAGCTGCAGGAGTCGGGCCCAGG ACTGGTGAAGCCTTCGGAGACCCTGTCCCT CACCTGCTCTGTCTCT**GGTGGCTCCATCAG TAGTTACTAC**TGGAGCTGGATCCGGCAGCC CCCAGGGAAGGCACTGGAGTGGATTGGATA T**ATCTATTACAGTGGGAGCACC**AACTACA ATTCATCCCTCAAGAGTCGAGTCACCATAT CACTAGACACGTCCAAGAACCAGTTCTCCC TGAAGCTGAGCTCTGTGGCCGCCGCAGACA CGGCCGTGTATTACTGT**GCGAGACATGAC CCTTTCAGGGCAGTGACTGGGCACTTTG ACTAC**TGGGGCCAGGGAACCCTGGTCACCG TCTCCTCAG
SARS-CoV-2 S2H66-v1 mAb VL (nt)	263	cagactgtgctgactcagccccactctgtgtcggagtctccggggaag acggtaaccatctcctgcacccgcagc**agtggcagcattgccagcaa ctat**gtgcagtggtaccaacagcgcccgggcagttccccaccattgt gatctat**gaggatagc**cgaagaccctctggggtccctgatcggttctct ggctccatcgacagctcctccaactctgcctccctcagcatctctagact gaagactgaggacgaggctgactactactgt**cagtcttattatagaaa cactgtggta**ttcggcggagggaccaagctgaccgtcctag
SARS-CoV-2 S2H70-v1 mAb VH (aa)	264	EVQLVQSGAEVKKPGASVKVSCKAS**GYTFT GYY**LHWVRQAPGQGLEWMGW**INPISGGT**N YAQKFQGRVTMTRDTSISTAYMELSRLRSDD TAVYYC**ARVDYDILTGYYWGWFDP**WGQG TLVTVSS

Sequence Description	SEQ ID NO.	Sequence
SARS-CoV-2 S2H70-v1 mAb CDRH1 (aa)	265	**GYTFTGYY**
SARS-CoV-2 S2H70-v1 mAb CDRH2 (aa)	266	**INPISGGT**
SARS-CoV-2 S2H70-v1 mAb CDRH3 (aa)	267	**ARVDYDILTGYYWGWFDP**
SARS-CoV-2 S2H70-v1 mAb VL (aa)	268	QTVVTQPASVSGSPGQSITISCTGT**SSDVGGY NY**VSWYQQHPGKAPKLMIY**DVS**NRPSGVSN RFSGSKSGNTASLTISGLQAEDEADYYC**SSYT SSSTYV**FGTGTKVTVL
SARS-CoV-2 S2H70-v1 mAb CDRL1 (aa)	269	**SSDVGGYNY**
SARS-CoV-2 S2H70-v1 mAb CDRL2 (aa)	270	**DVS**
SARS-CoV-2 S2H70-v1 mAb CDRL3 (aa)	271	**SSYTSSSTYV**
SARS-CoV-2 S2H70-v1 mAb VH (nt)	272	GAGGTGCAGCTGGTGCAGTCTGGGGCTGAG GTGAAGAAGCCTGGGGCCTCAGTGAAGGTC TCCTGCAAGGCTTCT**GGATACACCTTCACC GGCTACTAT**CTGCACTGGGTGCGACAGGC CCCTGGACAAGGGCTTGAGTGGATGGGATG G**ATCAACCCTATCAGTGGTGGCACA**AACT ATGCACAGAAGTTTCAGGGCAGGGTCACCA TGACCAGGGACACGTCCATCAGCACAGCCT ACATGGAGCTGAGCAGGCTGAGATCTGACG ACACGGCCGTGTATTACTGT**GCGAGAGTG GATTACGATATTTTGACTGGTTATTACTG GGGCTGGTTCGACCCC**TGGGGCCAGGGA

Sequence Description	SEQ ID NO.	Sequence
		ACCCTGGTCACCGTCTCCTCAG
SARS-CoV-2 S2H70-v1 mAb VL (nt)	273	CAGACTGTGGTGACTCAGCCTGCCTCCGTG TCTGGGTCTCCTGGACAGTCGATCACCATCT CCTGCACTGGAACC**AGCAGTGACGTTGGT GGTTATAACTAT**GTCTCCTGGTACCAACAG CACCCAGGCAAAGCCCCCAAACTCATGATT TAT**GATGTCAGT**AATCGGCCCTCAGGGGTT TCTAATCGCTTCTCTGGCTCCAAGTCTGGCA ACACGGCCTCCCTGACCATCTCTGGGCTCC AGGCTGAGGACGAGGCTGATTATTACTGC**A GCTCATATACAAGCAGCAGCACTTATGTC** TTCGGAACTGGGACCAAGGTCACCGTCCTA G
SARS-CoV-2 S2H71-v1 mAb VH (aa)	274	QITLKESGPTLVKPTQTLTLTCTFS**GFSLSTGG VG**VGWIRQPPGKALEWLAL**IYWDDDK**RYSP SLKSRLTITKDTSKNQVVLTMTNVDPVDTAT YYC**ARHTVTRIFDY**WGQGTLVTVSS
SARS-CoV-2 S2H71-v1 mAb CDRH1 (aa)	275	**GFSLSTGGVG**
SARS-CoV-2 S2H71-v1 mAb CDRH2 (aa)	276	**IYWDDDK**
SARS-CoV-2 S2H71-v1 mAb CDRH3 (aa)	277	**ARHTVTRIFDY**
SARS-CoV-2 S2H71-v1 mAb VL (aa)	278	QSVLTQPASVSGSPGQSITISCTGT**SSDVGGFL Y**VSWYQQLPGKAPKLMIY**EVS**DRPSGVSNRF SGSKSGNTASLTISGLQAEDEADYYC**SSYTTS STV**FGGGTKLTVL
SARS-CoV-2 S2H71-v1 mAb CDRL1 (aa)	279	**SSDVGGFLY**
SARS-CoV-2 S2H71-v1	280	**EVS**

Sequence Description	SEQ ID NO.	Sequence
mAb CDRL2 (aa)		
SARS-CoV-2 S2H71-v1 mAb CDRL3 (aa)	281	**SSYTTSSTV**
SARS-CoV-2 S2H71-v1 mAb VH (nt)	282	CAGATCACCTTGAAGGAGTCTGGTCCTACG CTGGTGAAACCCACACAGACCCTCACGCTG ACCTGCACCTTCTCT**GGGTTCTCACTCAGC ACTGGTGGAGTGGGT**GTGGGCTGGATCCG TCAGCCCCCAGGAAAGGCCCTGGAGTGGCT TGCACTC**ATTTATTGGGATGATGATAAG**C GCTACAGCCCATCTCTGAAGAGCAGGCTCA CCATCACCAAGGACACTTCCAAAAACCAGG TGGTCCTTACAATGACCAACGTGGACCCTG TGGACACAGCCACATATTACTGT**GCACGCC ATACGGTGACTAGGATATTTGACTAC**TGG GGCCAGGGAACCCTGGTCACCGTCTCCTCA G
SARS-CoV-2 S2H71-v1 mAb VL (nt)	283	CAGTCTGTGCTGACTCAGCCTGCCTCCGTGT CTGGGTCTCCTGGACAGTCGATCACCATCT CCTGCACTGGAACC**AGCAGTGACGTTGGT GGTTTTCTCTAT**GTCTCCTGGTACCAACAA CTCCCAGGCAAAGCCCCCAAACTCATGATT TAT**GAGGTCAGT**GATCGGCCCTCAGGGGTT TCTAATCGCTTCTCTGGCTCCAAGTCTGGCA ACACGGCCTCCCTGACCATCTCTGGGCTCC AGGCTGAGGACGAGGCTGATTATTACTGC**A GCTCATATACAACCAGCAGCACGGTG**TTC GGCGGAGGGACCAAGTTGACCGTCCTAG
SARS-CoV-2 S2H73-v1 mAb VH (aa)	284	QVQLVQSGAEVKKPGASVKVSCKAS**GYTFT GYY**IHWVRQAPGQGLEWMGW**INPNSGGT**N YAQKFQGRVTMTRDTSISTAYMELSRLRSDD TAVYYC**ARELLVPGAMSPYGMDV**WGQGTT VTVSS
SARS-CoV-2 S2H73-v1 mAb CDRH1 (aa)	285	**GYTFTGYY**
SARS-CoV-2	286	**INPNSGGT**

Sequence Description	SEQ ID NO.	Sequence
S2H73-v1 mAb CDRH2 (aa)		
SARS-CoV-2 S2H73-v1 mAb CDRH3 (aa)	287	**ARELLVPGAMSPYGMDV**
SARS-CoV-2 S2H73-v1 mAb VL (aa)	288	EIVMTQSPATLSLSPGERATLSCRAS**QSVSRY** LAWYQQKPGQAPRLLIY**DAS**NRAAGIPARFS GSGSGTDFTLTISSLEPEDFVVYYC**QQRSNWP PLA**FGGGTKVEIK
SARS-CoV-2 S2H73-v1 mAb CDRL1 (aa)	289	**QSVSRY**
SARS-CoV-2 S2H73-v1 mAb CDRL2 (aa)	290	**DAS**
SARS-CoV-2 S2H73-v1 mAb CDRL3 (aa)	291	**QQRSNWPPLA**
SARS-CoV-2 S2H73-v1 mAb VH (nt)	292	CAGGTCCAGCTGGTGCAGTCTGGGGCTGAG GTGAAGAAGCCTGGGGCCTCAGTGAAGGTC TCCTGCAAGGCTTCT**GGATACACCTTCACC GGCTACTAT**ATACACTGGGTGCGACAGGC CCCTGGACAAGGGCTTGAGTGGATGGGATG G**ATCAACCCTAACAGTGGTGGCACA**AACT ATGCACAGAAGTTTCAGGGCAGGGTCACCA TGACCAGGGACACGTCCATCAGCACAGCCT ACATGGAGCTGAGCAGGCTGAGATCTGACG ACACGGCCGTGTATTACTGT**GCGAGGGAA TTATTAGTACCAGGTGCTATGTCCCCTTA CGGTATGGACGTC**TGGGGCCAAGGGACCA CGGTCACCGTCTCCTCA
SARS-CoV-2 S2H73-v1 mAb VL (nt)	293	GAAATAGTGATGACGCAGTCTCCAGCCACC CTGTCTTTGTCTCCAGGGGAAAGAGCCACC CTCTCCTGCAGGGCCAGT**CAGAGTGTTAG CAGGTAC**TTAGCCTGGTACCAACAGAAAC CTGGCCAGGCTCCCAGGCTCCTCATCTAT**G**

Sequence Description	SEQ ID NO.	Sequence
		ATGCATCCAACAGGGCCGCTGGCATCCCA GCCAGGTTCAGTGGCAGTGGGTCTGGGACA GACTTCACTCTCACCATCAGCAGCCTAGAG CCTGAAGATTTTGTAGTTTATTACTGT**CAGC AGCGTAGCAACTGGCCTCCGCTCGCT**TTC GGCGGAGGGACCAAGGTGGAGATCAAAC
SARS-CoV-2 S2H66-v2 mAb VL (aa)	294	SYELTQPHSVSESPGKTVTISCTRS**SGSIASNY** VQWYQQRPGSSPTIVIY**EDS**RRPSGVPDRFSG SIDSSSNSASLSISRLKTEDEADYYC**QSYYRN TVV**FGGGTKLTVL
SARS-CoV-2 S2H66-v2 mAb VL (nt)	295	tcctatgagctgacacagccccactctgtgtcggagtctccggggaag acggtaaccatctcctgcacccgcagcagtggcagcattgccagcaac tatgtgcagtggtaccaacagcgcccgggcagttcccccaccattgtga tctatgaggatagccgaagaccctctggggtccctgatcggttctctgg ctccatcgacagctcctccaactctgcctccctcagcatctctagactga agactgaggacgaggctgactactactgtcagtcttattatagaaacact gtggtattcggcggagggaccaagctgaccgtccta
SARS-CoV-2 S2H66-v3 mAb VL (aa)	296	QPVLTQPHSVSESPGKTVTISCTRS**SGSIASNY** VQWYQQRPGSSPTIVIY**EDS**RRPSGVPDRFSG SIDSSSNSASLSISRLKTEDEADYYC**QSYYRN TVV**FGGGTKLTVL
SARS-CoV-2 S2H66-v3 mAb VL (nt)	297	Cagcctgtgctgactcagccccactctgtgtcggagtctccggggaag acggtaaccatctcctgcacccgcagcagtggcagcattgccagcaac tatgtgcagtggtaccaacagcgcccgggcagttcccccaccattgtga tctatgaggatagccgaagaccctctggggtccctgatcggttctctgg ctccatcgacagctcctccaactctgcctccctcagcatctctagactga agactgaggacgaggctgactactactgtcagtcttattatagaaacact gtggtattcggcggagggaccaagctgaccgtccta
SARS-CoV-2 S2N12-v1 mAb VH (aa)	298	QVRLQESGPGLVKPSETLSLTCTVS**GGSISSST YF**WGWIRQPPGKGLEWIGS**ISYSGST**YYNPSL KSRVTISVDTSKSQFSLKLSSVTAADTAVYYC **ARRGGYCSRVNCYNRYWYFDL**WGRGTLVT VSS
SARS-CoV-2 S2N12-v1 mAb CDRH1 (aa)	299	**GGSISSSTYF**
SARS-CoV-2	300	**ISYSGST**

Sequence Description	SEQ ID NO.	Sequence
S2N12-v1 mAb CDRH2 (aa)		
SARS-CoV-2 S2N12-v1 mAb CDRH3 (aa)	301	**ARRGGYCSRVNCYNRYWYFDL**
SARS-CoV-2 S2N12-v1 mAb VL (aa)	302	DIQLTQSPSSVSASVGDRVTVSCRAS**QDISSW** LAWYQQKPGKAPKLLIY**AAS**SLQSGVPSRFS GSGSGTDFTLTISSLQPEDFATYFC**QQANSFP VT**FGPGTKVDIK
SARS-CoV-2 S2N12-v1 mAb CDRL1 (aa)	303	**QDISSW**
SARS-CoV-2 S2N12-v1 mAb CDRL2 (aa)	304	**AAS**
SARS-CoV-2 S2N12-v1 mAb CDRL3 (aa)	305	**QQANSFPVT**
SARS-CoV-2 S2N12-v1 mAb VH (nt)	306	CAGGTGCGGCTGCAGGAGTCGGGCCCAGG ACTGGTGAAGCCTTCGGAGACCCTGTCCCT CACCTGCACTGTCTCT**GGTGGCTCCATCAG CAGTAGTACTTACTTC**TGGGGCTGGATCC GCCAGCCCCCAGGGAAGGGGCTGGAGTGG ATTGGGAGT**ATCTCTTATAGTGGGAGCAC C**TACTACAACCCGTCCCTCAAGAGTCGAGT CACCATATCCGTTGACACGTCCAAGAGCCA GTTCTCCCTGAAGCTGAGCTCTGTGACCGC CGCAGACACGGCTGTGTATTACTGT**GCGAG ACGGGGGGGATATTGTAGTCGTGTTAAC TGCTACAATCGCTACTGGTACTTCGATCT C**TGGGGCCGTGGCACCCTGGTCACTGTCTC CTCAG
SARS-CoV-2 S2N12-v1 mAb VL (nt)	307	GACATCCAGTTGACGCAGTCTCCATCTTCTG TGTCTGCATCTGTAGGAGACAGAGTCACCG TCAGTTGTCGGGCGAGT**CAGGATATTAGC AGCTGG**TTAGCCTGGTATCAGCAGAAACC

Sequence Description	SEQ ID NO.	Sequence
		AGGGAAAGCCCCTAAGCTCCTGATCTAT**GC TGCATCC**AGTTTGCAAAGTGGGGTCCCATC AAGGTTCAGCGGCAGTGGATCTGGGACAGA TTTCACTCTCACTATCAGCAGCCTGCAGCCT GAAGATTTTGCAACTTACTTTTGTCAACAG GCTAACAGTTTCCCTGTCACTTTCGGCCCTG GGACCAAAGTGGATATCAAAC
SARS-CoV-2 S2N12-v2 mAb VL (aa)	308	DIVMTQSPSSVSASVGDRVTVSCRAS**QDISSW** LAWYQQKPGKAPKLLIY**AAS**SLQSGVPSRFS GSGSGTDFTLTISSLQPEDFATYFC**QQANSFP VT**FGPGTKVDIK
SARS-CoV-2 S2N12-v2 mAb VL (nt)	309	GACATCGTGATGACCCAGTCTCCATCTTCTG TGTCTGCATCTGTAGGAGACAGAGTCACCG TCAGTTGTCGGGCGAGT**CAGGATATTAGC AGCTGG**TTAGCCTGGTATCAGCAGAAACC AGGGAAAGCCCCTAAGCTCCTGATCTAT**GC TGCATCC**AGTTTGCAAAGTGGGGTCCCATC AAGGTTCAGCGGCAGTGGATCTGGGACAGA TTTCACTCTCACTATCAGCAGCCTGCAGCCT GAAGATTTTGCAACTTACTTTTGT**CAACAG GCTAACAGTTTCCCTGTCACT**TTCGGCCC TGGGACCAAAGTGGATATCAAAC
SARS-CoV-2 S2N12-v3 mAb VL (aa)	310	NIQMTQSPSSVSASVGDRVTVSCRAS**QDISSW** LAWYQQKPGKAPKLLIY**AAS**SLQSGVPSRFS GSGSGTDFTLTISSLQPEDFATYFC**QQANSFP VT**FGPGTKVDIK
SARS-CoV-2 S2N12-v3 mAb VL (nt)	311	AACATCCAGATGACCCAGTCTCCATCTTCT GTGTCTGCATCTGTAGGAGACAGAGTCACC GTCAGTTGTCGGGCGAGT**CAGGATATTAG CAGCTGG**TTAGCCTGGTATCAGCAGAAAC CAGGGAAAGCCCCTAAGCTCCTGATCTAT**G CTGCATCC**AGTTTGCAAAGTGGGGTCCCAT CAAGGTTCAGCGGCAGTGGATCTGGGACAG ATTTCACTCTCACTATCAGCAGCCTGCAGCC TGAAGATTTTGCAACTTACTTTTGT**CAACA GGCTAACAGTTTCCCTGTCACT**TTCGGCC CTGGGACCAAAGTGGATATCAAAC
SARS-CoV-2 S2N22-v1	312	EVQLVESGGGLVQPGGSLRLSCAAS**GFTFSS YP**MSWVRQAPGKGLEWVSA**ISGSGNYT**YYA DSVKGRFTISRDNSKNTLYLQMNSLRAEDTA

Sequence Description	SEQ ID NO.	Sequence
mAb VH (aa)		VYYC**AKDPGGLSNFDF**WGQGTLVTVSS
SARS-CoV-2 S2N22-v1 mAb CDRH1 (aa)	313	**GFTFSSYP**
SARS-CoV-2 S2N22-v1 mAb CDRH2 (aa)	314	**ISGSGNYT**
SARS-CoV-2 S2N22-v1 mAb CDRH3 (aa)	315	**AKDPGGLSNFDF**
SARS-CoV-2 S2N22-v1 mAb VL (aa)	316	NIQMTQSPSSLSASVGDRVTITCRAS**QSISTY**L NWFQQKPGKAPKLLIY**AAS**SLQSGVPSRFSGS GSGTDFTLTISSLQREDFATYYC**QQTYSTPRI** FGQGTKLEIK
SARS-CoV-2 S2N22-v1 mAb CDRL1 (aa)	317	**QSISTY**
SARS-CoV-2 S2N22-v1 mAb CDRL2 (aa)	318	**AAS**
SARS-CoV-2 S2N22-v1 mAb CDRL3 (aa)	319	**QQTYSTPRI**
SARS-CoV-2 S2N22-v1 mAb VH (nt)	320	GAGGTGCAGCTGGTGGAGTCTGGGGGAGG CTTGGTACAGCCTGGGGGGTCCCTGAGACT CTCCTGTGCAGCCTCT**GGATTCACCTTTAG CAGTTATCCT**ATGAGCTGGGTCCGCCAGGC TCCAGGTAAGGGGCTGGAGTGGGTCTCAGC T**ATTAGTGGTAGTGGTAATTACACA**TACT ACGCAGACTCCGTGAAGGGCCGGTTCACCA TCTCCAGAGACAATTCCAAGAACACGTTGT ATCTGCAAATGAACAGCCTGAGAGCCGAGG ACACGGCCGTATATTACTGT**GCGAAAGATC CCGGTGGGTTGTCGAACTTTGACTTC**TGG

Sequence Description	SEQ ID NO.	Sequence
		GGCCAGGGAACCCTGGTCACCGTCTCCTCA G
SARS-CoV-2 S2N22-v1 mAb VL (nt)	321	AACATCCAGATGACCCAGTCTCCATCCTCC CTGTCTGCATCTGTAGGAGACAGAGTCACC ATCACTTGCCGGGCAAGT**CAGAGCATTAG CACCTAT**TTAAATTGGTTTCAGCAGAAACC AGGGAAAGCCCCTAAGCTCCTGATCTAT**GC TGCATCC**AGTTTGCAAAGTGGGGTCCCGTC AAGGTTCAGTGGCAGTGGATCTGGGACAGA TTTCACTCTCACCATCAGCAGTCTACAACGT GAAGATTTTGCAACTTACTACTGT**CAACAG ACTTACAGTACCCCTCGAATT**TTTGGCCA GGGGACCAAGCTGGAGATCAAAC
SARS-CoV-2 S2N25-v1 mAb VH (aa)	322	QVQLQESGPGLVKPSETLSLTCTVS**GGSISSS Y**WSWIRQPPGKGLEWIGY**LYYSGST**NYNPSL KSRVTISVDTSKNQFSLKLTSVTAADTAVYYC **ARDPGPYYYDSSGYYLDAFD**IWGQGTMVTV SS
SARS-CoV-2 S2N25-v1 mAb CDRH1 (aa)	323	**GGSISSSY**
SARS-CoV-2 S2N25-v1 mAb CDRH2 (aa)	324	**LYYSGST**
SARS-CoV-2 S2N25-v1 mAb CDRH3 (aa)	325	**ARDPGPYYYDSSGYYLDAFD**
SARS-CoV-2 S2N25-v1 mAb VL (aa)	326	AIWMTQSPSSLSASVGDRVTITCRAS**QSIVSY** LNWYQQKPGKAPKLLIY**AAS**SLQSGVPSRFS GSGSGTDFTLTISSLQPEDFATYYC**QQTYNTL SLT**FGGGTKVEIK
SARS-CoV-2 S2N25-v1 mAb CDRL1 (aa)	327	**QSIVSY**

Sequence Description	SEQ ID NO.	Sequence
SARS-CoV-2 S2N25-v1 mAb CDRL2 (aa)	328	**AAS**
SARS-CoV-2 S2N25-v1 mAb CDRL3 (aa)	329	**QQTYNTLSLT**
SARS-CoV-2 S2N25-v1 mAb VH (nt)	330	CAGGTGCAGCTGCAGGAGTCGGGCCCAGG ACTGGTGAAGCCTTCGGAGACCCTGTCCCT CACCTGCACTGTCTCT**GGTGGCTCCATCAG TAGTTCCTAC**TGGAGCTGGATCCGGCAGCC CCCAGGGAAGGGACTGGAGTGGATTGGCTA T**CTCTATTACAGTGGGAGCACC**AACTACA ACCCCTCCCTCAAGAGTCGAGTCACCATAT CAGTAGACACGTCCAAGAACCAGTTCTCCC TGAAGCTGACCTCTGTGACCGCTGCGGACA CGGCCGTGTATTACTGT**GCGAGAGACCCC GGGCCGTATTACTATGATAGTAGTGGTT ATTACCTGGATGCTTTTGAT**ATCTGGGGC CAAGGGACAATGGTCACCGTCTCTTCAG
SARS-CoV-2 S2N25-v1 mAb VL (nt)	331	GCCATCTGGATGACCCAGTCTCCATCCTCCC TGTCTGCATCTGTAGGAGACAGAGTCACCA TCACTTGCCGGGCAAGT**CAGAGCATTGTC AGCTAT**TTAAATTGGTATCAGCAGAAACCA GGGAAAGCCCCTAAGCTCCTGATCTAT**GCT GCATCC**AGTTTGCAAAGTGGGGTCCCATCA AGGTTCAGTGGCAGTGGATCTGGGACAGAT TTCACTCTCACCATCAGCAGTCTGCAACCTG AAGATTTTGCAACTTACTACTGT**CAACAGA CTTACAATACCCTTTCGCTCACT**TTCGGC GGAGGGACCAAGGTGGAGATCAAAC
SARS-CoV-2 S2N28-v1 mAb VH (aa)	332	EVQLVESGGGVVQPGRSLRLSCAAS**GFTFFS YG**MHWVRQAPGKGLEWVAF**IRYDGSNK**YY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDT AVYYC**AKDSPRVTSGGYYSYYYGMDV**WG QGTTVTVSS
SARS-CoV-2 S2N28-v1 mAb CDRH1	333	**GFTFFSYG**

Sequence Description	SEQ ID NO.	Sequence
(aa)		
SARS-CoV-2 S2N28-v1 mAb CDRH2 (aa)	334	**IRYDGSNK**
SARS-CoV-2 S2N28-v1 mAb CDRH3 (aa)	335	**AKDSPRVTSGGYYSYYYGMDV**
SARS-CoV-2 S2N28-v1 mAb VL (aa)	336	DIVMTQTPSSLSASVGDRVTITCRAS**QNISSY**L NWYQQKPRKAPKLLIY**PAS**SLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYC**QQSYSTPLT** FGGGTKVEIK
SARS-CoV-2 S2N28-v1 mAb CDRL1 (aa)	337	**QNISSY**
SARS-CoV-2 S2N28-v1 mAb CDRL2 (aa)	338	**PAS**
SARS-CoV-2 S2N28-v1 mAb CDRL3 (aa)	339	**QQSYSTPLT**
SARS-CoV-2 S2N28-v1 mAb VH (nt)	340	GAGGTGCAGCTGGTGGAGTCTGGGGGAGG CGTGGTCCAGCCTGGGAGGTCCCTGAGACT CTCCTGTGCAGCGTCT**GGATTCACCTTCTT TAGCTATGGA**ATGCACTGGGTCCGCCAGG CCCCGGGCAAGGGGCTGGAGTGGGTGGCAT TT**ATACGGTATGATGGAAGTAATAAA**TAC TATGCAGACTCCGTGAAGGGCCGATTCACC ATCTCCAGAGACAATTCCAAGAACACGCTG TATCTGCAAATGAACAGCCTGAGAGCTGAG GACACAGCTGTGTATTACTGT**GCGAAAGAC TCTCCTCGGGTTACCAGTGGCGGATATT ACTCCTACTACTACGGTATGGACGTC**TGG GGCCAAGGGACCACGGTCACCGTCTCCTCA
SARS-CoV-2 S2N28-v1	341	GATATTGTGATGACCCAGACTCCATCCTCC CTGTCTGCATCTGTAGGAGACAGAGTCACC

Sequence Description	SEQ ID NO.	Sequence
mAb VL (nt)		ATCACTTGCCGGGCAAGT**CAGAACATTAG CAGTTAT**TTAAATTGGTATCAGCAGAAACC ACGGAAAGCCCCTAAACTCCTGATCTAT**CC TGCATCC**AGTTTGCAAAGTGGGGTCCCATC AAGGTTCAGTGGCAGTGGATCTGGGACAGA TTTCACTCTCACCATCAGCAGTCTGCAACCT GAAGATTTTGCAACTTACTACTGT**CAACAG AGTTACAGTACGCCGCTCACT**TTCGGCGG AGGGACCAAGGTGGAGATCAAAC
SARS-CoV-2 S309-v2 mAb VH (aa)	342	QVQLVQSGAEVKKPGASVKVSCKAS**GYPFT SYG**ISWVRQAPGQGLEWMGW**ISTYQGNT**N YAQKFQGRVTMTTDTSTTTGYMELRRLRSD DTAVYYC**ARDYTRGAWFGESLIGGFDN**WG QGTLVTVSS
SARS-CoV-2 S309-v2 mAb CDRH1 (aa)	343	**GYPFTSYG**
SARS-CoV-2 S309-v2 mAb CDRH2 (aa)	344	**ISTYQGNT**
SARS-CoV-2 S309-v2 mAb CDRH3 (aa)	345	**ARDYTRGAWFGESLIGGFDN**
SARS-CoV-2 S309-v2 mAb VL (aa)	346	EIVLTQSPGTLSLSPGERATLSCRASQTVSSTS LAWYQQKPGQAPRLLIYGASSRATGIPDRFSG SGSGTDFTLTISRLEPEDFAVYYCQQHDTSLT FGGGTKVEIK
SARS-CoV-2 S309-v2 mAb CDRL1 (aa)	347	QTVSSTS
SARS-CoV-2 S309-v2 mAb CDRL2 (aa)	348	GAS
SARS-CoV-2 S309-v2 mAb CDRL3 (aa)	349	QQHDTSLT
SARS-CoV-2 S2H58-v3 mAb VH (aa)	350	EVQLVQSGAEVKKPGASVKVSCKAS**GYTFT GYY**IHWVRQAPGQGLEWMGF**INPNSGGT**NF AQKFQGRVTMTRATSFSTAYMELSSLRSDDT AVYYC**ASSGYLGYYYYGMDV**WGQGTTVTV SS

Sequence Description	SEQ ID NO.	Sequence
SARS-CoV-2 S2H58-v4 mAb VH (aa)	351	EVQLVQSGAEVKKPGASVKVSCKAS**GYTFT GYY**IHWVRQAPGQGLEWMGF**INPNAGGT**NF AQKFQGRVTMTRATSFSTAYMELSSLRSDDT AVYYC**ASSGYLGYYYYGMDV**WGQGTTVTV SS
SARS-CoV-2 S2H58-v4 mAb CDRH2 (aa)	352	**INPNAGGT**
SARS-CoV-2 S2H58-v5 mAb VH (aa)	353	EVQLVQSGAEVKKPGASVKVSCKAS**GYTFT GYY**IHWVRQAPGQGLEWMGF**INPASGGT**NF AQKFQGRVTMTRATSFSTAYMELSSLRSDDT AVYYC**ASSGYAGYYYYGMDV**WGQGTTVTV SS
SARS-CoV-2 S2H58-v5 mAb CDRH3 (aa)	354	**ASSGYAGYYYYGMDV**
SARS-CoV-2 S2H58-v6 mAb VL (aa)	355	DIVMTQTPLSLPVTPGEPASISCRSS**QSLLHSN GYNY**LDWYLQKPGQSPQLLIY**LGS**NRASGVP DRFSGSGSGTDFTLKISRVEAEDVGVYYC**MQ ALQTPHT**FGQGTKLEIK
SARS-CoV-2 S2H58-v6 mAb CDRL1 (aa)	356	**QSLLHSNGYNY**
SARS-CoV-2 S2H58-v7 mAb VL (aa)	357	DIVMTQTPLSLPVTPGEPASISCRSS**QSLLHSN VYNY**LDWYLQKPGQSPQLLIY**LGS**NRASGVP DRFSGSGSGTDFTLKISRVEAEDVGVYYC**IQA LQTPHT**FGQGTKLEIK
SARS-CoV-2 S2H58-v7 mAb CDRL3 (aa)	358	**IQALQTPHT**
SARS-CoV-2 S2N22-v2 mAb VH (aa)	359	EVQLVESGGGLVQPGGSLRLSCAAS**GFTFSS YP**MSWVRQAPGKGLEWVSA**ISGSGQYT**YYA DSVKGRFTISRDNSKNTLYLQMNSLRAEDTA VYYC**AKDPGGLSNFDF**WGQGTLVTVSS

Sequence Description	SEQ ID NO.	Sequence
SARS-CoV-2 S2N22-v2 mAb CDRH2 (aa)	360	**ISGSGQYT**
SARS-CoV-2 S2N22-v3 mAb VH (aa)	361	EVQLVESGGGLVQPGGSLRLSCAAS**GFTFSS YP**MSWVRQAPGKGLEWVSA**ISGSGGYT**YYA DSVKGRFTISRDNSKNTLYLQMNSLRAEDTA VYYC**AKDPGGLSNFDF**WGQGTLVTVSS
SARS-CoV-2 S2N22-v3 mAb CDRH2 (aa)	362	**ISGSGGYT**
SARS-CoV-2 S2N22-v4 mAb VH (aa)	363	EVQLVESGGGLVQPGGSLRLSCAAS**GFTFSS YP**MSWVRQAPGKGLEWVSA**ISGSGNYA**YYA DSVKGRFTISRDNSKNTLYLQMNSLRAEDTA VYYC**AKDPGGLSNFDF**WGQGTLVTVSS
SARS-CoV-2 S2N22-v4 mAb CDRH2 (aa)	364	**ISGSGNYA**
SARS-CoV-2 S2N22-v5 mAb VH (aa)	365	EVQLVESGGGLVQPGGSLRLSCAAS**GFTFSS YP**MSWVRQAPGKGLEWVSA**ISGSGNPT**YYA DSVKGRFTISRDNSKNTLYLQMNSLRAEDTA VYYC**AKDPGGLSNFDF**WGQGTLVTVSS
SARS-CoV-2 S2N22-v5 mAb CDRH2 (aa)	366	**ISGSGNPT**
SARS-CoV-2 S2N22-v6 mAb VH (aa)	367	EVQLVESGGGLVQPGGSLRLSCAAS**GFTFSS YP**MSWVRQAPGKGLEWVSA**ISGSGNYA**YYA DAVKGRFTISRDNSKNTLYLQMNSLRAEDTA VYYC**AKDPGGLSNFDF**WGQGTLVTVSS
SARS-CoV-2 S2N22-v7 mAb VH (aa)	368	EVQLVESGGGLVQPGGSLRLSCAAS**GFTFSS YP**ISWVRQAPGKGLEWVSA**ISGSGNYA**YYA DAVKGRFTISRDNSKNTLYLQMNSLRAEDTA VYYC**AKDPGGLSNFDF**WGQGTLVTVSS

Sequence Description	SEQ ID NO.	Sequence
SARS-CoV-2 S2E6-v1 mAb VH (aa)	369	QITLKESGPTLVKPTQTLTLTCTFS**GFSLSTSG VG**VGWIRQPPGEALEWLAL**IFWDDDK**RYRP SLKSRLTITKDTSKNQVVLTMTNMDPVDTAT YYC**AHRRTSYGSYYFDY**WGQGTLVTVSS
SARS-CoV-2 S2E6-v1 mAb CDRH1 (aa)	370	**GFSLSTSGVG**
SARS-CoV-2 S2E6-v1 mAb CDRH2 (aa)	371	**IFWDDDK**
SARS-CoV-2 S2E6-v1 mAb CDRH3 (aa)	372	**AHRRTSYGSYYFDY**
SARS-CoV-2 S2E6-v1 mAb VL (aa)	373	DIEMTQSPSTLSASVGDRVTITCRAS**QSISNW** LAWYQQKPGRAPKLLIY**RAS**NLESGVPSRFS GSGSGTEFTLTISSLQPDDFATYYC**QQYNSYP T**FGQGTKVEIK
SARS-CoV-2 S2E6-v1 mAb CDRL1 (aa)	374	**QSISNW**
SARS-CoV-2 S2E6-v1 mAb CDRL2 (aa)	375	**RAS**
SARS-CoV-2 S2E6-v1 mAb CDRL3 (aa)	376	**QQYNSYPT**
SARS-CoV-2 S2E6-v1 mAb VH (nt)	377	CAGATCACCTTGAAGGAGTCTGGTCCTACG CTGGTGAAACCCACACAGACCCTCACGCTG ACCTGCACCTTCTCT**GGGTTCTCACTCAGC ACTAGTGGAGTGGGT**GTGGGCTGGATCCG TCAGCCCCCAGGAGAGGCCCTGGAGTGGCT TGCACTC**ATTTTTTGGGATGATGATAAG**C GCTACAGGCCATCTCTGAAGAGCAGGCTCA CCATCACCAAGGACACCTCCAAAAACCAGG TGGTCCTTACAATGACCAACATGGACCCTG TGGACACAGCCACATATTACTGT**GCACACA GACGTACCAGCTATGGTTCTTACTACTTT GACTAT**TGGGGCCAGGGAACCCTGGTCACC GTCTCCTCAG
SARS-CoV-2 S2E6-v1 mAb VL (nt)	378	GACATCGAGATGACCCAGTCTCCTTCCACC CTGTCTGCATCTGTAGGAGACAGAGTCACC ATCACTTGCCGGGCCAGT**CAGAGTATTAGT**

Sequence Description	SEQ ID NO.	Sequence
		AACTGGTTGGCCTGGTATCAGCAGAAACCA GGGAGAGCCCCTAAGCTCCTAATCTAT**AGG GCGTCT**AATTTAGAAAGTGGGGTCCCATCA AGGTTCAGCGGCAGTGGATCTGGGACAGAA TTCACTCTCACCATCAGCAGCCTGCAGCCT GATGATTTTGCAACTTATTACTGC**CAACAG TATAATAGTTATCCGACG**TTCGGCCAAGG GACCAAGGTGGAAATCAAAC
SARS-CoV-2 S2E7-v1 mAb VH (aa)	379	EVQLVESGGGLVQPGGSLRLSCAAS**GLTVSS NY**MTWVRQAPGKGLEWVSI**IYSGGST**FYAD SVKGRFTISRDNSKNTLNLQMNSLRVEDTAV YYC**ARPIVGSRAGMDV**WGQGTTVTVSS
SARS-CoV-2 S2E7-v1 mAb CDRH1 (aa)	380	**GLTVSSNY**
SARS-CoV-2 S2E7-v1 mAb CDRH2 (aa)	381	**IYSGGST**
SARS-CoV-2 S2E7-v1 mAb CDRH3 (aa)	382	**ARPIVGSRAGMDV**
SARS-CoV-2 S2E7-v1 mAb VH (aa)	383	EIVMTQSPSSLSASVGDRVTITCQAS**QDINKY** LNWYQQKPGKAPKLLIY**DAS**NLETGVPSRFS GSGSGTDFAFTISSLQPEDVATYYC**HQYDNL PLT**FGGGTKVEIK
SARS-CoV-2 S2E7-v1 mAb CDRL1 (aa)	384	**QDINKY**
SARS-CoV-2 S2E7-v1 mAb CDRL2 (aa)	385	**DAS**
SARS-CoV-2 S2E7-v1 mAb CDRL3 (aa)	386	**HQYDNLPLT**
SARS-CoV-2 S2E7-v1 mAb VH (nt)	387	GAGGTGCAGCTGGTGGAGTCTGGGGGAGG CTTGGTCCAGCCTGGGGGGTCCCTGAGACT CTCCTGTGCAGCCTCT**GGATTAACTGTCAG TAGCAACTAC**ATGACCTGGGTCCGCCAGG CTCCAGGGAAGGGGCTGGAGTGGGTCTCAA TT**ATTTATAGCGGTGGTAGCACA**TTCTAC GCAGACTCCGTGAAGGGCCGATTCACCATC TCCAGAGACAATTCCAAGAACACGCTGAAT

Sequence Description	SEQ ID NO.	Sequence
		CTTCAAATGAACAGCCTGAGAGTTGAGGAC ACGGCTGTGTATTACTGT**GCGAGACCCATA GTGGGATCCAGAGCCGGTATGGACGTC**T GGGGCCAAGGGACCACGGTCACCGTCTCCT CA
SARS-CoV-2 S2E7-v1 mAb VL (nt)	388	GAAATAGTGATGACGCAGTCTCCATCCTCC CTGTCTGCATCTGTAGGAGACAGAGTCACC ATCACTTGCCAGGCGAGT**CAAGACATTAA CAAGTAT**TTAAATTGGTATCAGCAGAAACC AGGGAAAGCCCCTAAACTCCTTATCTAC**GA TGCATCC**AATTTGGAAACAGGGGTCCCATC AAGGTTCAGTGGAAGTGGGTCTGGGACAGA TTTTGCTTTCACCATCAGCAGCCTGCAGCCT GAAGATGTTGCAACATATTACTGT**CACCAG TATGATAATCTCCCGCTCACT**TTCGGCGG AGGGACCAAGGTGGAGATCAAAC
SARS-CoV-2 S2E9-v1 mAb VH (aa)	389	EVQLVESGGGLIQPGGSLRLSCAAS**GLTVSSN Y**MSWVRQAPGKGLEWVSV**IYSGGST**FYAES VKGRFTISRDNSKNTLYLQLNSLRAADTAVY YC**ARDLEIHGMDV**WGQGTTVTVSS
SARS-CoV-2 S2E9-v1 mAb CDRH1 (aa)	390	**GLTVSSNY**
SARS-CoV-2 S2E9-v1 mAb CDRH2 (aa)	391	**IYSGGST**
SARS-CoV-2 S2E9-v1 mAb CDRH3 (aa)	392	**ARDLEIHGMDV**
SARS-CoV-2 S2E9-v1 mAb VL (aa)	393	EIVLTQSPSFLSASVGDRVTITCRAS**QGISNY**L AWYQQKPGKAPQLLIY**AAS**TLQSGVPSRFSG SGSGTEFTLTISSLQPEDFATYYC**QQLNSYPP VT**FGPGTKVDIK
SARS-CoV-2 S2E9-v1 mAb CDRL1 (aa)	394	**QGISNY**
SARS-CoV-2 S2E9-v1 mAb CDRL2 (aa)	395	**AAS**
SARS-CoV-2 S2E9-v1 mAb CDRL3 (aa)	396	**QQLNSYPPVT**

Sequence Description	SEQ ID NO.	Sequence
SARS-CoV-2 S2E9-v1 mAb VH (nt)	397	GAGGTGCAGCTGGTGGAGTCTGGAGGAGG CTTGATCCAGCCTGGGGGGTCCCTGAGACT CTCCTGTGCAGCCTCT**GGGTTAACCGTCAG TAGCAACTAC**ATGAGCTGGGTCCGCCAGG CTCCAGGGAAGGGGCTGGAGTGGGTCTCAG TT**ATTTATAGCGGTGGTAGCACA**TTCTAC GCAGAATCCGTGAAGGGCCGATTCACCATC TCCAGAGACAATTCCAAGAACACGCTGTAT CTTCAATTGAACAGCCTGAGAGCCGCGGAC ACGGCCGTGTATTACTGT**GCGAGAGATCTT GAGATTCACGGTATGGACGTC**TGGGGCCA AGGGACCACGGTCACCGTCTCCTCA
SARS-CoV-2 S2E9-v1 mAb VL (nt)	398	GAAATTGTGCTGACTCAGTCTCCATCCTTCC TGTCTGCATCTGTAGGAGACAGAGTCACCA TCACTTGCCGGGCCAGT**CAGGGCATTAGC AATTAT**TTAGCCTGGTATCAGCAAAAACCA GGGAAAGCCCCTCAGCTCCTGATCTAT**GCT GCATCC**ACTTTGCAAAGTGGGGTCCCATCA AGGTTCAGCGGCAGTGGATCTGGGACAGAA TTCACTCTCACAATCAGCAGCCTGCAGCCT GAAGATTTTGCAACTTATTACTGT**CAACAG CTTAATAGTTACCCTCCGGTCACT**TTCGG CCCTGGGACCAAAGTGGATATCAAAC
SARS-CoV-2 S2E12-v1 mAb VH (aa)	399	QVQLVQSGPEVKKPGTSVRVSCKAS**GFTFTS SA**VQWVRQARGQRLEWVGW**IVVGSGNT**NY AQKFHERVTITRDMSTSTAYMELSSLRSEDTA VYYCAS**PYCSGGSCSDGFDI**WGQGTMVTVS S
SARS-CoV-2 S2E12-v1 mAb CDRH1 (aa)	400	**GFTFTSSA**
SARS-CoV-2 S2E12-v1 mAb CDRH2 (aa)	401	**IVVGSGNT**
SARS-CoV-2 S2E12-v1 mAb CDRH3 and N-terminal Ala-Ser (aa)	402	**ASPYCSGGSCSDGFDI**
SARS-CoV-2	403	DIVLTQTPGTLSLSPGERATLSCRAS**QSVSSSY**

Sequence Description	SEQ ID NO.	Sequence
S2E12-v1 mAb VL (aa)		LAWYQQKPGQAPRLLIY**GAS**SRATGIPDRFSG SGSGTDFTLTISRLEPEDFAVYYC**QQYVGLT GWT**FGQGTKVEIK
SARS-CoV-2 S2E12-v1 mAb CDRL1 (aa)	404	**QSVSSSY**
SARS-CoV-2 S2E12-v1 mAb CDRL2 (aa)	405	**GAS**
SARS-CoV-2 S2E12-v1 mAb CDRL3 (aa)	406	**QQYVGLTGWT**
SARS-CoV-2 S2E12-v1 mAb VH (nt)	407	CAGGTGCAGCTGGTGCAGTCTGGGCCTGAG GTGAAGAAGCCTGGGACCTCAGTGAGGGTC TCCTGCAAGGCTTCT**GGATTCACCTTTACT AGCTCTGCT**GTACAGTGGGTGCGACAGGC TCGTGGACAACGCCTTGAGTGGGTGGGATG G**ATCGTCGTTGGCAGTGGTAACACA**AACT ACGCACAGAAGTTCCACGAAAGAGTCACCA TTACCAGGGACATGTCCACAAGCACAGCCT ACATGGAGCTGAGCAGCCTGAGATCCGAGG ACACGGCCGTGTATTACTGTGCGTCA**CCTT ATTGTAGTGGTGGTAGCTGCTCTGATGG TTTTGATATC**TGGGGCCAAGGGACAATGG TCACCGTCTCTTCAG
SARS-CoV-2 S2E12-v1 mAb VL (nt)	408	GATATTGTGTTGACGCAGACTCCAGGCACC CTGTCTTTGTCTCCAGGGGAAAGAGCCACC CTCTCCTGCAGGGCCAGT**CAGAGTGTTAG CAGCAGTTAC**TTAGCCTGGTACCAGCAGA AACCTGGCCAGGCTCCCAGGCTCCTCATCT AT**GGTGCATCC**AGCAGGGCCACTGGCATC CCAGACAGGTTCAGTGGCAGTGGGTCTGGG ACAGACTTCACTCTCACCATCAGCAGACTG GAGCCTGAAGATTTTGCAGTGTATTACTGT **CAGCAGTATGTTGGCTTAACAGGGTGGA CG**TTCGGCCAAGGGACCAAGGTGGAAATC AAAC

Sequence Description	SEQ ID NO.	Sequence
SARS-CoV-2 S2E13-v1 mAb VH (aa)	409	QVQLVQSGTEVKKPGASVKVSCKAS**GYTFIS YG**ISWVRQAPGQGLEWMGW**ISPYNGNT**HY AKRVQGRVTMTTDTSTNTSYMELRSLRSDDT AVYYC**ARDGELLGWFDP**WGQGTLVTVSS
SARS-CoV-2 S2E13-v1 mAb CDRH1 (aa)	410	**GYTFISYG**
SARS-CoV-2 S2E13-v1 mAb CDRH2 (aa)	411	**ISPYNGNT**
SARS-CoV-2 S2E13-v1 mAb CDRH3 (aa)	412	**ARDGELLGWFDP**
SARS-CoV-2 S2E13-v1 mAb VL (aa)	413	HTELTQPASVSGSPGQSITISCTGT**SSDVGNYN L**VSWYQQHPGKAPKLMIY**AGT**KRPSGVSNR FSGSKSGNTASLTISGLQAEDEADYYC**CSYA GSSTWV**FGGGTKLTVL
SARS-CoV-2 S2E13-v1 mAb CDRL1 (aa)	414	**SSDVGNYNL**
SARS-CoV-2 S2E13-v1 mAb CDRL2 (aa)	415	**AGT**
SARS-CoV-2 S2E13-v1 mAb CDRL3 (aa)	416	**CSYAGSSTWV**
SARS-CoV-2 S2E13-v1 mAb VH (nt)	417	CAGGTGCAGCTGGTGCAGTCTGGAACTGAG GTGAAGAAGCCTGGGGCCTCAGTGAAGGTC TCCTGCAAGGCTTCT**GGTTACACCTTTATC AGCTATGGT**ATCAGCTGGGTGCGACAGGC CCCTGGACAAGGGCTTGAGTGGATGGGATG G**ATCAGCCCTTACAATGGTAACACA**CATT ATGCAAAGAGGGTCCAGGGCAGAGTCACC ATGACCACAGACACATCCACGAACACATCC

Sequence Description	SEQ ID NO.	Sequence
		TACATGGAGCTGAGGAGCCTGAGATCTGAC GACACGGCCGTGTATTACTGT**GCGAGAGA TGGAGAACTCCTCGGCTGGTTCGATCCC** TGGGGCCAGGGAACCCTGGTCACCGTCTCC TCAG
SARS-CoV-2 S2E13-v1 mAb VL (nt)	418	CACACTGAGCTGACTCAGCCTGCCTCCGTG TCTGGGTCTCCTGGACAGTCGATCACCATCT CCTGCACTGGAACC**AGCAGTGATGTTGGG AATTATAACCTT**GTCTCCTGGTACCAACAG CACCCAGGCAAAGCCCCCAAACTCATGATT TAT**GCGGGCACT**AAGCGGCCCTCAGGGGT TTCTAATCGCTTCTCTGGCTCCAAGTCTGGC AACACGGCCTCCCTGACAATCTCTGGGCTC CAGGCTGAGGACGAGGCTGACTATTACTGC **TGCTCATATGCAGGTAGTAGCACTTGGG TG**TTCGGCGGAGGGACCAAGCTGACCGTCC TAG
SARS-CoV-2 S2E14-v1 mAb VH (aa)	419	EVQLVESGGGVVQPGRSLRLSCAAS**GFTFSS YA**MHWVRQAPGKGLEWVTV**ISSDGSNK**YY AESVKGRFTISRDNSKNTLYLQMNSLRAEDT ALYYC**ARDLPVIVATMWHYYNGMDV**WGQ GTTVTVSS
SARS-CoV-2 S2E14-v1 mAb CDRH1 (aa)	420	**GFTFSSYA**
SARS-CoV-2 S2E14-v1 mAb CDRH2 (aa)	421	**ISSDGSNK**
SARS-CoV-2 S2E14-v1 mAb CDRH3 (aa)	422	**ARDLPVIVATMWHYYNGMDV**
SARS-CoV-2 S2E14-v1 mAb VL (aa)	423	DIRMTQSPSSVSASVGDRVTITCRAS**EGISSW** LGWYQQKPGKAPKLLIY**GAS**SLQSGVPSRFS GSGFGTDFTLTISSLQPEDFATYYC**QQAKSFP IT**FGQGTRLEIK
SARS-CoV-2 S2E14-v1 mAb CDRL1	424	**EGISSW**

Sequence Description	SEQ ID NO.	Sequence
(aa)		
SARS-CoV-2 S2E14-v1 mAb CDRL2 (aa)	425	**GAS**
SARS-CoV-2 S2E14-v1 mAb CDRL3 (aa)	426	**QQAKSFPIT**
SARS-CoV-2 S2E14-v1 mAb VH (nt)	427	GAGGTGCAGCTGGTGGAGTCTGGGGGAGG CGTGGTCCAGCCTGGGAGGTCCCTGAGACT CTCCTGTGCAGCCTCT**GGATTCACCTTCAG TAGCTATGCT**ATGCACTGGGTCCGCCAGGC TCCAGGCAAGGGGCTGGAGTGGGTGACAGT T**ATTTCATCTGATGGAAGCAATAAA**TACT ACGCGGAGTCCGTGAAGGGCCGATTCACCA TCTCCAGAGACAATTCCAAGAACACGCTGT ATCTGCAAATGAACAGCCTGAGAGCTGAGG ACACGGCTCTATATTACTGT**GCGAGAGACC TTCCTGTTATAGTGGCTACGATGTGGCAC TACTATAACGGAATGGACGTC**TGGGGCCA AGGGACCACGGTCACCGTCTCCTCG
SARS-CoV-2 S2E14-v1 mAb VL (nt)	428	GACATCCGGATGACCCAGTCTCCATCTTCC GTGTCTGCATCTGTAGGAGACAGAGTCACC ATCACTTGTCGGGCGAGT**GAAGGTATTAG CAGCTGG**TTAGGCTGGTATCAGCAGAAAC CAGGGAAGGCCCCTAAACTCCTGATCTAC**G GTGCATCC**AGTTTGCAAAGTGGGGTCCCAT CAAGGTTCAGCGGCAGTGGATTTGGGACAG ATTTCACTCTCACCATCAGCAGTCTGCAGCC TGAAGATTTTGCAACTTACTATTGT**CAACA GGCTAAGAGTTTCCCGATCACC**TTCGGCC AAGGGACACGACTGGAGATTAAAC
SARS-CoV-2 S2K4-v1 mAb VH (aa)	429	QVQLVQSGAEVKKPGASVKVSCKAS**GYTFT GYY**MHWVRQAPGQGLEWMGW**INPNSGGT** NYTQKFQGWVTMTRDTSISTAYMELSRLSSD DTAVYYC**ARDLAYSYVTGAFDI**WGHGTMV TVSS
SARS-CoV-2 S2K4-v1 mAb CDRH1 (aa)	430	**GYTFTGYY**
SARS-CoV-2	431	**INPNSGGT**

Sequence Description	SEQ ID NO.	Sequence
S2K4-v1 mAb CDRH2 (aa)		
SARS-CoV-2 S2K4-v1 mAb CDRH3 (aa)	432	**ARDLAYSYVTGAFDI**
SARS-CoV-2 S2K4-v1 mAb VH (nt)	433	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAG GTGAAGAAGCCTGGGGCCTCAGTGAAGGTC TCCTGCAAGGCTTCT**GGATACACCTTCACC GGCTACTAT**ATGCACTGGGTGCGACAGGC CCCTGGACAAGGGCTTGAGTGGATGGGATG G**ATCAACCCTAACAGTGGTGGCACA**AACT ATACACAGAAGTTTCAGGGCTGGGTCACCA TGACCAGGGACACGTCCATCAGCACAGCCT ACATGGAGCTGAGCAGGCTGAGCTCTGACG ACACGGCCGTGTATTACTGT**GCGAGAGAT CTCGCATACAGCTATGTCACGGGGGCTT TTGATATC**TGGGGCCACGGGACAATGGTC ACCGTCTCTTCAG
SARS-CoV-2 S2X193-v1 mAb VH (aa)	434	EVHLVESGGGLVQPGGSLRLSCAAS**GIIVSRN Y**MSWVRQAPGKGLEWVSV**IYSGGST**FYADS VKGRFTISRDNSKNTLYLQMNSLRAGDTAVY YC**ARDMMNDAFDI**WGQGTMVTVSS
SARS-CoV-2 S2X193-v1 mAb CDRH1 (aa)	435	**GIIVSRNY**
SARS-CoV-2 S2X193-v1 mAb CDRH2 (aa)	436	**IYSGGST**
SARS-CoV-2 S2X193-v1 mAb CDRH3 (aa)	437	**ARDMMNDAFDI**
SARS-CoV-2 S2X193-v1 mAb VH (aa)	438	DIQMTQSPSSLSASVGDRVTITCRAS**QGISSY**L AWYQQKPGKAPKLLIY**SAS**TLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYC**QQLNSYPPE VT**FGQGTRLEIK
SARS-CoV-2 S2X193-v1	439	**QGISSY**

Sequence Description	SEQ ID NO.	Sequence
mAb CDRL1 (aa)		
SARS-CoV-2 S2X193-v1 mAb CDRL2 (aa)	440	**SAS**
SARS-CoV-2 S2X193-v1 mAb CDRL3 (aa)	441	**QQLNSYPPEVT**
SARS-CoV-2 S2X193-v1 mAb VH (nt)	442	GAGGTGCATCTGGTGGAGTCTGGGGGAGGT TTGGTCCAGCCGGGGGGGTCCCTGAGACTC TCCTGTGCAGCCTCT**GGAATCATCGTCAGT AGGAATTAC**ATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGGAGTGGGTCTCAGT T**ATTTATAGCGGTGGTAGTACA**TTCTACG CAGACTCCGTGAAGGGCCGATTCACCATCT CCAGAGACAATTCCAAGAACACGCTGTATC TTCAAATGAACAGCCTGAGAGCTGGGGACA CGGCTGTGTATTACTGT**GCGAGGGATATG ATGAATGATGCTTTTGATATC**TGGGGCCA AGGGACAATGGTCACCGTCTCTTCAG
SARS-CoV-2 S2X193-v1 mAb VL (nt)	443	GACATCCAGATGACCCAGTCTCCATCCTCC CTGTCTGCATCTGTAGGAGACAGAGTCACC ATCACTTGCCGGGCCAGT**CAGGGCATTAG CAGTTAT**TTAGCCTGGTATCAGCAAAAACC AGGGAAAGCCCCTAAGCTCCTGATCTAT**TC TGCATCC**ACTTTGCAAAGTGGGGTCCCATC GAGGTTCAGCGGCAGTGGATCTGGGACAGA TTTCACTCTCACCATCAGCAGCCTGCAGCCT GAAGATTTTGCAACTTATTACTGT**CAACAG CTTAATAGTTACCCTCCGGAGGTCACC**TT CGGCCAAGGGACACGACTGGAGATTAAAC
SARS-CoV-2 S2X195-v1 mAb VH (aa)	444	EVHLVQSGAEVKKPGASVKVSCKAS**GYTFT DYY**MHWVRQAPGQGLEWMGW**INPKIGGT**N YAQKFQGRVTMTRDTSINTAYMELSRLRSDD TAVYYC**AKDLQPSYCTDGVCWPDDAFDI**W GQGTMVTVSS
SARS-CoV-2 S2X195-v1	445	**GYTFTDYY**

Sequence Description	SEQ ID NO.	Sequence
mAb CDRH1 (aa)		
SARS-CoV-2 S2X195-v1 mAb CDRH2 (aa)	446	**INPKIGGT**
SARS-CoV-2 S2X195-v1 mAb CDRH3 (aa)	447	**AKDLQPSYCTDGVCWPDDAFDI**
SARS-CoV-2 S2X195-v1 mAb VL (aa)	448	AIRMTQTPLSLSVTPGQPASISCKSS**QSLLHSDGKTY**LYWYLQKPGQSPQLLIY**EVS**NRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC**MQSIQLPPT**FGQGTKVEIK
SARS-CoV-2 S2X195-v1 mAb CDRL1 (aa)	449	**QSLLHSDGKTY**
SARS-CoV-2 S2X195-v1 mAb CDRL2 (aa)	450	**EVS**
SARS-CoV-2 S2X195-v1 mAb CDRL3 (aa)	451	**MQSIQLPPT**
SARS-CoV-2 S2X195-v1 mAb VH (nt)	452	GAGGTGCATCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT**GGATACACCTTCACCGACTACTAT**ATGCACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATG**GATCAACCCTAAGATTGGTGGCACA**AACTATGCACAGAAGTTTCAGGGCAGGGTCACCATGACCAGGGACACGTCCATCAACACAGCCTACATGGAACTGAGCAGGCTGAGATCTGACGACACGGCCGTATATTACTGT**GCGAAAGATCTACAACCTTCATATTGTACTGATGGTGTATGCTGGCCCGATGATGCTTTTGATATC**TGGGGCCAAGGGACAATGGTCACCGTCTCTTCAG

Sequence Description	SEQ ID NO.	Sequence
SARS-CoV-2 S2X195-v1 mAb VL (nt)	453	GCCATCCGGATGACCCAGACTCCACTCTCT CTGTCCGTCACCCCTGGACAGCCGGCCTCC ATCTCCTGCAAGTCTAGT**CAGAGCCTCCTG CATAGTGATGGAAAGACCTAT**TTGTATTG GTACCTGCAGAAGCCAGGCCAGTCTCCACA GCTCCTGATCTAT**GAAGTTTCC**AACCGCTT CTCTGGAGTGCCAGATAGGTTCAGTGGCAG CGGGTCAGGGACAGATTTCACACTGAAAAT CAGCCGGGTGGAGGCTGAGGATGTTGGGGT TTATTACTGC**ATGCAAAGTATACAGCTTC CTCCGACG**TTCGGCCAAGGGACCAAGGTG GAAATCAAAC
SARS-CoV-2 S2X219-v1 mAb VH (aa)	454	EVQLVESGGGLIQPGGSLRLSCAAT**GITVSRN YI**NWVRQAPGKGLEWVSI**IYSGGTT**YYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYY C**ARDLNVVGGFDI**WGQGTMVTVSS
SARS-CoV-2 S2X219-v1 mAb CDRH1(aa)	455	**GITVSRNY**
SARS-CoV-2 S2X219-v1 mAb CDRH2 (aa)	456	**IYSGGTT**
SARS-CoV-2 S2X219-v1 mAb CDRH3 (aa)	457	**ARDLNVVGGFDI**
SARS-CoV-2 S2X219-v1 mAb VL (aa)	458	EIVMTQSPGTLSLSPGERATLSCRAS**QSISSSY** LAWYQQKPGQAPRLLIY**GAS**SRATGIPDRFSG SGSGTDFTLTISRLEPEDFAVYYC**QQYGSSPPI T**FGQGTRLEIK
SARS-CoV-2 S2X219-v1 mAb CDRL1 (aa)	459	**QSISSSY**
SARS-CoV-2 S2X219-v1 mAb CDRL2	460	**GAS**

Sequence Description	SEQ ID NO.	Sequence
(aa)		
SARS-CoV-2 S2X219-v1 mAb CDRL3 (aa)	461	**QQYGSSPPIT**
SARS-CoV-2 S2X219-v1 mAb VH (nt)	462	GAGGTGCAGCTGGTGGAGTCTGGAGGAGG CTTGATCCAGCCTGGGGGGTCCCTGAGACT CTCCTGTGCAGCCACT**GGGATCACCGTCA GTAGGAACTAC**ATAAACTGGGTCCGCCAG GCTCCAGGGAAGGGGCTGGAGTGGGTCTCA ATT**ATTTATAGCGGTGGTACTACA**TACTA CGCAGACTCCGTGAAGGGCCGATTCACCAT CTCCAGAGACAATTCCAAGAACACGCTGTA TCTTCAAATGAACAGCCTGAGAGCCGAGGA CACGGCCGTGTATTACTGT**GCGAGAGATTT AAACGTAGTGGGTGGTTTTGATATC**TGGG GCCAAGGGACAATGGTCACCGTCTCTTCAG
SARS-CoV-2 S2X219-v1 mAb VL (nt)	463	GAAATAGTGATGACGCAGTCTCCAGGCACC CTGTCTTTGTCTCCAGGGGAAAGAGCCACC CTCTCCTGCAGGGCCAGT**CAGAGTATTAGC AGCAGCTAC**TTAGCCTGGTACCAGCAGAA ACCTGGCCAGGCTCCCAGGCTCCTCATCTA T**GGTGCATCC**AGCAGGGCCACTGGCATCC CAGACAGGTTCAGTGGCAGTGGGTCTGGGA CAGACTTCACTCTCACCATCAGCAGACTGG AGCCTGAAGATTTTGCAGTGTATTACTGT**C AGCAGTATGGTAGCTCACCTCCGATCAC C**TTCGGCCAAGGGACACGACTGGAGATTAA AC
SARS-CoV-2 S2X244-v1 mAb VH (aa)	464	QVQLVQSGTEVKKPGSSVKVSCKAS**GGTFST FS**INWVRQAPGQGLEWMGR**IIPILKIA**DYAQ KFQGRVTITADKSTSTAYMELSSLRSEDTAVY YC**AREAGFFEEYGSGSSGLDP**WGQGTLVTV SS
SARS-CoV-2 S2X244-v1 mAb CDRH1 (aa)	465	**GGTFSTFS**
SARS-CoV-2 S2X244-v1	466	**IIPILKIA**

Sequence Description	SEQ ID NO.	Sequence
mAb CDRH2 (aa)		
SARS-CoV-2 S2X244-v1 mAb CDRH3 (aa)	467	**AREAGFFEEYGSGSSGLDP**
SARS-CoV-2 S2X244-v1 mAb VL (aa)	468	EIVLTQSPLSLPVTPGEPASISCRSN**LSLLHSN GYNY**LDWYLQKPGQSPQLLIY**LGS**NRASGVP DRFSGSGSGTDFILKISRVEAEDVGVYYC**MQ ALQTPR**FGGGTKVEIK
SARS-CoV-2 S2X244-v1 mAb CDRL1 (aa)	469	**LSLLHSNGYNY**
SARS-CoV-2 S2X244-v1 mAb CDRL2 (aa)	470	**LGS**
SARS-CoV-2 S2X244-v1 mAb CDRL3 (aa)	471	**MQALQTPR**
SARS-CoV-2 S2X244-v1 mAb VH (nt)	472	CAGGTCCAGCTGGTGCAATCTGGGACTGAG GTGAAGAAGCCTGGGTCCTCGGTGAAGGTC TCCTGCAAGGCTTCT**GGAGGCACCTTCAG CACCTTTAGT**ATCAACTGGGTGCGACAGG CCCCTGGACAAGGGCTTGAGTGGATGGGAA GG**ATCATCCCTATCCTTAAAATAGCA**GAC TACGCACAGAAGTTCCAGGGCAGAGTCACG ATTACCGCGGACAAATCCACGAGCACAGCC TACATGGAGCTGAGCAGCCTGAGATCTGAG GACACGGCCGTGTATTACTGT**GCGAGAGA GGCAGGCTTCTTCGAGGAGTATGGTTCG GGGAGTTCAGGGCTCGACCCC**TGGGGCC AGGGAACCCTGGTCACCGTCTCCTCAG
SARS-CoV-2 S2X244-v1 mAb VL (nt)	473	GAAATTGTGTTGACACAGTCTCCACTCTCCC TGCCCGTCACCCCTGGAGAGCCGGCCTCCA TCTCCTGCAGGTCTAAT**CTGAGTCTCCTGC ATAGTAATGGATACAACTAT**TTGGATTGG TACCTGCAGAAGCCAGGGCAGTCTCCACAG CTCCTGATCTAT**TTGGGTTCT**AATCGGGCC

Sequence Description	SEQ ID NO.	Sequence
		TCCGGGGTCCCTGACAGGTTCAGTGGCAGT GGATCAGGCACAGATTTTATACTGAAAATC AGCAGAGTGGAGGCTGAGGATGTTGGGGTT TATTACTGC**ATGCAAGCTCTCCAAACTCC TCGT**TTCGGCGGAGGGACCAAGGTGGAGA TCAAAC
SARS-CoV-2 S2X246-v1 mAb VH (aa)	474	QVQLVESGGGLVQPGGSLRLSCAAS**GFTFSI YE**MNWVRQAPGKGLEWVSY**ITSGGHTI**FYA DSVKGRFTISRDNAKNSLYLQMNSLRAEDTA VYYC**ASNPSSGYFFDY**WGQGTLVTVSS
SARS-CoV-2 S2X246-v1 mAb CDRH1 (aa)	475	**GFTFSIYE**
SARS-CoV-2 S2X246-v1 mAb CDRH2 (aa)	476	**ITSGGHTI**
SARS-CoV-2 S2X246-v1 mAb CDRH3 (aa)	477	**ASNPSSGYFFDY**
SARS-CoV-2 S2X246-v1 mAb VL (aa)	478	AIRMTQSPSTLSASVGDRVTITCRAS**QSISSW**L AWYQQKPGKAPKLLIY**KAS**SLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYC**QQYNSYPYT** FGQGTKLDIK
SARS-CoV-2 S2X246-v1 mAb CDRL1 (aa)	479	**QSISSW**
SARS-CoV-2 S2X246-v1 mAb CDRL2 (aa)	480	**KAS**
SARS-CoV-2 S2X246-v1 mAb CDRL3 (aa)	481	**QQYNSYPYT**
SARS-CoV-2	482	CAGGTACAGCTGGTGGAGTCTGGGGGAGGC

Sequence Description	SEQ ID NO.	Sequence
S2X246-v1 mAb VH (nt)		TTGGTCCAGCCTGGAGGGTCCCTGAGGCTC TCCTGTGCAGCCTCT**GGATTCACCTTCAGT ATTTATGAA**ATGAACTGGGTCCGCCAGGCT CCAGGGAAGGGGCTGGAGTGGGTTTCATAC **ATTACTAGTGGTGGTCATACCATA**TTCTA CGCAGACTCTGTGAAGGGCCGATTCACCAT CTCCAGAGACAACGCCAAGAACTCACTGTA TCTGCAAATGAACAGCCTGCGAGCCGAGGA CACGGCTGTTTATTACTGT**GCGAGCAACCC GAGTAGTGGTTATTTTTTTGACTAC**TGGG GCCAGGGAACCCTGGTCACCGTCTCCTCAG
SARS-CoV-2 S2X246-v1 mAb VL (nt)	483	GCCATCCGGATGACCCAGTCTCCTTCCACC CTGTCTGCATCTGTAGGAGACAGAGTCACC ATCACTTGCCGGGCCAGT**CAGAGTATTAGT AGCTGG**TTGGCCTGGTATCAGCAGAAACC AGGGAAAGCCCCTAAGCTCCTGATCTAT**AA GGCGTCT**AGTTTAGAAAGTGGGGTCCCATC AAGGTTCAGCGGCAGTGGATCTGGGACAGA ATTCACTCTCACCATCAGCAGCCTGCAGCC TGATGATTTTGCAACTTATTACTGC**CAACA GTATAATAGTTATCCCTACACT**TTTGGCC AGGGGACCAAGCTGGACATCAAAC
SARS-CoV-2 S2X256-v1 mAb VH (aa)	484	EVQLVESGGGLIQPGGSLRLSCAAS**GIIVSSN Y**MNWVRQAPGRGLEWVSV**IYSGGST**FYADS VKGRFTISRDSSKNTLYLQMNGLRAEDTAVY YC**ARDLGESGMDV**WGQGTTVTVSS
SARS-CoV-2 S2X256-v1 mAb CDRH1 (aa)	485	**GIIVSSNY**
SARS-CoV-2 S2X256-v1 mAb CDRH2 (aa)	486	**IYSGGST**
SARS-CoV-2 S2X256-v1 mAb CDRH3 (aa)	487	**ARDLGESGMDV**
SARS-CoV-2 S2X256-v1	488	AIRMTQSPSSVSASVGDRVTITCRAS**QGISSW** LAWYQQKPGKAPKLLIS**AAS**NLQSGVPSRFS

Sequence Description	SEQ ID NO.	Sequence
mAb VL (aa)		GSGSGTDFTLTISSLQPEDFATYYC**QQANSFP** **R**FGPGTKVDIK
SARS-CoV-2 S2X256-v1 mAb CDRL1 (aa)	489	**QGISSW**
SARS-CoV-2 S2X256-v1 mAb CDRL2 (aa)	490	**AAS**
SARS-CoV-2 S2X256-v1 mAb CDRL3 (aa)	491	**QQANSFPR**
SARS-CoV-2 S2X256-v1 mAb VH (nt)	492	GAGGTGCAGCTGGTGGAGTCTGGAGGGGG CTTGATCCAGCCTGGGGGGTCCCTGAGACT CTCCTGTGCAGCCTCT**GGGATCATCGTCAG** **TAGCAACTAC**ATGAACTGGGTCCGCCAGG CTCCAGGGAGGGGGCTGGAGTGGGTCTCAG TT**ATTTATAGCGGTGGTAGCACA**TTCTAC GCAGACTCCGTGAAGGGCCGATTCACCATC TCCAGAGACAGTTCCAAGAACACACTGTAT CTTCAAATGAACGGCCTGAGAGCCGAGGAC ACGGCCGTGTATTACTGT**GCGAGAGATCT** **GGGAGAGAGCGGTATGGACGTC**TGGGGC CAAGGGACCACGGTCACCGTCTCCTCA
SARS-CoV-2 S2X256-v1 mAb VL (nt)	493	GCCATCCGGATGACCCAGTCTCCATCTTCC GTGTCTGCATCTGTAGGAGACAGAGTCACC ATCACTTGTCGGGCGAGT**CAGGGTATTAG** **CAGCTGG**TTAGCCTGGTATCAGCAGAAAC CAGGGAAAGCCCCTAAGCTCCTGATCTCT**G** **CTGCATCC**AATTTGCAAAGTGGGGTCCCAT CTAGGTTCAGCGGCAGTGGATCTGGGACAG ATTTCACTCTCACCATCAGCAGCCTGCAGC CTGAAGATTTTGCAACTTACTATTGT**CAAC** **AGGCTAACAGTTTCCCTCGG**TTCGGCCCT GGGACCAAAGTGGATATCAAAC
SARS-CoV-2 S2X269-v1 mAb VH (aa)	494	EVQLVESGGGVVQPGRSLRLSCAAS**GFAFRI** **YG**MHWVRQAPGKGLEWVAL**IWFDGNNK**Y YADSVKGRFTISRDSSKNTLFLQMNSLRAEDT

Sequence Description	SEQ ID NO.	Sequence
		ALYYC**ARAMCPGETGNLLGICYAPDY**WGQ GTLVTVSS
SARS-CoV-2 S2X269-v1 mAb CDRH1 (aa)	495	**GFAFRIYG**
SARS-CoV-2 S2X269-v1 mAb CDRH2 (aa)	496	**IWFDGNNK**
SARS-CoV-2 S2X269-v1 mAb CDRH3 (aa)	497	**ARAMCPGETGNLLGICYAPDY**
SARS-CoV-2 S2X269-v1 mAb VL (aa)	498	QSALTQPPSASGTPGQRVTISCSGS**TSNIGSNH** VCWYQQLPGTAPKLLIY**SNN**QRPSGVPDRFS GSKSGTSASLAISGLRSEDEADYYC**AAWDDR LSGWV**FGGGTKLTVL
SARS-CoV-2 S2X269-v1 mAb CDRL1 (aa)	499	**TSNIGSNH**
SARS-CoV-2 S2X269-v1 mAb CDRL2 (aa)	500	**SNN**
SARS-CoV-2 S2X269-v1 mAb CDRL3 (aa)	501	**AAWDDRLSGWV**
SARS-CoV-2 S2X269-v1 mAb VH (nt)	502	GAGGTGCAGCTGGTGGAGTCTGGGGGAGG CGTGGTCCAGCCTGGGAGGTCCCTGAGACT CTCCTGTGCAGCGTCT**GGATTCGCCTTCAG AATCTATGGC**ATGCACTGGGTCCGCCAGG CTCCAGGCAAGGGGCTGGAGTGGGTGGCAC TT**ATATGGTTTGATGGAAATAATAAA**TAC TATGCCGACTCCGTGAAGGGCCGATTCACC ATCTCCAGAGACAGTTCCAAGAACACACTG TTTCTGCAAATGAACAGCCTGAGAGCCGAG GACACGGCTCTGTATTACTGT**GCGAGAGC**

Sequence Description	SEQ ID NO.	Sequence
		GATGTGCCCAGGCGAAACGGGAAATCTT CTGGGTATCTGCTACGCCCCTGACTACTG GGGCCAGGGAACCCTGGTCACCGTCTCCTC AG
SARS-CoV-2 S2X269-v1 mAb VL (nt)	503	CAGTCTGCCCTGACTCAGCCACCCTCAGCG TCTGGGACCCCCGGGCAGAGGGTCACCATC TCTTGTTCTGGAAGC**ACCTCCAACATCGGA AGTAATCAT**GTATGCTGGTACCAGCAGCTC CCAGGAACGGCCCCCAAACTCCTCATCTAT **AGTAATAAT**CAACGGCCCTCAGGGGTCCCT GACCGATTCTCTGGCTCCAAGTCTGGCACC TCAGCCTCCCTGGCCATCAGTGGGCTCCGG TCCGAGGATGAGGCTGATTATTACTGT**GCA GCATGGGATGACAGACTGAGTGGCTGGG TG**TTCGGCGGAGGGACCAAGCTGACCGTCC TAG
SARS-CoV-2 S2X278-v1 mAb VH (aa)	504	QVRLQESGPGLVKPSETLSLTCAVS**GYSISSG YY**WGWIRQPPGKGLEWIGS**IYESGST**YNNPS LKSRVTMSVDTSKNQFSLKLTSVTAADTAVY YC**ARDLWEGDYYRVGDY**WGQGTLVTVSS
SARS-CoV-2 S2X278-v1 mAb CDRH1 (aa)	505	**GYSISSGYY**
SARS-CoV-2 S2X278-v1 mAb CDRH2 (aa)	506	**IYESGST**
SARS-CoV-2 S2X278-v1 mAb CDRH3 (aa)	507	**ARDLWEGDYYRVGDY**
SARS-CoV-2 S2X278-v1 mAb VL (aa)	508	QSVLTQPPSVSAAPGQKVTISCSGS**SSNVGNN Y**VSWYQQLPGTAPKLLIY**DNT**KRPSWIPDRFS GSKSGTSATLDITGLQTGDEADYYC**GTWDSS LSVV**FGGGTKLTVL
SARS-CoV-2 S2X278-v1 mAb CDRL1	509	**SSNVGNNY**

Sequence Description	SEQ ID NO.	Sequence
(aa)		
SARS-CoV-2 S2X278-v1 mAb CDRL2 (aa)	510	**DNT**
SARS-CoV-2 S2X278-v1 mAb CDRL3 (aa)	511	**GTWDSSLSVV**
SARS-CoV-2 S2X278-v1 mAb VH (nt)	512	CAGGTGCGGCTGCAGGAGTCGGGCCCAGG ACTGGTGAAGCCTTCGGAGACCCTGTCCCT CACCTGCGCTGTCTCT**GGTTACTCCATCAG CAGTGGTTACTAC**TGGGGCTGGATCCGGC AGCCCCCAGGGAAGGGGCTGGAGTGGATT GGGAGT**ATCTATGAGAGTGGGAGCACC**T ACAACAACCCGTCCCTCAAGAGTCGAGTCA CCATGTCAGTAGACACGTCCAAGAACCAGT TCTCCCTGAAGCTGACCTCTGTGACCGCCG CAGACACGGCCGTATATTACTGT**GCGAGA GACCTCTGGGAAGGTGACTACTACCGAG TGGGGGACTAC**TGGGGCCAGGGAACCCTG GTCACCGTCTCCTCAG
SARS-CoV-2 S2X278-v1 mAb VL (nt)	513	CAGTCTGTGTTGACGCAGCCGCCCTCAGTG TCTGCGGCCCCAGGACAGAAGGTCACCATC TCCTGCTCTGGAAGC**AGCTCCAACGTTGG GAATAATTAT**GTATCCTGGTACCAGCAGCT CCCAGGAACAGCCCCCAAACTCCTCATTTA T**GACAATACT**AAGCGACCCTCATGGATTCC TGACCGATTCTCTGGCTCCAAGTCTGGCAC GTCAGCCACCCTGGACATCACCGGACTCCA GACTGGGGACGAGGCCGATTATTACTGC**GG AACATGGGATAGCAGTCTGAGTGTTGTC** TTCGGCGGAGGGACCAAGCTGACCGTCCTA G
SARS-CoV-2 S2M7-v1 mAb VH (aa)	514	QVQLVQSGAEVKKPGASVKVSCKAS**GYTFT SYY**MHWVRQAPGQGLEWMGI**INPSGTST**SY AQKFQGRVTMTRDTSTSTVYLDLSSLRSGDT AVYYC**ATGSWELPSYFDY**WGQGTLITVSS
SARS-CoV-2 S2M7-v1 mAb CDRH1 (aa)	515	**GYTFTSYY**

Sequence Description	SEQ ID NO.	Sequence
SARS-CoV-2 S2M7-v1 mAb CDRH2 (aa)	516	**INPSGTST**
SARS-CoV-2 S2M7-v1 mAb CDRH3 (aa)	517	**ATGSWELPSYFDY**
SARS-CoV-2 S2M7-v1 mAb VL (aa)	518	DIVMMQSPGTLSLSPGERATLSCRAS**QSIYSS YLAWYQQKPGQAPRLLIS**GAS**SRATGIPDRFS** GSGSGTDFTLTISRLEPADFAVYYC**QQYGSSP PT**FGQGTKVEIK
SARS-CoV-2 S2M7-v1 mAb CDRL1 (aa)	519	**QSIYSSY**
SARS-CoV-2 S2M7-v1 mAb CDRL2 (aa)	520	**GAS**
SARS-CoV-2 S2M7-v1 mAb CDRL3 (aa)	521	**QQYGSSPPT**
SARS-CoV-2 S2M7-v1 mAb VH (nt)	522	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAG GTGAAGAAGCCTGGGGCCTCAGTGAAGGTT TCCTGCAAGGCATCT**GGATACACCTTCAC CAGCTACTAT**ATGCACTGGGTGCGACAGG CCCCTGGACAAGGGCTTGAGTGGATGGGAA TA**ATCAACCCTAGTGGTACTAGCACA**AGC TACGCACAGAAGTTCCAGGGCAGAGTCACT ATGACCAGGGACACGTCCACGAGCACAGTC TACTTGGACCTGAGCAGCCTGAGATCTGGT GACACGGCCGTGTATTACTGT**GCGACCGG GTCGTGGGAGCTACCTTCCTACTTTGACT AC**TGGGGCCAGGGAACCCTGATCACCGTCT CCTCAG
SARS-CoV-2 S2M7-v1 mAb VL (nt)	523	GACATCGTGATGATGCAGTCTCCAGGCACC CTGTCTTTGTCTCCAGGGGAAAGAGCCACC CTCTCCTGCAGGGCCAGT**CAGAGTATTTAC AGCAGCTAT**TTAGCCTGGTACCAGCAGAA ACCTGGCCAGGCTCCCAGGCTCCTCATCTCT **GGTGCATCC**AGCAGGGCCACTGGCATCCC AGACAGGTTCAGTGGCAGTGGGTCTGGGAC AGACTTCACTCTCACCATCAGCAGACTGGA

Sequence Description	SEQ ID NO.	Sequence
		GCCTGCGGATTTTGCAGTGTATTACTGT**CA GCAGTATGGTAGCTCACCTCCGACG**TTCG GCCAAGGGACCAAGGTGGAAATCAAAC
SARS-CoV-2 S2M11-v1 mAb VH (aa)	524	EVQLVQSGAEVKKPGASVKVSCKAS**GYTFT GYY**MHWVRQAPGQGLEWMGW**INPISSGT**S YAQTFQGRVTMTSDTSITTAYMELSRLRSDD TAVYYC**ARAAPFYDFWSGYSYFDY**WGQGT LVTVSS
SARS-CoV-2 S2M11-v1 mAb CDRH1 (aa)	525	**GYTFTGYY**
SARS-CoV-2 S2M11-v1 mAb CDRH2 (aa)	526	**INPISSGT**
SARS-CoV-2 S2M11-v1 mAb CDRH3 (aa)	527	**ARAAPFYDFWSGYSYFDY**
SARS-CoV-2 S2M11-v1 mAb VL (aa)	528	EIVMMQSPGTLSLSPGERATLSCRAS**QSVSSS YL**AWYQQKPGQAPRLLIY**GAS**SRATGIPDRFS GSGSGTDFTLTISRLEPEDFAVYYC**QQYGSSA WT**FGQGTKVEIK
SARS-CoV-2 S2M11-v1 mAb CDRL1 (aa)	529	**QSVSSSY**
SARS-CoV-2 S2M11-v1 mAb CDRL2 (aa)	530	**GAS**
SARS-CoV-2 S2M11-v1 mAb CDRL3 (aa)	531	**QQYGSSAWT**
SARS-CoV-2 S2M11-v1 mAb VH (nt)	532	GAGGTGCAGCTGGTGCAGTCTGGGGCTGAG GTGAAGAAGCCTGGGGCCTCAGTGAAGGTC TCCTGCAAGGCTTCT**GGATACACCTTCACC**

Sequence Description	SEQ ID NO.	Sequence
		GGCTACTATATGCACTGGGTGCGACAGGC CCCTGGACAAGGGCTTGAGTGGATGGGATG G**ATCAACCCTATCAGTAGTGGCACA**AGCT ATGCACAGACATTTCAGGGCAGGGTCACCA TGACCAGTGACACGTCCATCACCACAGCCT ACATGGAGCTCAGCAGGCTGAGATCTGACG ACACGGCCGTATATTACTGT**GCGAGAGCA GCCCCGTTTTACGATTTTTGGAGTGGTTA TTCTTACTTTGACTAC**TGGGGCCAGGGAA CCCTGGTCACCGTCTCCTCAG
SARS-CoV-2 S2M11-v1 mAb VL (nt)	533	GAAATAGTGATGATGCAGTCTCCAGGCACC CTGTCTTTGTCTCCAGGGGAAAGAGCCACC CTCTCCTGCAGGGCCAGT**CAGAGTGTTAG CAGCAGCTAC**TTAGCCTGGTACCAGCAGA AACCTGGCCAGGCTCCCAGGCTCCTCATCT AT**GGTGCATCC**AGCAGGGCCACTGGCATC CCAGACAGGTTCAGTGGCAGTGGGTCTGGG ACAGACTTCACTCTCACCATCAGCAGACTG GAGCCTGAAGATTTTGCAGTGTATTACTGT **CAGCAGTATGGTAGCTCAGCGTGGACG**T TCGGCCAAGGGACCAAGGTGGAAATCAAA C
SARS-CoV-2 S2M16-v1 mAb VH (aa)	534	EVQLVESGGGMVLPGRSLRLSCAAS**GFTFSN YA**MHWVRQAPGKGLEWVAV**ISYDGSTK**YF ADSVKGRFTISRDTSKNTLYLQMNSLRAEDT AVYYC**AKDSETCSSFTCYCDY**WGRGTLVTV SS
SARS-CoV-2 S2M16-v1 mAb CDRH1 (aa)	535	**GFTFSNYA**
SARS-CoV-2 S2M16-v1 mAb CDRH2 (aa)	536	**ISYDGSTK**
SARS-CoV-2 S2M16-v1 mAb CDRH3 (aa)	537	**AKDSETCSSFTCYCDY**
SARS-CoV-2	538	DIVLTQSPDSLAVSLGERATINCKSS**QSVLYSS**

Sequence Description	SEQ ID NO.	Sequence
S2M16-v1 mAb VL (aa)		**NNKNY**LAWYQQKPGQPPKLLIY**WAS**TRESG VPDRFSGSGSGTDFTLTIGSLQAEDVAVYYC**Q QYYNTPFT**FGPGTKVDIK
SARS-CoV-2 S2M16-v1 mAb CDRL1 (aa)	539	**QSVLYSSNNKNY**
SARS-CoV-2 S2M16-v1 mAb CDRL2 (aa)	540	**WAS**
SARS-CoV-2 S2M16-v1 mAb CDRL3 (aa)	541	**QQYYNTPFT**
SARS-CoV-2 S2M16-v1 mAb VH (nt)	542	GAGGTGCAACTGGTGGAGTCTGGGGGAGG CATGGTCCTGCCTGGGAGGTCCCTGAGACT CTCCTGTGCAGCCTCT**GGATTCACCTTCAG TAACTATGCC**ATGCACTGGGTCCGCCAGGC TCCAGGCAAGGGGCTGGAGTGGGTGGCAGT T**ATATCGTATGATGGAAGTACTAAA**TACT TTGCAGACTCCGTGAAGGGCCGATTCACCA TCTCCAGAGACACTTCCAAGAACACGCTGT ATCTGCAAATGAACAGCCTGAGAGCTGAGG ACACGGCTGTGTATTACTGT**GCGAAAGATT CAGAGACTTGTAGTAGTTTCACCTGCTAT TGCGACTAC**TGGGGCCGGGGAACCCTGGT CACCGTCTCCTCAG
SARS-CoV-2 S2M16-v1 mAb VL (nt)	543	GATATTGTGCTGACTCAGTCTCCAGACTCCC TGGCTGTGTCTCTGGGCGAGAGGGCCACCA TCAACTGCAAGTCCAGC**CAGAGTGTTTTAT ACAGCTCCAACAATAAGAACTAC**TTAGCT TGGTACCAGCAGAAACCAGGACAGCCTCCT AAGCTGCTCATTTAC**TGGGCATCT**ACCCGG GAATCCGGGGTCCCTGACCGATTCAGTGGC AGCGGGTCTGGGACAGATTTCACTCTCACC ATCGGCAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGT**CAGCAATATTATAATACT CCCTTCACT**TTCGGCCCTGGGACCAAAGTG GATATCAAAC

Sequence Description	SEQ ID NO.	Sequence
SARS-CoV-2 S2M28-v1 mAb VH (aa)	544	EVQLVESGGGVVQPGRSLRLSCAAS**GFTFSS YG**MHWVRQAPGKGLEWVTV**IWYDGSNR**Y YADSVKGRFTISRDNSKNTLYLQMDSLRAED TAVYYC**ARAVAGEWYFDY**WGQGTLVTVSS
SARS-CoV-2 S2M28-v1 mAb CDRH1 (aa)	545	**GFTFSSYG**
SARS-CoV-2 S2M28-v1 mAb CDRH2 (aa)	546	**IWYDGSNR**
SARS-CoV-2 S2M28-v1 mAb CDRH3 (aa)	547	**ARAVAGEWYFDY**
SARS-CoV-2 S2M28-v1 mAb VL (aa)	548	SYELTQPPSVSVSPGQTARITCSGD**ALAKHY**A YWYRQKPGQAPVLVIY**KDS**ERPSGIPERFSGS SSGTTVTLTISGVQAEDEADYYC**QSADSIGSS WV**FGGGTKLTVL
SARS-CoV-2 S2M28-v1 mAb CDRL1 (aa)	549	**ALAKHY**
SARS-CoV-2 S2M28-v1 mAb CDRL2 (aa)	550	**KDS**
SARS-CoV-2 S2M28-v1 mAb CDRL3 (aa)	551	**QSADSIGSSWV**
SARS-CoV-2 S2M28-v1 mAb VH (nt)	552	GAGGTGCAGCTGGTGGAGTCTGGGGGAGG CGTGGTCCAGCCTGGGAGGTCCCTGAGACT CTCCTGTGCAGCGTCT**GGATTCACCTTCAG TAGCTATGGC**ATGCACTGGGTCCGCCAGG CTCCAGGCAAGGGGCTGGAGTGGGTGACA GTT**ATTTGGTATGATGGAAGTAATCGA**TA CTATGCAGACTCCGTGAAGGGCCGATTCAC CATCTCCAGAGACAATTCCAAGAACACGCT GTATCTGCAAATGGACAGCCTGAGAGCCGA

Sequence Description	SEQ ID NO.	Sequence
		GGACACGGCTGTTTATTACTGT**GCGAGAGC AGTGGCCGGGGAATGGTACTTTGACTAC** TGGGGCCAGGGAACCCTGGTCACCGTCTCC TCAG
SARS-CoV-2 S2M28-v1 mAb VL (nt)	553	TCCTATGAGCTGACACAGCCACCCTCGGTG TCAGTGTCCCCAGGACAGACGGCCAGGATC ACCTGCTCCGGAGAT**GCATTGGCAAAACA CTAT**GCTTATTGGTACCGGCAGAAGCCAGG CCAGGCCCCTGTGCTGGTGATATAT**AAAGA CAGT**GAGAGGCCCTCAGGGATCCCTGAGC GATTCTCTGGCTCCAGCTCAGGGACAACAG TCACGTTGACCATCAGTGGAGTCCAGGCAG AAGACGAGGCTGACTATTACTGT**CAATCAG CAGACAGCATTGGTAGTTCTTGGGTG**TTC GGCGGAGGGACCAAGCTGACCGTCCTAG
SARS-CoV-2 S2L49-v1 mAb VH (aa)	554	EVQLLESGGGVVQPGGSLRLSCAAS**GFNFSS YG**MHWVRQAPGKGLEWVAF**MRYDETNK**Y YADSVKGRFTISRDNSKNTLYLQMNSLRAED TAVYYC**AKDRLLGGPYYDSIGLDY**WGQGT LVTVSS
SARS-CoV-2 S2L49-v1 mAb CDRH1 (aa)	555	**GFNFSSYG**
SARS-CoV-2 S2L49-v1 mAb CDRH2 (aa)	556	**MRYDETNK**
SARS-CoV-2 S2L49-v1 mAb CDRH3 (aa)	557	**AKDRLLGGPYYDSIGLDY**
SARS-CoV-2 S2L49-v1 mAb VL (aa)	558	DIVMTQSPSSVSASVGDRVTITCRAS**QGISSW** LAWYQQKPGKAPKLLIY**TAS**SLQSGVPSRFS GSESGTDFTLTISSLQPEDFATYYC**QQGYSFP YT**FGQGTKLEIK
SARS-CoV-2 S2L49-v1 mAb CDRL1 (aa)	559	**QGISSW**
SARS-CoV-2 S2L49-v1	560	**TAS**

Sequence Description	SEQ ID NO.	Sequence
mAb CDRL2 (aa)		
SARS-CoV-2 S2L49-v1 mAb CDRL3 (aa)	561	**QQGYSFPYT**
SARS-CoV-2 S2L49-v1 mAb VH (nt)	562	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGC GTGGTCCAGCCTGGGGGGTCCCTGAGACTC TCCTGTGCAGCGTCT**GGATTCAACTTCAGT AGCTATGGC**ATGCACTGGGTCCGCCAGGC TCCAGGCAAGGGGCTGGAGTGGGTGGCATT T**ATGCGGTATGATGAAACTAATAAA**TACT ATGCAGACTCCGTGAAGGGCCGATTCACCA TCTCCAGAGACAATTCCAAGAACACGCTGT ATCTGCAAATGAACAGCCTGAGAGCTGAGG ACACGGCTGTGTATTACTGT**GCGAAAGATC GGCTATTAGGAGGTCCATATTATGATAG CATTGGGCTTGACTAC**TGGGGCCAGGGAA CCCTGGTCACCGTCTCCTCAG
SARS-CoV-2 S2L49-v1 mAb VL (nt)	563	GATATTGTGATGACTCAGTCTCCATCTTCCG TGTCTGCATCTGTAGGAGACAGAGTCACCA TCACTTGTCGGGCGAGT**CAGGGTATTAGC AGCTGG**TTAGCCTGGTATCAGCAGAAACC AGGTAAAGCCCCTAAGCTCTTGATCTAT**AC TGCATCC**AGTTTGCAAAGTGGGGTCCCATC AAGGTTCAGCGGCAGTGAATCTGGGACAGA TTTCACTCTCACCATCAGCAGCCTGCAGCCT GAAGATTTTGCAACTTACTATTGT**CAACAG GGTTACAGTTTCCCGTACACT**TTTGGCCA GGGGACCAAGCTGGAGATCAAAC
SARS-CoV-2 S2D65-v1 mAb VH (aa)	564	EVQLVESGGGLAQPGRSLRLSCAVS**GFSFDD YAMHWVRQVPGKGLEWVSGISWNSGNI**GY ADSAKGRFTISRDNAKNSLYLQMNSLRPEDT ALYYC**VKDKHYDSSGYVVNGFDY**WGQGTL VTVSP
SARS-CoV-2 S2D65-v1 mAb CDRH1 (aa)	565	**GFSFDDYA**
SARS-CoV-2	566	**ISWNSGNI**

Sequence Description	SEQ ID NO.	Sequence
S2D65-v1 mAb CDRH2 (aa)		
SARS-CoV-2 S2D65-v1 mAb CDRH3 (aa)	567	**VKDKHYDSSGYVVNGFDY**
SARS-CoV-2 S2D65-v1 mAb VL (aa)	568	DIQLTQSPSFLSASVGDRVTITCRAS**QDISSY**L AWYQQKPGKAPKLLIY**AAS**TLQSGVPSRFSG SGSGTEFTLTIRSLQPEDFATYYC**QQLHSYPA** TFGQGTKVEIK
SARS-CoV-2 S2D65-v1 mAb CDRL1 (aa)	569	**QDISSY**
SARS-CoV-2 S2D65-v1 mAb CDRL2 (aa)	570	**AAS**
SARS-CoV-2 S2D65-v1 mAb CDRL3 (aa)	571	**QQLHSYPAT**
SARS-CoV-2 S2D65-v1 mAb VH (nt)	572	GAGGTGCAGCTGGTGGAGTCGGGGGGAGG CTTGGCACAGCCTGGCAGGTCCCTGAGACT CTCCTGTGCAGTCTCT**GGATTCAGCTTTGA TGATTATGCC**ATGCACTGGGTCCGGCAAGT TCCAGGGAAGGGCCTGGAGTGGGTCTCAGG **TATTAGTTGGAATAGTGGTAACATA**GGCT ATGCGGACTCTGCGAAGGGCCGATTCACCA TCTCCAGAGACAACGCCAAGAACTCCCTGT ATCTGCAAATGAACAGTCTGAGACCTGAGG ACACGGCCTTGTATTACTGT**GTAAAAGATA AACATTATGATAGTAGTGGTTACGTAGTA AATGGATTTGACTAC**TGGGGCCAGGGAAC CCTGGTCACCGTCTCCCCAG
SARS-CoV-2 S2D65-v1 mAb VL (nt)	573	GACATCCAGTTGACCCAGTCTCCATCCTTCC TGTCTGCATCTGTAGGAGACAGAGTCACCA TCACTTGCCGGGCCAGT**CAGGACATTAGC AGTTAT**TTGGCCTGGTATCAGCAAAAACCA

Sequence Description	SEQ ID NO.	Sequence
		GGGAAAGCCCCTAAGCTCCTGATCTATGCT GCATCCACTTTGCAAAGTGGGGTCCCATCA AGGTTCAGCGGCAGTGGATCTGGGACAGAA TTCACTCTCACAATCCGCAGCCTGCAGCCT GAAGATTTTGCAACTTATTACTGTCAACAG CTTCACAGTTACCCTGCGACGTTCGGCCA AGGGACCAAGGTGGAAATCAAAC
SARS-CoV-2 S2D97-v1 mAb VH (aa)	574	QITLKESGPTLVKPTQTLTLTCSFSGFSLTTSG VGVAWIRQPPGKALEWLALIYWDDDKRYSP TLRSRLTITKDTSKNQVVLTMTNMDPVDTAT YYCALHQIMTVFDLWGRGALVTVSS
SARS-CoV-2 S2D97-v1 mAb CDRH1 (aa)	575	GFSLTTSGVG
SARS-CoV-2 S2D97-v1 mAb CDRH2 (aa)	576	IYWDDDK
SARS-CoV-2 S2D97-v1 mAb CDRH3 (aa)	577	ALHQIMTVFDL
SARS-CoV-2 S2D97-v1 mAb VL (aa)	578	QSVLTQPASVSGSPGQSITISCTGTSSDVGDYN YVSWYQHHPGKAPKLMIYQVTNRPSGVSNR FSGSKSGNTASLTISGLQAEDEADYYCTSYTT SSTLVEFGGGTKLTVL
SARS-CoV-2 S2D97-v1 mAb CDRL1 (aa)	579	SSDVGDYNY
SARS-CoV-2 S2D97-v1 mAb CDRL2 (aa)	580	QVT
SARS-CoV-2 S2D97-v1 mAb CDRL3	581	TSYTTSSTLVE

Sequence Description	SEQ ID NO.	Sequence
(aa)		
SARS-CoV-2 S2D97-v1 mAb VH (nt)	582	CAGATCACCTTGAAGGAGTCTGGTCCTACC CTGGTGAAACCCACACAGACCCTCACGCTG ACCTGCAGTTTCTCT**GGGTTCTCACTCACC ACTAGTGGAGTGGGT**GTGGCCTGGATCCG TCAGCCCCCAGGAAAGGCCCTGGAGTGGCT TGCACTC**ATTTATTGGGATGATGACAAG**C GCTACAGCCCAACTCTGAGGAGCAGGCTCA CCATCACCAAGGACACCTCCAAGAACCAGG TGGTCCTTACAATGACCAACATGGACCCTG TGGACACAGCCACATATTACTGT**GCACTAC ACCAGATTATGACGGTCTTCGATCTC**TGG GGCCGTGGCGCCCTGGTCACTGTCTCCTCA G
SARS-CoV-2 S2D97-v1 mAb VL (nt)	583	CAGTCTGTGCTGACTCAGCCTGCCTCCGTGT CTGGGTCTCCTGGCCAGTCGATCACCATCTC CTGCACTGGAACC**AGCAGTGACGTTGGTG ATTATAACTAT**GTGTCCTGGTACCAACACC ACCCAGGCAAAGCCCCCAAACTCATGATTT AT**CAGGTCACT**AATCGGCCCTCAGGGGTTT CTAATCGCTTCTCTGGCTCCAAGTCTGGCAA CACGGCCTCCCTGACCATCTCTGGGCTCCA GGCTGAGGACGAGGCTGATTATTACTGC**AC TTCCTATACAACCAGTAGTACTCTCGTGG AA**TTCGGCGGAGGGACCAAGTTGACCGTCT TAG
SARS-CoV-2 S2D106-v1 mAb VH (aa)	584	EVQLVQSGAEVKKPGSSVKVSCKAS**GGPFSS SA**ISWVRQAPGQGLEWMGG**IIPMVGTA**NYA QKFQGRVTITADESTSTAYMELSSLRSEDTAV YYC**ARDSRYCSGGSCYSVWFDP**WGQGTLV TVSS
SARS-CoV-2 S2D106-v1 mAb CDRH1 (aa)	585	**GGPFSSSA**
SARS-CoV-2 S2D106-v1 mAb CDRH2 (aa)	586	**IIPMVGTA**

Sequence Description	SEQ ID NO.	Sequence
SARS-CoV-2 S2D106-v1 mAb CDRH3 (aa)	587	**ARDSRYCSGGSCYSVWFDP**
SARS-CoV-2 S2D106-v1 mAb VL (aa)	588	DIQLTQSPSSLSASVGDRVTITCRAS**QSISSY**L NWYQQKPGKAPKVLIY**AAS**SLQSGVPSRFSG SGSGTDFTLTISSLQPEDFATYYC**QQSYSTPR** TFGQGTKVEMK
SARS-CoV-2 S2D106-v1 mAb CDRL1 (aa)	589	**QSISSY**
SARS-CoV-2 S2D106-v1 mAb CDRL2 (aa)	590	**AAS**
SARS-CoV-2 S2D106-v1 mAb CDRL3 (aa)	591	**QQSYSTPRT**
SARS-CoV-2 S2D106-v1 mAb VH (nt)	592	GAGGTGCAGCTGGTGCAGTCTGGGGCTGAG GTGAAGAAGCCTGGGTCCTCGGTGAAGGTT TCCTGCAAGGCTTCT**GGAGGCCCCTTCAG CAGCTCTGCT**ATCAGCTGGGTGCGACAGG CCCCTGGACAAGGGCTTGAGTGGATGGGAG **GGATCATCCCTATGGTAGGTACAGCA**AAC TATGCACAGAAGTTCCAGGGCAGAGTCACG ATTACCGCGGACGAATCCACGAGCACAGCC TACATGGAGCTGAGCAGCCTGAGATCTGAG GACACGGCCGTGTATTACTGT**GCGAGAGA TTCGCGCTATTGTAGTGGTGGTAGCTGC TACTCCGTCTGGTTCGACCCC**TGGGGCCA GGGAACCCTGGTCACCGTCTCCTCAG
SARS-CoV-2 S2D106-v1 mAb VL (nt)	593	GACATCCAGTTGACCCAGTCTCCATCCTCCC TGTCTGCATCTGTAGGAGACAGAGTCACCA TCACTTGCCGGGCAAGT**CAGAGCATTAGC AGCTAT**TTAAATTGGTATCAGCAGAAACCA GGGAAAGCCCCTAAGGTCCTGATCTAT**GCT GCATCC**AGTTTGCAAAGTGGGGTCCCATCA AGGTTCAGTGGCAGTGGATCTGGGACAGAT

Sequence Description	SEQ ID NO.	Sequence
		TTCACTCTCACCATCAGCAGTCTCCAACCTG AAGATTTTGCAACTTACTACTGT**CAACAGA GTTACAGTACCCCTCGAACG**TTCGGCCAA GGGACCAAGGTGGAAATGAAAC
SARS-CoV-2 S2X149-v1 mAb VH (aa)	594	QVQLVQSGADVKKPGASVKVSCKAS**GYTFT GYF**IHWVRQAPGQGLEWMGW**INPISGGR**NY TRKFQGRITMNRDTSITTAYMELSRLRSDDTA VYYC**ARDSGGMDYGSGSYFSPPRYGMDV**W GQGTTVTVSS
SARS-CoV-2 S2X149-v1 mAb CDRH1 (aa)	595	**GYTFTGYF**
SARS-CoV-2 S2X149-v1 mAb CDRH2 (aa)	596	**INPISGGR**
SARS-CoV-2 S2X149-v1 mAb CDRH3 (aa)	597	**ARDSGGMDYGSGSYFSPPRYGMDV**
SARS-CoV-2 S2X149-v1 mAb VL (aa)	598	QSVLTQPASVSGSPGQSITISCTGA**SSDVGAY NF**VSWYQQHPGKAPKLMIY**EVS**NRPSGVSNR FSGSKSGNTASLTISGLQAEDEAAYYC**SSYTS SNTVV**FGGGTSLTVL
SARS-CoV-2 S2X149-v1 mAb CDRL1 (aa)	599	**SSDVGAYNF**
SARS-CoV-2 S2X149-v1 mAb CDRL2 (aa)	600	**EVS**
SARS-CoV-2 S2X149-v1 mAb CDRL3 (aa)	601	**SSYTSSNTVV**
SARS-CoV-2	602	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAC

Sequence Description	SEQ ID NO.	Sequence
S2X149-v1 mAb VH (nt)		GTGAAGAAGCCTGGGGCCTCAGTGAAGGTC TCCTGCAAGGCTTCT**GGATACACCTTCACC GGCTACTTT**ATACACTGGGTGCGACAGGC CCCTGGACAAGGGCTTGAGTGGATGGGATG **GATCAACCCTATCAGTGGTGGCAGA**AACT ATACACGGAAGTTTCAGGGCAGGATCACCA TGAACAGGGACACGTCCATCACCACAGCCT ACATGGAGCTGAGCAGGCTGAGATCTGACG ACACGGCCGTGTATTACTGT**GCGAGAGATT CGGGGGGGATGGACTATGGTTCGGGGAG TTATTTTTCCCCCCCCCGATACGGTATGG ACGTC**TGGGGCCAAGGGACCACGGTCACC GTCTCCTCA
SARS-CoV-2 S2X149-v1 mAb VL (nt)	603	CAGTCTGTGCTGACTCAGCCTGCCTCCGTGT CTGGGTCTCCTGGACAGTCGATCACCATCT CCTGCACTGGAGCC**AGCAGTGACGTTGGT GCTTATAACTTT**GTCTCCTGGTACCAACAG CACCCAGGCAAAGCCCCCAAACTCATGATT TAT**GAGGTCAGT**AATCGGCCCTCAGGGGTT TCTAATCGCTTCTCTGGCTCCAAGTCTGGCA ACACGGCCTCCCTGACCATCTCTGGGCTCC AGGCTGAGGACGAGGCTGCTTATTACTGCA **GCTCATATACAAGCAGTAACACTGTGGT** ATTCGGCGGAGGGACCAGCCTGACCGTCCT AG
SARS-CoV-2 S2X179-v1 mAb VH (aa)	604	EVQLVESGGGLVQPGGSLRLSCAAS**GITVSSN** **Y**MTWVRQAPGKGLEWVSV**IYSGGST**FYADS VRGRFTISRDNSKNTLYLQMNSLRPDDTAVY YC**ARDLNELGIDC**WGQGTLVTVSS
SARS-CoV-2 S2X179-v1 mAb CDRH1 (aa)	605	**GITVSSNY**
SARS-CoV-2 S2X179-v1 mAb CDRH2 (aa)	606	**IYSGGST**
SARS-CoV-2 S2X179-v1	607	**ARDLNELGIDC**

Sequence Description	SEQ ID NO.	Sequence
mAb CDRH3 (aa)		
SARS-CoV-2 S2X179-v1 mAb VL (aa)	608	DIVMTQTPSSVSASVGDRVTITCRAS**QGISRW** LAWYQQKPGKAPKLLIY**AAS**TLQSGVPSRFS GSGSGTDFTLTIRSLQPEDYATYYC**QQANSFP** **F**FGGGTKVEIK
SARS-CoV-2 S2X179-v1 mAb CDRL1 (aa)	609	**QGISRW**
SARS-CoV-2 S2X179-v1 mAb CDRL2 (aa)	610	**AAS**
SARS-CoV-2 S2X179-v1 mAb CDRL3 (aa)	611	**QQANSFPF**
SARS-CoV-2 S2X179-v1 mAb VH (nt)	612	GAGGTGCAGCTGGTGGAGTCTGGGGGAGG CTTGGTCCAGCCTGGGGGGTCCCTGAGACT CTCCTGTGCAGCCTCT**GGTATCACCGTCAG** **TAGCAATTAT**ATGACCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGGAATGGGTCTCAGT **TATTTATAGCGGTGGCAGCACA**TTCTACG CAGACTCCGTGAGGGGCCGATTCACCATCT CCAGAGACAATTCCAAGAACACCCTGTATC TTCAAATGAACAGCCTGAGACCTGACGACA CGGCTGTGTATTACTGT**GCGAGAGATCTG** **AACGAGCTGGGGATTGACTGC**TGGGGCC AGGGAACCCTGGTCACCGTCTCCTCAG
SARS-CoV-2 S2X179-v1 mAb VL (nt)	613	GATATTGTGATGACCCAGACTCCATCTTCC GTGTCTGCATCTGTAGGAGACAGAGTCACC ATCACTTGTCGGGCGAGT**CAGGGTATTAG** **CCGCTGG**TTAGCCTGGTATCAGCAGAAAC CAGGGAAAGCCCCTAAGCTCCTGATCTAT**G** **CTGCATCC**ACTTTACAAAGTGGGGTCCCAT CAAGGTTCAGCGGCAGTGGATCTGGGACAG ATTTCACTCTCACCATCAGGAGCCTGCAGC CTGAAGATTATGCAACTTACTATTGT**CAAC** **AGGCTAACAGTTTCCCTTTT**TTCGGCGGA

Sequence Description	SEQ ID NO.	Sequence
		GGGACCAAGGTGGAGATCAAAC
SARS-CoV-2 S2H101-v1 mAb VH (aa)	614	EVHLVESGGGLVQPGGSLRLSCAAS**GFTFIN YAMSWVRQAPGKGLEWVSAIGLSGGST**NY ADSVKGRFTISRDNSKNTLSLEMNNLRAEDT AVYYC**TKGRGGYFDPFDP**WGQGTLVTVSS
SARS-CoV-2 S2H101-v1 mAb CDRH1 (aa)	615	**GFTFINYA**
SARS-CoV-2 S2H101-v1 mAb CDRH2 (aa)	616	**IGLSGGST**
SARS-CoV-2 S2H101-v1 mAb CDRH3 (aa)	617	**TKGRGGYFDPFDP**
SARS-CoV-2 S2H101-v1 mAb VL (aa)	618	DIVMTQSPSSLSASVGDRVTITCRAS**QSISSY**L NWYQQIPGKAPNLLIH**AAS**SLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYC**QQSYSSPPT**F GQGTKLEIK
SARS-CoV-2 S2H101-v1 mAb CDRL1 (aa)	619	**QSISSY**
SARS-CoV-2 S2H101-v1 mAb CDRL2 (aa)	620	**AAS**
SARS-CoV-2 S2H101-v1 mAb CDRL3 (aa)	621	**QQSYSSPPT**
SARS-CoV-2 S2H101-v1 mAb VH (nt)	622	GAGGTGCATCTGGTGGAGTCTGGGGGAGGC TTGGTACAGCCTGGGGGGTCCCTGAGACTC TCCTGTGCAGCCTCT**GGATTCACCTTTATC AACTATGCC**ATGAGCTGGGTCCGCCAGGCT CCAGGGAAGGGGCTGGAATGGGTCTCAGCT

Sequence Description	SEQ ID NO.	Sequence
		ATTGGTCTTAGTGGTGGTAGTACAAACTA CGCAGACTCCGTGAAGGGCCGGTTCACCAT CTCCAGAGACAACTCCAAGAACACGCTGTC TTTGGAAATGAACAACCTGCGAGCCGAGGA CACGGCCGTATATTACTGT**ACAAAAGGGA GGGGAGGATATTTTGACCCGTTCGACCC C**TGGGGCCAGGGAACCCTGGTCACCGTCTC CTCAG
SARS-CoV-2 S2H101-v1 mAb VL (nt)	623	GACATCGTGATGACCCAGTCTCCATCCTCC CTGTCTGCATCTGTTGGGGACAGAGTCACC ATCACTTGCCGGGCAAGT**CAGAGCATTAG CAGCTA**TTTAAATTGGTATCAGCAGATACC AGGGAAAGCCCCTAACCTCCTGATCCAT**GC TGCATCC**AGTTTGCAAAGTGGGGTCCCATC AAGGTTCAGTGGCAGTGGATCTGGGACAGA TTTCACTCTCACCATCAGCAGTCTGCAACCT GAAGATTTTGCAACTTACTACTGT**CAGCAG AGTTACAGTTCCCCTCCCACT**TTTGGCCA GGGGACCAAGCTGGAGATCAAAC
Antibody 409_11_1_v2 VH	624	EVQLVQSGAEVKKPGSSVKVSCKAS**GGPFSS SA**ISWVRQAPGQGLEWMGG**IIPIVGTA**NYAQ KFQGRVTITADESTSTAYMELSSLRSEDTAVY YC**ARDSRYCSGGSCYSVWFDP**WGQGTLVT VSS
Antibody 409_11_1_v2 CDRH2	625	**IIPIVGTA**
Antibody 409_11_1_v3 VH	626	EVQLVQSGAEVKKPGSSVKVSCKAS**GGPFSS SA**ISWVRQAPGQGLEWMGG**IIPMVGTA**NYA QKFQGRVTITADESTSTAYMELSSLRSEDTAV YYC**ARDSRYCSGGSCYSVFFDP**WGQGTLVT VSS
Antibody 409_11_1_v3 CDRH3	627	**ARDSRYCSGGSCYSVFFDP**
Antibody 409_11_1_v4 VH	628	EVQLVQSGAEVKKPGSSVKVSCKAS**GGPFSS SA**ISWVRQAPGQGLEWMGG**IIPIVGTA**NYAQ KFQGRVTITADESTSTAYMELSSLRSEDTAVY YC**ARDSRYCSGGSCYSVFFDP**WGQGTLVTV SS

Sequence Description	SEQ ID NO.	Sequence
[reserved]	629	**[reserved]**
Antibody 409_11_2_v1 VH	630	QITLKESGPTLVKPTQTLTLTCTFS**GFSVTTSG VG**VGWIRQPPGKALEYLAL**IYWDDDK**RYST SLKSRLTITKDTSKNQVVLTMTNMDPVDTAT YYC**ARHTIPSIFDY**WGQGILVTVSS
Antibody 409_11_2_v1 CDRH1	631	**GFSVTTSGVG**
Antibody 409_11_2_v1 CDRH2	632	**IYWDDDK**
Antibody 409_11_2_v1 CDRH3	633	**ARHTIPSIFDY**
Antibody 409_11_2_v2 VH	634	QITLKESGPTLVKPTQTLTLTCTFSGFSVTTSG VGVGWIRQPPGKALEYLAL**IYFDDDK**RYSTS LKSRLTITKDTSKNQVVLTMTNMDPVDTATY YCARHTIPSIFDYWGQGILVTVSS
Antibody 409_11_2_v2 CDRH2	635	**IYFDDDK**
Antibody 409_11_2_v3 VH	636	QITLKESGPTLVKPTQTLTLTCTFSGFSVTTSG VGVGWIRQPPGKALEYLAL**IYYDDDK**RYSTS LKSRLTITKDTSKNQVVLTMTNMDPVDTATY YCARHTIPSIFDYWGQGILVTVSS
Antibody 409_11_2_v3 CDRH2	637	**IYYDDDK**
Antibody 409_11_2_v4 VH	638	QITLKESGPTLVKPTQTLTLTCTFSGFSVTTSG VGVGWIRQPPGKALEYLAL**IYWEDDK**RYSTS LKSRLTITKDTSKNQVVLTMTNMDPVDTATY YCARHTIPSIFDYWGQGILVTVSS
Antibody 409_11_2_v4 CDRH2	639	**IYWEDDK**
Antibody 409_11_2_v5 VH	640	QITLKESGPTLVKPTQTLTLTCTFSGFSVTTSG VGVGWIRQPPGKALEYLAL**IYWNDDK**RYST SLKSRLTITKDTSKNQVVLTMTNMDPVDTAT YYCARHTIPSIFDYWGQGILVTVSS
Antibody 409_11_2_v5	641	**IYWNDDK**

Sequence Description	SEQ ID NO.	Sequence
CDRH2		
Antibody 409_11_2_v6 VH	642	QITLKESGPTLVKPTQTLTLTCTFSGFSVTTSG VGVGWIRQPPGKALEYLAL**IYWDEDK**RYSTS LKSRLTITKDTSKNQVVLTMTNMDPVDTATY YCARHTIPSIFDYWGQGILVTVSS
Antibody 409_11_24_v6 CDRH2	643	**IYWDEDK**
Antibody 409_11_2_v7 VH	644	QITLKESGPTLVKPTQTLTLTCTFSGFSVTTSG VGVGWIRQPPGKALEYLAL**IYWDNDK**RYST SLKSRLTITKDTSKNQVVLTMTNMDPVDTAT YYCARHTIPSIFDYWGQGILVTVSS
Antibody 409_11_2_v7 CDRH2	645	**IYWDNDK**
Antibody 409_11_2_v8 VH	646	QITLKESGPTLVKPTQTLTLTCTFSGFSVTTSG VGVGWIRQPPGKALEYLAL**IYFEDDK**RYSTS LKSRLTITKDTSKNQVVLTMTNMDPVDTATY YCARHTIPSIFDYWGQGILVTVSS
Antibody 409_11_2_v8 CDRH2	647	**IYFEDDK**
Antibody 409_11_2_v9 VH	648	QITLKESGPTLVKPTQTLTLTCTFSGFSVTTSG VGVGWIRQPPGKALEYLAL**IYFNDDK**RYSTS LKSRLTITKDTSKNQVVLTMTNMDPVDTATY YCARHTIPSIFDYWGQGILVTVSS
Antibody 409_11_2_v9 CDRH2	649	**IYFNDDK**
Antibody 409_11_2_v10 VH	650	QITLKESGPTLVKPTQTLTLTCTFSGFSVTTSG VGVGWIRQPPGKALEYLAL**IYYEDDK**RYSTS LKSRLTITKDTSKNQVVLTMTNMDPVDTATY YCARHTIPSIFDYWGQGILVTVSS
Antibody 409_11_2_v10 CDRH2	651	**IYYEDDK**
Antibody 409_11_2_v11 VH	652	QITLKESGPTLVKPTQTLTLTCTFSGFSVTTSG VGVGWIRQPPGKALEYLAL**IYYNDDK**RYSTS LKSRLTITKDTSKNQVVLTMTNMDPVDTATY YCARHTIPSIFDYWGQGILVTVSS
Antibody 409_11_2_v11	653	**IYYNDDK**

Sequence Description	SEQ ID NO.	Sequence
CDRH2		
Antibody 409_11_2_v12 VH	654	QITLKESGPTLVKPTQTLTLTCTFSGFSVTTSG VGVGWIRQPPGKALEYLAL**IYFDEDK**RYSTS LKSRLTITKDTSKNQVVLTMTNMDPVDTATY YCARHTIPSIFDYWGQGILVTVSS
Antibody 409_11_2_v12 CDRH2	655	**IYFDEDK**
Antibody 409_11_2_v13 VH	656	QITLKESGPTLVKPTQTLTLTCTFSGFSVTTSG VGVGWIRQPPGKALEYLAL**IYFDNDK**RYSTS LKSRLTITKDTSKNQVVLTMTNMDPVDTATY YCARHTIPSIFDYWGQGILVTVSS
Antibody 409_11_2_v13 CDRH2	657	**IYFDNDK**
Antibody 409_11_2_v14 VH	658	QITLKESGPTLVKPTQTLTLTCTFSGFSVTTSG VGVGWIRQPPGKALEYLAL**IYYDEDK**RYSTS LKSRLTITKDTSKNQVVLTMTNMDPVDTATY YCARHTIPSIFDYWGQGILVTVSS
Antibody 409_11_2_v14 CDRH2	659	**IYYDEDK**
Antibody 409_11_2_v15 VH	660	QITLKESGPTLVKPTQTLTLTCTFSGFSVTTSG VGVGWIRQPPGKALEYLAL**IYYDNDK**RYSTS LKSRLTITKDTSKNQVVLTMTNMDPVDTATY YCARHTIPSIFDYWGQGILVTVSS
Antibody 409_11_2_v15 CDRH2	661	**IYYDNDK**
Antibody 409_11_2_v16 VH	662	QITLKESGPTLVKPTQTLTLTCTFSGFSVTTSG VGVGWIRQPPGKALEYLAL**IYWEEDK**RYSTS LKSRLTITKDTSKNQVVLTMTNMDPVDTATY YCARHTIPSIFDYWGQGILVTVSS
Antibody 409_11_2_v16 CDRH2	663	**IYWEEDK**
Antibody 409_11_2_v17 VH	664	QITLKESGPTLVKPTQTLTLTCTFSGFSVTTSG VGVGWIRQPPGKALEYLAL**IYWENDK**RYSTS LKSRLTITKDTSKNQVVLTMTNMDPVDTATY YCARHTIPSIFDYWGQGILVTVSS
Antibody 409_11_2_v17	665	**IYWENDK**

Sequence Description	SEQ ID NO.	Sequence
CDRH2		
Antibody 409_11_2_v18 VH	666	QITLKESGPTLVKPTQTLTLTCTFSGFSVTTSG VGVGWIRQPPGKALEYLAL**IYWNEDK**RYSTS LKSRLTITKDTSKNQVVLTMTNMDPVDTATY YCARHTIPSIFDYWGQGILVTVSS
Antibody 409_11_2_v18 CDRH2	667	**IYWNEDK**
Antibody 409_11_2_v19 VH	668	QITLKESGPTLVKPTQTLTLTCTFSGFSVTTSG VGVGWIRQPPGKALEYLAL**IYWNNDK**RYST SLKSRLTITKDTSKNQVVLTMTNMDPVDTAT YYCARHTIPSIFDYWGQGILVTVSS
Antibody 409_11_2_v19 CDRH2	669	**IYWNNDK**
Antibody 409_11_2_v20 VH	670	QITLKESGPTLVKPTQTLTLTCTFSGFSVTTSG VGVGWIRQPPGKALEYLAL**IYFEEDK**RYSTS LKSRLTITKDTSKNQVVLTMTNMDPVDTATY YCARHTIPSIFDYWGQGILVTVSS
Antibody 409_11_2_v20 CDRH2	671	**IYFEEDK**
Antibody 409_11_2_v21 VH	672	QITLKESGPTLVKPTQTLTLTCTFSGFSVTTSG VGVGWIRQPPGKALEYLAL**IYFENDK**RYSTS LKSRLTITKDTSKNQVVLTMTNMDPVDTATY YCARHTIPSIFDYWGQGILVTVSS
Antibody 409_11_2_v21 CDRH2	673	**IYFENDK**
Antibody 409_11_2_v22 VH	674	QITLKESGPTLVKPTQTLTLTCTFSGFSVTTSG VGVGWIRQPPGKALEYLAL**IYFNEDK**RYSTS LKSRLTITKDTSKNQVVLTMTNMDPVDTATY YCARHTIPSIFDYWGQGILVTVSS
S2X324_v22 CDRH2	675	**IYFNEDK**
Antibody 409_11_2_v23 VH	676	QITLKESGPTLVKPTQTLTLTCTFSGFSVTTSG VGVGWIRQPPGKALEYLAL**IYFNNDK**RYSTS LKSRLTITKDTSKNQVVLTMTNMDPVDTATY YCARHTIPSIFDYWGQGILVTVSS
Antibody 409_11_2_v23 CDRH2	677	**IYFNNDK**

Sequence Description	SEQ ID NO.	Sequence
Antibody 409_11_2_v24 VH	678	QITLKESGPTLVKPTQTLTLTCTFSGFSVTTSG VGVGWIRQPPGKALEYLAL**IYYEEDK**RYSTS LKSRLTITKDTSKNQVVLTMTNMDPVDTATY YCARHTIPSIFDYWGQGILVTVSS
Antibody 409_11_2_v24 CDRH2	679	**IYYEEDK**
Antibody 409_11_2_v25 VH	680	QITLKESGPTLVKPTQTLTLTCTFSGFSVTTSG VGVGWIRQPPGKALEYLAL**IYYENDK**RYSTS LKSRLTITKDTSKNQVVLTMTNMDPVDTATY YCARHTIPSIFDYWGQGILVTVSS
Antibody 409_11_2_v25 CDRH2	681	**IYYENDK**
Antibody 409_11_2_v26 VH	682	QITLKESGPTLVKPTQTLTLTCTFSGFSVTTSG VGVGWIRQPPGKALEYLAL**IYYNEDK**RYSTS LKSRLTITKDTSKNQVVLTMTNMDPVDTATY YCARHTIPSIFDYWGQGILVTVSS
Antibody 409_11_2__v26 CDRH2	683	**IYYNEDK**
Antibody 409_11_2_v27 VH	684	QITLKESGPTLVKPTQTLTLTCTFSGFSVTTSG VGVGWIRQPPGKALEYLAL**IYYNNDK**RYSTS LKSRLTITKDTSKNQVVLTMTNMDPVDTATY YCARHTIPSIFDYWGQGILVTVSS
S2X324_v27 CDRH2	685	**IYYNNDK**
Antibody 409_11_2 VL	686	QPVLTQPASVSGSPGQSITISCTAT**SSDVGNYN Y**VSWYQHHPGKAPKLMIY**EVS**NRPSGVSNRF SGSKSGNTASLTISGLQAEDEADYYC**SSYTSS SLL**FGGGTKLTVL
Antibody 409_11_2 CDRL1	687	**SSDVGNYNY**
Antibody 409_11_2 CDRL2	688	**EVS**
Antibody 409_11_2 CDRL3	689	**SSYTSSSLL**
Antibody	690	CAGATCACCTTGAAGGAGTCTGGTCCTACG

Sequence Description	SEQ ID NO.	Sequence
409_11_2 VH (nt)		CTGGTGAAACCCACACAGACCCTCACGCTG ACCTGCACCTTCTCTGGGTTCTCAGTCACT ACTAGTGGAGTGGGTGTGGGCTGGATCCG TCAGCCCCCAGGAAAGGCCCTGGAGTACCT TGCACTCATTTATTGGGATGATGATAAGC GCTACAGTACATCTCTGAAGAGCAGGCTCA CTATCACCAAGGACACCTCCAAAAACCAGG TGGTCCTTACAATGACCAACATGGACCCTG TGGACACAGCCACATATTACTGTGCACGCC ATACTATACCTTCGATCTTTGACTACTGG GGCCAGGGAATCCTGGTCACCGTCTCCTCA G
Antibody 409_11_2 VL (nt)	691	CAGCCTGTGCTGACTCAGCCTGCCTCCGTGT CTGGGTCTCCTGGACAGTCGATCACCATCT CCTGCACTGCAACCAGCAGTGACGTTGGT AATTATAACTATGTCTCCTGGTACCAACAC CACCCAGGCAAAGCCCCCAAACTCATGATT TATGAGGTCAGTAATCGGCCCTCAGGGGTT TCTAATCGCTTCTCTGGCTCCAAGTCTGGCA ACACGGCCTCCCTGACCATCTCTGGGCTCC AGGCTGAGGACGAGGCTGATTATTATTGCA GCTCATATACAAGCAGCAGTCTACTATTC GGCGGAGGGACCAAGCTGACCGTCCTAG
Antibody 409_11_3_v1 VH	692	EVQLVQSGAAVKKTGASVKVSCKASEYIFTE YYIHWVRQAPGQGLEWMGWINPNSGRTHY AQKFQGRVTMTRDTSITTAYMELSSLRSDDT AVYYCACLAGEWGYCSTTSCKRGIDGMDV WGQGTTVTVSS
Antibody 409_11_3_v1 CDRH1	693	EYIFTEYY
Antibody 409_11_3_v1 CDRH2	694	INPNSGRT
Antibody 409_11_3_v1 CDRH3	695	ACLAGEWGYCSTTSCKRGIDGMDV
Antibody 409_11_3_v1 VL	696	EIVLTQSPLSLPVTPGEPASISCRSSQSLLHSN GYNYLNWYLQKPGQSPQLLIYLGSNRASGVP DRFSGSGSGTDFTLKISRVEAEDVGVYYCMQ ALQTMYTFGQGTKLEIR
Antibody 409_11_3_v1	697	QSLLHSNGYNY

Sequence Description	SEQ ID NO.	Sequence
CDRL1		
Antibody 409_11_3_v1 CDRL2	698	**LGS**
Antibody 409_11_3_v1 CDRL3	699	**MQALQTMYT**
Antibody 409_11_3_v1 VH (nt)	700	GAGGTGCAACTGGTGCAGTCTGGGGCTGCG GTGAAGAAGACTGGGGCCTCAGTGAAGGTC TCCTGCAAGGCTTCT**GAATACATCTTCACC GAATACTAT**ATACACTGGGTGCGACAGGC CCCTGGACAAGGGCTTGAGTGGATGGGATG G**ATCAACCCTAACAGTGGTCGCACA**CACT ATGCACAGAAGTTTCAGGGCAGGGTCACCA TGACCAGGGACACGTCCATCACCACAGCCT ACATGGAGCTGAGTAGCCTGAGATCTGACG ACACGGCCGTGTATTACTGT**GCGTGCCTTG CGGGTGAGTGGGGATATTGTAGTACGAC CAGCTGCAAAAGAGGGATTGACGGTATG GACGTC**TGGGGCCAAGGGACCACGGTCAC CGTCTCCTCA
Antibody 409_11_3_v1 VL (nt)	701	GAAATTGTGTTGACGCAGTCTCCACTCTCCC TGCCCGTCACCCCTGGAGAGCCGGCCTCCA TCTCCTGCAGGTCTAGT**CAGAGCCTCCTGC ATAGTAATGGATACAACTAT**TTGAATTGG TACCTGCAGAAGCCAGGGCAGTCTCCACAA CTCCTGATCTAT**TTGGGTTCT**AATCGGGCC TCCGGGGTCCCTGACAGGTTCAGTGGCAGT GGATCAGGCACAGATTTTACACTGAAAATC AGCAGAGTGGAGGCTGAGGATGTTGGGGTT TATTACTGC**ATGCAAGCTCTACAAACTAT GTACACT**TTTGGCCAGGGGACCAAGCTGG AGATCAGAC
S2D106-v1 mAb VH (nt-CO)	702	GAAGTGCAACTAGTGCAAAGTGGTGCAGA AGTGAAGAAGCCTGGCTCTTCTGTGAAAGT GTCTTGCAAGGCCTCTGGCGGCCCATTTTCC AGCTCTGCCATCTCCTGGGTCAGACAGGCT CCCGGCCAAGGACTGGAGTGGATGGGCGG AATCATCCCTATGGTGGGCACCGCCAACTA CGCCCAGAAGTTCCAGGGCAGAGTGACCAT CACCGCTGATGAGTCCACCTCTACAGCCTA

Sequence Description	SEQ ID NO.	Sequence
		CATGGAACTGTCCTCCCTGAGATCCGAGGA CACCGCTGTGTACTACTGTGCTCGGGACTCT CGGTATTGCTCCGGCGGCAGCTGCTACTCC GTGTGGTTCGACCCTTGGGGCCAGGGCACA CTGGTGACCGTGTCCAGC
Antibody 409_11_1_v2 VH (nt-CO)	703	GAAGTGCAACTAGTGCAAAGTGGTGCAGA AGTCAAGAAGCCAGGCTCCAGCGTTAAAGT GTCTTGCAAGGCCTCTGGCGGACCTTTCTCC TCCAGCGCCATCTCCTGGGTGCGGCAGGCT CCTGGCCAAGGCCTGGAGTGGATGGGCGGC ATCATCCCCATCGTGGGCACCGCCAACTAC GCCCAGAAGTTCCAGGGCAGAGTGACCATC ACAGCCGACGAGTCTACCTCCACCGCTTAT ATGGAACTGTCTTCTCTGCGGTCCGAGGAC ACCGCTGTGTACTACTGTGCTAGAGATTCT AGATACTGCTCCGGCGGCAGCTGCTACTCC GTGTGGTTTGACCCTTGGGGCCAGGGAACC CTGGTGACAGTGTCCTCT
Antibody 409_11_1_v3 VH (nt-CO)	704	GAAGTGCAACTAGTGCAAAGTGGTGCAGA AGTCAAGAAGCCTGGATCTTCTGTGAAAGT GTCCTGCAAGGCCTCTGGCGGACCATTTAG CTCCTCTGCCATCTCCTGGGTGCGGCAGGCT CCTGGCCAAGGCCTGGAGTGGATGGGCGGC ATCATCCCCATGGTGGGCACCGCCAACTAC GCCCAGAAGTTCCAGGGCAGAGTGACCATC ACCGCTGACGAGTCCACCTCCACAGCCTAC ATGGAACTGTCCAGCCTGAGATCCGAGGAC ACCGCTGTGTACTACTGTGCTAGAGATTCTC GGTATTGCTCCGGCGGCTCTTGCTACTCCGT GTTCTTCGACCCTTGGGGCCAGGGCACCCT GGTGACCGTGTCTAGC
Antibody 409_11_1_v4 VH (nt-CO)	705	GAAGTGCAACTAGTGCAAAGTGGTGCAGA AGTCAAGAAGCCTGGCTCCTCTGTGAAAGT GTCCTGCAAGGCCTCTGGCGGCCCATTTAG CAGCTCTGCCATCTCCTGGGTGCGGCAGGC TCCTGGACAAGGCCTGGAGTGGATGGGCGG CATCATCCCCATCGTGGGCACAGCTAACTA CGCCCAGAAGTTCCAGGGCAGAGTGACCAT CACCGCCGACGAGTCCACATCTACCGCCTA CATGGAACTGTCCTCCCTGAGATCCGAGGA CACCGCTGTGTACTACTGTGCTAGAGATTCT CGGTATTGCTCCGGCGGATCTTGCTACTCCG

Sequence Description	SEQ ID NO.	Sequence
		TGTTCTTCGACCCTTGGGGCCAGGGCACCC TGGTGACCGTGTCTAGC
Antibody 409_11_2_v1 VH (nt - CO)	706	CAAATCACTCTAAAGGAAAGTGGTCCAACT CTCGTGAAGCCTACCCAGACCCTGACACTG ACCTGTACCTTTTCTGGCTTCTCCGTGACCA CCTCTGGAGTCGGCGTGGGCTGGATCCGGC AGCCTCCAGGCAAGGCCCTGGAGTACCTGG CTCTGATCTACTGGGACGACGATAAACGGT ATAGCACTAGCCTGAAGTCCAGACTGACAA TCACCAAGGATACATCCAAGAACCAAGTGG TGCTGACCATGACCAACATGGACCCTGTGG ACACCGCTACCTACTACTGCGCCAGACACA CCATCCCCTCCATCTTCGACTACTGGGGCCA GGGCATCCTGGTGACCGTGTCCTCT
Antibody 409_11_2_v2 VH (nt - CO)	707	CAAATCACTCTAAAGGAAAGTGGTCCAACT CTGGTGAAGCCTACCCAGACCCTGACACTG ACCTGTACTTTTTCTGGCTTCTCCGTGACCA CCTCCGGCGTGGGAGTGGGCTGGATCAGAC AGCCTCCAGGCAAGGCCCTCGAGTACCTGG CTCTGATCTACTTCGATGATGACAAGCGGT ATAGCACCTCTCTGAAATCTCGGCTGACAA TCACCAAGGACACATCCAAGAACCAAGTGG TGCTGACCATGACCAACATGGACCCTGTGG ACACCGCTACCTACTACTGCGCCAGACACA CCATCCCCTCCATCTTCGACTACTGGGGCCA GGGCATCCTGGTCACCGTGTCCAGC
Antibody 409_11_2_v3 VH (nt - CO)	708	CAAATCACTCTAAAGGAAAGTGGTCCAACT CTCGTGAAGCCTACCCAGACCCTGACACTG ACCTGTACTTTTAGCGGCTTCTCCGTGACCA CCTCTGGAGTCGGCGTGGGCTGGATCCGGC AGCCTCCTGGCAAAGCTCTGGAGTACCTGG CCCTGATCTACTACGACGATGACAAGCGGT ATAGCACATCTCTGAAGTCCAGACTGACCA TCACCAAGGACACCTCCAAGAACCAAGTGG TGCTGACCATGACCAACATGGACCCAGTGG ATACAGCTACCTACTACTGCGCCAGACACA CCATCCCCTCCATCTTCGACTACTGGGGCCA GGGCATCCTGGTGACCGTGTCCTCT
Antibody 409_11_2_v4 VH (nt - CO)	709	CAAATCACTCTAAAGGAAAGTGGTCCAACT CTGGTGAAACCAACACAGACCCTGACACTG ACCTGTACTTTTAGCGGCTTCTCCGTGACCA CCTCTGGCGTGGGAGTGGGCTGGATCAGAC

Sequence Description	SEQ ID NO.	Sequence
		AGCCTCCTGGCAAGGCCCTGGAATATCTCG CTCTGATCTACTGGGAGGACGACAAGCGGT ACTCCACCAGCCTGAAGTCTCGGCTGACCA TCACCAAGGACACCTCCAAGAACCAAGTGG TGCTGACCATGACCAACATGGATCCTGTGG ATACAGCTACCTACTACTGCGCCAGACACA CCATCCCCTCCATCTTCGACTACTGGGGCCA GGGCATCCTGGTCACCGTGTCCTCT
Antibody 409_11_2_v5 VH (nt - CO)	710	CAAATCACTCTAAAGGAAAGTGGTCCAACT CTGGTGAAGCCTACACAGACCCTGACACTG ACCTGTACTTTTTCTGGCTTCTCCGTGACCA CCAGCGGCGTGGGCGTGGGCTGGATCCGGC AGCCTCCAGGAAAAGCTCTCGAGTACCTGG CCCTGATCTACTGGAACGACGACAAGCGGT ACTCCACCTCTCTGAAGTCCAGACTGACAA TCACCAAGGACACCTCCAAGAACCAAGTGG TGCTGACCATGACCAACATGGATCCTGTGG ATACCGCTACCTACTACTGCGCCAGACACA CCATCCCCAGCATCTTCGACTATTGGGGCC AGGGCATCCTGGTCACCGTGTCCTCT
Antibody 409_11_2_v6 VH (nt - CO)	711	CAAATCACTCTAAAGGAAAGTGGTCCAACT CTCGTGAAGCCTACCCAGACCCTGACACTG ACCTGTACTTTTAGCGGCTTCTCCGTGACCA CATCTGGCGTGGGAGTGGGCTGGATCAGAC AGCCTCCAGGCAAGGCCCTGGAATACCTGG CTCTGATCTACTGGGACGAGGACAAGCGGT ATTCCACCTCTCTGAAATCTCGGCTGACAAT CACCAAGGACACCTCCAAGAACCAAGTGGT GCTGACCATGACCAACATGGATCCTGTGGA TACCGCTACCTACTACTGCGCCAGACACAC CATCCCCTCCATCTTCGACTACTGGGGCCA GGGCATCCTGGTCACCGTGTCCAGC
Antibody 409_11_2_v7 VH (nt - CO)	712	CAAATCACTCTAAAGGAAAGTGGTCCAACT CTGGTGAAACCAACCCAGACCCTGACACTG ACCTGTACCTTTTCTGGCTTCTCCGTGACCA CCAGCGGCGTGGGAGTGGGCTGGATCCGGC AGCCTCCTGGCAAGGCCCTCGAGTACCTGG CTCTGATCTACTGGGACAACGACAAGCGGT ATAGCACTTCTCTGAAGTCCAGACTGACAA TCACCAAGGACACCTCCAAGAACCAAGTGG TGCTGACCATGACCAACATGGATCCTGTGG ATACAGCTACCTACTACTGCGCCAGACACA

Sequence Description	SEQ ID NO.	Sequence
		CCATCCCCTCCATCTTCGACTACTGGGGCCA GGGCATCCTGGTCACCGTGTCCTCT
Antibody 409_11_2_v8 VH (nt - CO)	713	CAAATCACTCTAAAGGAAAGTGGTCCAACT CTCGTGAAGCCTACACAGACCCTGACACTG ACCTGTACTTTTTCTGGCTTCTCCGTGACCA CCAGCGGCGTGGGAGTGGGCTGGATCAGAC AGCCTCCAGGCAAGGCCCTGGAATACCTGG CTCTGATCTACTTCGAGGACGACAAGCGGT ATTCCACCTCTCTGAAATCTCGGCTGACAAT CACCAAGGACACCTCCAAGAACCAAGTGGT GCTGACCATGACCAACATGGATCCTGTGGA TACCGCTACCTACTACTGCGCCAGACACAC CATCCCCTCCATCTTCGACTACTGGGGCCA GGGCATCCTGGTCACCGTGTCCAGC
Antibody 409_11_2_v9 VH (nt - CO)	714	CAAATCACTCTAAAGGAAAGTGGTCCAACT CTGGTGAAACCAACCCAGACCCTGACACTG ACCTGTACCTTCTCCGGCTTTTCTGTGACCA CCTCTGGCGTGGGAGTGGGCTGGATCCGGC AGCCTCCTGGCAAGGCCCTCGAGTACCTGG CTCTGATCTACTTCAACGACGACAAGCGGT ATAGCACTAGCCTGAAGTCCAGACTGACAA TCACCAAGGATACATCCAAGAACCAAGTGG TGCTGACCATGACCAACATGGATCCTGTGG ACACCGCTACCTACTACTGCGCCAGACACA CCATCCCCTCCATCTTCGACTACTGGGGCCA GGGCATCCTGGTCACCGTGTCCTCT
Antibody 409_11_2_v10 VH (nt - CO)	715	CAAATCACTCTAAAGGAAAGTGGTCCAACT CTGGTGAAGCCTACCCAGACCCTGACACTC ACATGTACCTTTTCTGGCTTCTCCGTGACCA CTAGCGGCGTGGGAGTGGGCTGGATCCGGC AACCACCTGGCAAAGCTCTGGAATACCTGG CCCTGATCTACTACGAGGACGACAAGCGGT ATTCTACCTCTCTGAAGTCCAGACTGACCAT CACCAAGGATACATCCAAGAACCAGGTGGT GCTGACCATGACCAACATGGATCCTGTGGA CACCGCTACCTACTACTGCGCCAGACACAC CATCCCCTCCATCTTCGACTACTGGGGCCA GGGCATCCTGGTCACCGTGTCCAGC
Antibody 409_11_2_v11 VH (nt - CO)	716	CAAATCACTCTAAAGGAAAGTGGTCCAACT CTGGTGAAGCCTACCCAGACCCTGACACTG ACCTGTACCTTTTCTGGCTTCTCCGTGACCA CATCTGGAGTGGGCGTGGGCTGGATCAGAC

Sequence Description	SEQ ID NO.	Sequence
		AGCCTCCAGGCAAGGCCCTCGAGTACCTGG CTCTGATCTACTACAACGACGACAAGCGGT ATTCCACCTCTCTGAAAAGCCGGCTGACTA TCACCAAGGACACCTCCAAGAACCAAGTGG TGCTGACCATGACCAACATGGATCCTGTGG ATACAGCTACCTACTACTGCGCCAGACACA CCATCCCCTCCATCTTCGACTACTGGGGCCA GGGCATCCTGGTCACCGTGTCCAGC
Antibody 409_11_2_v12 VH (nt - CO)	717	CAAATCACTCTAAAGGAAAGTGGTCCAACT CTCGTGAAACCAACCCAGACCCTGACACTG ACCTGTACCTTTTCTGGCTTCTCCGTGACAA CTAGCGGAGTCGGCGTGGGCTGGATCCGGC AGCCTCCTGGCAAGGCCCTGGAATACCTGG CTCTGATCTACTTCGATGAGGACAAGCGGT ATAGCACCTCTCTGAAGTCCAGACTGACAA TCACCAAGGACACCTCCAAGAACCAAGTGG TGCTGACCATGACCAACATGGACCCTGTGG ATACCGCTACCTACTACTGCGCCAGACACA CCATCCCCTCCATCTTCGACTACTGGGGCCA GGGCATCCTGGTGACCGTGTCCTCT
Antibody 409_11_2_v13 VH (nt - CO)	718	CAAATCACTCTAAAGGAAAGTGGTCCAACT CTCGTGAAGCCTACCCAGACCCTGACACTG ACCTGTACCTTTTCTGGCTTCTCCGTGACCA CCAGCGGCGTCGGCGTGGGCTGGATCCGGC AGCCTCCAGGAAAAGCTCTGGAGTACCTGG CCCTGATCTACTTCGACAACGACAAGCGGT ATTCTACTTCTCTGAAGTCCAGACTGACCAT CACCAAGGACACCTCCAAGAACCAAGTGGT GCTGACCATGACCAACATGGATCCTGTGGA TACCGCTACCTACTACTGCGCCAGACACAC AATCCCCTCCATCTTCGACTACTGGGGCCA GGGCATCCTGGTGACCGTGTCCAGC
Antibody 409_11_2_v14 VH (nt - CO)	719	CAAATCACTCTAAAGGAAAGTGGTCCAACT CTCGTGAAGCCTACCCAGACCCTGACACTG ACATGTACTTTTTCTGGCTTCTCCGTGACCA CCAGCGGAGTCGGCGTGGGCTGGATCAGAC AGCCTCCAGGCAAGGCCCTGGAATACCTGG CTCTGATCTACTACGACGAGGACAAGCGGT ATTCCACCTCTCTGAAATCTCGGCTGACAAT CACCAAGGACACCTCCAAGAACCAAGTGGT GCTGACCATGACCAACATGGATCCTGTGGA TACCGCTACCTACTACTGCGCCAGACACAC

Sequence Description	SEQ ID NO.	Sequence
		CATCCCCTCCATCTTCGACTACTGGGGCCA GGGCATCCTGGTGACCGTGTCCAGC
Antibody 409_11_2_v15 VH (nt - CO)	720	CAAATCACTCTAAAGGAAAGTGGTCCAACT CTGGTGAAGCCCACACAGACCCTGACACTG ACCTGCACCTTTTCTGGCTTCTCCGTGACCA CCTCCGGCGTGGGAGTGGGCTGGATCAGAC AGCCTCCAGGCAAAGCTCTCGAGTACCTGG CCCTGATCTACTACGACAACGACAAGCGGT ACTCCACCTCTCTGAAGTCTCGGCTGACTAT CACCAAGGATACAAGCAAGAACCAAGTGG TGCTGACCATGACCAACATGGATCCTGTGG ACACCGCTACCTACTATTGTGCCAGACACA CCATCCCTTCCATCTTCGACTACTGGGGCCA GGGCATCCTGGTCACCGTGTCCAGC
Antibody 409_11_2_v16 VH (nt - CO)	721	CAAATCACTCTAAAGGAAAGTGGTCCAACT CTCGTGAAGCCTACACAGACCCTGACACTG ACCTGTACCTTTTCTGGCTTCTCCGTGACCA CAAGCGGAGTCGGCGTGGGCTGGATCCGGC AGCCTCCAGGCAAAGCTCTGGAATACCTGG CCCTGATCTACTGGGAGGAGGACAAGCGGT ATTCCACCTCTCTGAAGTCCAGACTGACTAT CACCAAGGACACCTCCAAGAACCAAGTGGT GCTGACCATGACCAACATGGACCCTGTGGA TACCGCTACCTACTACTGCGCCAGACACAC CATCCCCTCTATCTTCGACTACTGGGGCCAG GGCATCCTGGTGACCGTGTCCAGC
Antibody 409_11_2_v17 VH (nt - CO)	722	CAAATCACTCTAAAGGAAAGTGGTCCAACT CTCGTGAAACCAACCCAGACCCTGACACTG ACCTGTACCTTTAGCGGCTTCTCCGTGACCA CCTCTGGCGTGGGAGTGGGCTGGATCCGGC AGCCTCCTGGCAAGGCCCTGGAATACCTGG CTCTGATCTACTGGGAGAACGACAAGCGGT ATAGCACATCTCTGAAGTCCAGACTGACAA TCACCAAGGACACTTCCAAGAACCAAGTGG TGCTGACCATGACCAACATGGACCCTGTGG ATACCGCTACCTACTACTGCGCCAGACACA CCATCCCCTCCATCTTCGACTACTGGGGCCA GGGCATCCTGGTCACCGTGTCCTCT
Antibody 409_11_2_v18 VH (nt - CO)	723	CAAATCACTCTAAAGGAAAGTGGTCCAACT CTCGTCAAACCAACTCAGACCCTGACACTG ACCTGTACCTTTTCCGGCTTCTCCGTGACCA CATCTGGCGTGGGAGTGGGCTGGATCCGGC

Sequence Description	SEQ ID NO.	Sequence
		AGCCTCCTGGCAAGGCCCTGGAATACCTGG CTCTGATCTACTGGAACGAGGACAAGCGGT ATAGCACCTCTCTGAAGTCCAGACTGACAA TCACCAAGGACACCTCCAAGAACCAAGTGG TGCTGACCATGACCAACATGGACCCTGTGG ATACCGCTACCTACTACTGCGCCAGACACA CCATCCCCTCTATCTTCGACTACTGGGGCCA GGGCATCCTGGTGACCGTGTCCAGC
Antibody 409_11_2_v19 VH (nt - CO)	724	CAAATCACTCTAAAGGAAAGTGGTCCAACT CTGGTGAAGCCTACCCAGACCCTGACACTG ACCTGTACTTTTTCTGGCTTCTCCGTGACCA CCTCTGGAGTGGGCGTGGGCTGGATCCGGC AGCCTCCAGGCAAGGCCCTCGAGTACCTGG CTCTGATCTACTGGAACAACGACAAGCGGT ATAGCACATCTCTGAAGTCCAGACTGACAA TCACCAAAGATACCTCCAAGAATCAAGTGG TGCTGACCATGACCAACATGGACCCTGTGG ACACCGCTACCTACTACTGCGCCAGACACA CCATCCCCTCCATCTTCGACTACTGGGGCCA GGGCATCCTGGTCACCGTGTCCAGC
Antibody 409_11_2_v20 VH (nt - CO)	725	CAAATCACTCTAAAGGAAAGTGGTCCAACT CTGGTGAAACCAACCCAGACCCTGACACTG ACCTGTACTTTTTCTGGCTTCTCCGTGACCA CAAGCGGAGTGGGCGTGGGCTGGATCAGA CAGCCTCCTGGCAAGGCCCTGGAATACCTG GCTCTGATCTACTTCGAGGAGGACAAGCGG TATTCCACCTCTCTGAAGTCTCGGCTCACAA TCACCAAGGACACCTCCAAGAACCAAGTGG TGCTGACCATGACCAACATGGACCCTGTGG ATACCGCTACCTACTACTGCGCCAGACACA CCATCCCCTCCATCTTCGACTACTGGGGCCA GGGCATCCTGGTCACCGTGTCCAGC
Antibody 409_11_2_v21 VH (nt - CO)	726	CAAATCACTCTAAAGGAAAGTGGTCCAACT CTCGTGAAGCCTACCCAGACCCTGACACTG ACCTGTACCTTTAGCGGCTTCTCCGTGACTA CATCTGGCGTGGGAGTCGGCTGGATCCGGC AGCCTCCAGGCAAGGCCCTGGAATACCTGG CTCTGATCTACTTCGAGAACGACAAGCGGT ATAGCACCTCTCTGAAGTCCAGACTGACAA TCACCAAAGATACCTCCAAGAACCAAGTGG TGCTGACCATGACCAACATGGACCCTGTGG ACACCGCTACCTACTACTGCGCCAGACACA

Sequence Description	SEQ ID NO.	Sequence
		CCATCCCCTCCATCTTCGACTACTGGGGCCA GGGCATCCTGGTGACCGTGTCCTCT
Antibody 409_11_2_v22 VH (nt - CO)	727	CAAATCACTCTAAAGGAAAGTGGTCCAACT CTCGTGAAACCAACCCAGACCCTGACACTG ACCTGTACCTTCTCCGGCTTTTCTGTGACCA CATCTGGCGTGGGAGTGGGCTGGATCCGGC AGCCTCCTGGCAAGGCCCTGGAATACCTGG CTCTGATCTACTTCAACGAGGACAAGCGGT ATAGCACCTCTCTGAAGTCCAGACTGACAA TCACCAAGGACACCTCCAAGAACCAAGTG GTGCTGACCATGACCAACATGGACCCTGTG GATACTGCTACCTACTACTGCGCCAGACAC ACCATCCCCTCCATCTTCGACTACTGGGGCC AGGGCATCCTGGTCACCGTGTCCAGC
Antibody 409_11_2_v23 VH (nt - CO)	728	CAAATCACTCTAAAGGAAAGTGGTCCAACT CTCGTGAAACCAACCCAGACCCTGACACTG ACCTGTACCTTTTCTGGCTTCTCCGTGACTA CCTCTGGAGTCGGCGTGGGCTGGATCCGGC AGCCTCCTGGCAAGGCCCTGGAGTACCTGG CTCTGATCTACTTCAACAACGACAAGCGGT ATAGCACATCTCTGAAGTCCAGACTGACAA TCACCAAGGACACCTCCAAGAATCAAGTGG TGCTGACCATGACCAACATGGACCCTGTGG ATACCGCTACCTACTACTGCGCCAGACACA CCATCCCCTCCATCTTCGACTACTGGGGCCA GGGCATCCTGGTGACCGTGTCCAGC
Antibody 409_11_2_v24 VH (nt - CO)	729	CAAATCACTCTAAAGGAAAGTGGTCCAACT CTGGTGAAACCAACCCAGACCCTGACACTC ACATGTACTTTTTCTGGCTTCTCCGTGACCA CAAGCGGCGTGGGAGTGGGCTGGATCCGGC AGCCTCCTGGCAAGGCCCTGGAATACCTGG CTCTGATCTACTACGAGGAGGACAAGCGGT ATTCTACCTCTCTGAAGTCCAGACTGACCAT CACCAAGGACACCTCCAAGAACCAAGTGGT GCTGACCATGACCAACATGGACCCTGTGGA TACCGCTACCTACTACTGCGCCAGACACAC CATCCCCTCCATCTTCGACTACTGGGGCCA GGGCATCCTGGTCACCGTGTCCAGC
Antibody 409_11_2_v25 VH (nt - CO)	730	CAAATCACTCTAAAGGAAAGTGGTCCAACT CTCGTCAAACCAACCCAGACCCTGACACTG ACCTGTACCTTCTCCGGCTTTTCTGTGACTA CATCTGGCGTGGGAGTGGGCTGGATCCGGC

Sequence Description	SEQ ID NO.	Sequence
		AGCCTCCTGGCAAGGCCCTGGAATACCTGG CTCTGATCTACTACGAGAACGACAAGCGGT ATTCCACCTCTCTGAAGTCCAGACTGACAA TCACCAAGGACACCTCCAAGAACCAAGTGG TGCTGACCATGACCAACATGGACCCTGTGG ATACCGCTACCTACTACTGCGCCAGACACA CCATCCCCAGCATCTTCGACTACTGGGGCC AGGGCATCCTGGTGACCGTGTCCAGC
Antibody 409_11_2_v26 VH (nt - CO)	731	CAAATCACTCTAAAGGAAAGTGGTCCAACT CTCGTGAAGCCTACCCAGACCCTGACACTG ACCTGTACCTTTTCTGGCTTCTCCGTGACTA CAAGCGGCGTGGGAGTGGGCTGGATCCGGC AGCCTCCAGGCAAAGCTCTGGAATACCTGG CCCTGATCTACTACAACGAGGACAAGCGGT ATTCTACCTCTCTGAAGTCCAGACTGACAA TCACCAAGGACACCTCCAAGAACCAAGTGG TGCTGACCATGACCAACATGGACCCTGTGG ATACCGCTACCTACTACTGCGCCAGACACA CCATCCCCTCCATCTTCGACTACTGGGGCCA GGGCATCCTGGTCACCGTGTCCAGC
Antibody 409_11_2_v27 VH (nt - CO)	732	CAAATCACTCTAAAGGAAAGTGGTCCAACT CTGGTGAAGCCTACCCAGACCCTGACACTG ACCTGTACCTTTTCTGGCTTCTCCGTGACCA CCTCTGGCGTGGGAGTGGGCTGGATCCGGC AGCCTCCAGGCAAGGCCCTCGAGTACCTGG CTCTGATCTACTACAACAACGACAAGCGGT ATTCTACTAGCCTGAAGTCCAGACTGACAA TCACCAAGGATACATCCAAAAATCAAGTGG TGCTGACCATGACCAACATGGACCCTGTGG ACACCGCTACCTACTACTGCGCCAGACACA CCATCCCCTCCATCTTCGACTACTGGGGCCA GGGCATCCTGGTCACCGTGTCCAGC
Antibody S2D106-v1.1 VH (nt)	733	GAGGTGCAGCTGGTGCAGTCTGGGGCTGAG GTGAAGAAGCCTGGGTCCTCGGTGAAGGTT TCCTGCAAGGCTTCT**GGAGGCCCCTTCAG** **CAGCTCTGCT**ATCAGCTGGGTGCGACAGG CCCCTGGACAAGGGCTTGAGTGGATGGGAG **GGATCATCCCTATGGTAGGTACAGCA**AAAC TATGCACAGAAGTTCCAGGGCAGAGTCACG ATTACCGCGGACGAATCCACGAGCACAGCC TACATGGAGCTGAGCAGCCTGAGATCTGAG GACACGGCCGTGTATTACTGT**GCGAGAGA** **TTCGCGCTATTGTAGTGGTGGTAGCTGC**

Sequence Description	SEQ ID NO.	Sequence
		TACTCCGTCTGGTTCGACCCCTGGGGCCA GGGAACCCTGGTCACCGTCTCCTCA
Antibody 409_11_1_v2 VH (nt)	734	GAGGTGCAGCTGGTGCAGTCTGGGGCTGAG GTGAAGAAGCCTGGGTCCTCGGTGAAGGTT TCCTGCAAGGCTTCTGGAGGCCCCTTCAG CAGCTCTGCTATCAGCTGGGTGCGACAGG CCCCTGGACAAGGGCTTGAGTGGATGGGAG GGATCATCCCTATAGTAGGTACAGCAAAC TATGCACAGAAGTTCCAGGGCAGAGTCACG ATTACCGCGGACGAATCCACGAGCACAGCC TACATGGAGCTGAGCAGCCTGAGATCTGAG GACACGGCCGTGTATTACTGTGCGAGAGA TTCGCGCTATTGTAGTGGTGGTAGCTGC TACTCCGTCTGGTTCGACCCCTGGGGCCA GGGAACCCTGGTCACCGTCTCCTCA
Antibody 409_11_1_v3 VH (nt)	735	GAGGTGCAGCTGGTGCAGTCTGGGGCTGAG GTGAAGAAGCCTGGGTCCTCGGTGAAGGTT TCCTGCAAGGCTTCTGGAGGCCCCTTCAG CAGCTCTGCTATCAGCTGGGTGCGACAGG CCCCTGGACAAGGGCTTGAGTGGATGGGAG GGATCATCCCTATGGTAGGTACAGCAAAC TATGCACAGAAGTTCCAGGGCAGAGTCACG ATTACCGCGGACGAATCCACGAGCACAGCC TACATGGAGCTGAGCAGCCTGAGATCTGAG GACACGGCCGTGTATTACTGTGCGAGAGA TTCGCGCTATTGTAGTGGTGGTAGCTGC TACTCCGTCTTCTTCGACCCCTGGGGCCA GGGAACCCTGGTCACCGTCTCCTCA
Antibody 409_11_1_v4 VH (nt)	736	GAGGTGCAGCTGGTGCAGTCTGGGGCTGAG GTGAAGAAGCCTGGGTCCTCGGTGAAGGTT TCCTGCAAGGCTTCTGGAGGCCCCTTCAG CAGCTCTGCTATCAGCTGGGTGCGACAGG CCCCTGGACAAGGGCTTGAGTGGATGGGAG GGATCATCCCTATAGTAGGTACAGCAAAC TATGCACAGAAGTTCCAGGGCAGAGTCACG ATTACCGCGGACGAATCCACGAGCACAGCC TACATGGAGCTGAGCAGCCTGAGATCTGAG GACACGGCCGTGTATTACTGTGCGAGAGA TTCGCGCTATTGTAGTGGTGGTAGCTGC TACTCCGTCTTCTTCGACCCCTGGGGCCA GGGAACCCTGGTCACCGTCTCCTCA
Antibody S2E12-v1.1 VL (nt)	737	GATATTGTGTTGACGCAGACTCCAGGCACC CTGTCTTTGTCTCCAGGGGAAAGAGCCACC CTCTCCTGCAGGGCCAGTCAGAGTGTTAG CAGCAGTTACTTAGCCTGGTACCAGCAGA

Sequence Description	SEQ ID NO.	Sequence
		AACCTGGCCAGGCTCCCAGGCTCCTCATCT ATGGTGCATCCAGCAGGGCCACTGGCATC CCAGACAGGTTCAGTGGCAGTGGGTCTGGG ACAGACTTCACTCTCACCATCAGCAGACTG GAGCCTGAAGATTTTGCAGTGTATTACTGT CAGCAGTATGTTGGCTTAACAGGGTGGA CGTTCGGCCAAGGGACCAAGGTGGAAATC AAA
Antibody 409_11_4_v2 VL (aa)	738	DIVLTQTPGTLSLSPGERATLSCRASQSVSSSY LAWYQQKPGQAPRALIYGASSRATGIPDRFS GSGSGTDFTLTISRLEPEDFAVYYCQQYVGL TGWTFGQGTKVEIK
Antibody 409_11_4_v2 VL (nt)	739	GATATTGTGTTGACGCAGACTCCAGGCACC CTGTCTTTGTCTCCAGGGGAAAGAGCCACC CTCTCCTGCAGGGCCAGTCAGAGTGTTAG CAGCAGTTACTTAGCCTGGTACCAGCAGA AACCTGGCCAGGCTCCCAGGGCCCTCATCT ATGGTGCATCCAGCAGGGCCACTGGCATC CCAGACAGGTTCAGTGGCAGTGGGTCTGGG ACAGACTTCACTCTCACCATCAGCAGACTG GAGCCTGAAGATTTTGCAGTGTATTACTGT CAGCAGTATGTTGGCTTAACAGGGTGGA CGTTCGGCCAAGGGACCAAGGTGGAAATC AAA
Antibody 409_3_1_v2 VH (aa)	740	QVQLVQSGAEVKKPGASVKVSCKASGYTFT GYYIHWVRQAPGQGLEWMGWINPNSGGTN FAQKFQGRVTMTRDTSISTAYMELSRLRSDD TAVYYCASSGYLGYYYYGMDVWGQGTTVT VSS
Antibody 409_3_1_v3 VH (aa)	741	EVQLVQSGAEVKKPGASVKVSCKASGYTFT GYYIHWVRQAPGQGLEWMGWINPNSGGTN FAQKFQGRVTMTRDTSISTAYMELSSLRSDDT AVYYCASSGYLGYYYYGMDVWGQGTTVTV SS
Antibody 409_3_1_v4 VH (aa)	742	EVQLVQSGAEVKKPGASVKVSCKASGYTFT GYYIHWVRQAPGQGLEWMGWINPNSGGTN FAQKFQGRVTMTRATSISTAYMELSRLRSDD TAVYYCASSGYLGYYYYGMDVWGQGTTVT VSS
Antibody 409_3_1_v5 VH (aa)	743	EVQLVQSGAEVKKPGASVKVSCKASGYTFT GYYIHWVRQAPGQGLEWMGWINPNSGGTN FAQKFQGRVTMTRDTSFSTAYMELSRLRSDD TAVYYCASSGYLGYYYYGMDVWGQGTTVT VSS

Sequence Description	SEQ ID NO.	Sequence
Antibody 409_11_4_v3 VL (aa)	744	DIVLTQTPGTLSLSPGERATLSCRAS**QSVS SSY**LAWYQQKPGQAPRLLIY**GAS**SRATGIP DRFSGSGSGTDFTLTISRLEPEDFAVYYC**Q QYVGLTGFT**FGQGTKVEIK
Antibody 409_11_4_v3 CDRL3 (aa)	745	**QQYVGLTGFT**
Antibody 409_11_4_v4 VL (aa)	746	DIVLTQTPGTLSLSPGERATLSCRAS**QSVS SSY**LAWYQQKPGQAPRLLIY**GAS**SRATGIP DRFSGSGSGTDFTLTISRLEPEDFAVYYC**Q QYVGLTGYT**FGQGTKVEIK
Antibody 409_11_4_v4 CDRL3 (aa)	747	**QQYVGLTGYT**
Antibody 409_11_4_v5 VH (aa)	748	QVQLVQSGPEVKKPGTSVRVSCKAS **GFTFTSSA**VQWVRQARGQRLEWVGF **IVVGSGNT**NYAQKFHERVTITRDMS TSTAYMELSSLRSEDTAVYYCAS**PY CSGGSCSDGFDI**WGQGTMVTVSS
Antibody 409_11_4_v6 VH (aa)	749	QVQLVQSGPEVKKPGTSVRVSCKAS **GFTFTSSA**VQWVRQARGQRLEWVGY **IVVGSGNT**NYAQKFHERVTITRDMS TSTAYMELSSLRSEDTAVYYCAS**PY CSGGSCSDGFDI**WGQGTMVTVSS
Antibody 409_11_4_v7 VH (aa)	750	QVQLVQSGPEVKKPGTSVRVSCKAS **GFTFTSSA**VQWVRQARGQRLEWVGW **IVVGSGNT**NYAQKFH ERVTITRDMS TSTAYMELSSLRSEDTAVYYCAS**PY CSGGSCSDAFDI**WGQGTMVTVSS
Antibody 409_11_4_v7 CDRH3 and N-terminal Ala-Ser (aa)	751	**ASPYCSGGSCSDAFDI**
Antibody 409_11_4_v8 VH (aa)	752	QVQLVQSGPEVKKPGTSVRVSCKAS **GFTFTSSA**VQWVRQARGQRLEWVGW **IVVGSGNT**NYAQKFHERVTITRDMS TSTAYMELSSLRSEDTAVYYCAS**PY SSGGSSSDGFDI**WGQGTMVTVSS

Sequence Description	SEQ ID NO.	Sequence
Antibody 409_11_4_v8 CDRH3 and N-terminal Ala-Ser (aa)	753	**ASPYSSGGSSSDGFDI**
Antibody 409_11_4_v9 VH (aa)	754	QVQLVQSGPEVKKPGTSVRVSCKAS **GFTFT SSA**VQWVRQARGQRLEWVGW **IVVGSGNT**NYAQKFHERVTITRDMS TSTAYMELSSLRSEDTAVYYCAS**PY PSGGSPSDGFDI**WGQGTMVTVSS
Antibody 409_11_4_v9 CDRH3 and N-terminal Ala-Ser (aa)	755	**ASPYPSGGSPSDGFDI**
Antibody 409_11_4_v10 VH (aa)	756	QVQLVQSGPEVKKPGTSVRVSCKAS **GFTFTSSA**VQWVRQARGQRLEWVGW **IVVGSGNT**NYAQKFHERVTITRDMSTSTA MELSSLRSEDTAVYYCAS**PY ASGGSASDGFDI**WGQGTMVTVSS
Antibody 409_11_4_v10 CDRH3 and N-terminal Ala-Ser (aa)	757	**ASPYASGGSASDGFDI**
Antibody 409_11_4_v11 VH (aa)	758	QVQLVQSGPEVKKPGTSVRVSCKAS **GFTFTSSA**VQWVRQARGQRLEWVGF **IVVGSGNT**NYAQKFH ERVTITRDMS TSTAYMELSSLRSEDTAVYYCAS**PY CSGGSCSEGFDI**WGQGTMVTVSS
Antibody 409_11_4_v12 VH (aa)	759	QVQLVQSGPEVKKPGTSVRVSCKAS **GFTFTSSA**VQWVRQARGQRLEWVGW **IVVGSGNT**NYAQKFHERVTITRDMS TSTAYMELSSLRSEDTAVYYCAS**PY CSGGSCSEGFDI**WGQGTMVTVSS
Antibody 409_11_4_v12 CDRH3 with N-terminal Ala-Ser (aa)	760	**ASPYCSGGSCSEGFDI**
Antibody	761	QVQLVQSGPEVKKPGTSVRVSCKAS**GFTFTS SA**VQWVRQARGQRLEWVGA**IVVGSGNT**NY

Sequence Description	SEQ ID NO.	Sequence
409_11_4_v13 VH (aa)		AQKFHERVTITRDMSTSTAYMELSSLRSEDTA VYYCAS**PYCSGGSCSDGFDI**WGQGTMVTVS S
Antibody 409_11_1_v5 VH (aa)	762	EVQLVQSGAEVKKPGSSVKVSCKAS**GGPFSS SA**ISWVRQAPGQGLEWMGG**IIPMVGTA**NYA QKFQGRVTITADESTSTAYMELSSLRSEDTAV YYC**ARDSRYASGGSAYSVWFDP**WGQGTLV TVSS
Antibody 409_11_1_v5 CDRH3 (aa)	763	**ARDSRYASGGSAYSVWFDP**
Antibody 409_11_1_v6 VH (aa)	764	EVQLVQSGAEVKKPGSSVKVSCKAS**GGPFSS SA**ISWVRQAPGQGLEWMGG**IIPMVGTA**NYA QKFQGRVTITADESTSTAYMELSSLRSEDTAV YYC**ARDSRYSSGGSSYSVWFDP**WGQGTLVT VSS
Antibody 409_11_1_v6 CDRH3 (aa)	765	**ARDSRYSSGGSSYSVWFDP**
SARS-CoV-2 S2E12-v1 mAb CDRH3 (IMGT) (aa)	766	**PYCSGGSCSDGFDI**
SARS-CoV-2 S2E12-v1 heavy chain (MLNS)	767	QVQLVQSGPEVKKPGTSVRVSCKAS**GFTFTS SA**VQWVRQARGQRLEWVGW**IVVGSGNT**NY AQKFHERVTITRDMSTSTAYMELSSLRSEDTA VYYCAS**PYCSGGSCSDGFDI**WGQGTMVTVS SASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPREEQYNSTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSRDELTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVLHE ALHSHYTQKSLSLSPGK
SARS-CoV-2 409_11_4_v2 VL light chain	768	DIVLTQTPGTLSLSPGERATLSCRAS**QSVSSSY** LAWYQQKPGQAPRALIY**GAS**SRATGIPDRFS GSGSGTDFTLTISRLEPEDFAVYYC**QQYVGL TGWT**FGQGTKVEIKRTVAAPSVFIFPPSDEQL

Sequence Description	SEQ ID NO.	Sequence
		KSGTASVVCLLNNFYPREAKVQWKVDNALQ SGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
SARS-CoV-2 409_11_4_v7 CDRH3 (IMGT) (aa)	769	**PYCSGGSCSDAFDI**
SARS-CoV-2 409_11_4_v8 CDRH3 (IMGT) (aa)	770	**PYSSGGSSSDGFDI**
SARS-CoV-2 409_11_4_v9 CDRH3 (IMGT) (aa)	771	**PYPSGGSPSDGFDI**
SARS-CoV-2 409_11_4_v10 CDRH3 (IMGT) (aa)	772	**PYASGGSASDGFDI**
SARS-CoV-2 409_11_4_v11 and 409_11_4_v12 CDRH3 (IMGT) (aa)	773	**PYCSGGSCSEGFDI**

EXAMPLES

EXAMPLE 1

HUMAN ANTIBODIES BINDING SARS-COV-2 SPIKE PROTEIN

Monoclonal antibodies were isolated from human patients who recovered from SARS-CoV-2 infection. Briefly, EBV-immortalized memory B cells were sorted based on binding to the full ectodomain of SARS-CoV-2 Spike protein in the trimeric prefusion conformation. A biotin moiety was attached to the C-terminus of the Spike protein and the biotinylated Spike was coupled to fluorescent streptavidin (AF647 fluorophore) and used to stain the B cells, which were then sorted for binding to trimeric prefusion Spike protein based on fluorescence. Monoclonal antibodies identified by this process were recombinantly expressed in ExpiCHO cells transiently co-transfected with plasmids expressing the heavy and light chains.

EXAMPLE 2

BINDING OF ANTIBODIES TO SARS-COV-1 RBD AND SARS-COV-2 RBD

Binding of monoclonal antibodies isolated from patients who recovered from SARS-CoV-2 infection to the RBD of SARS-CoV-1 and SARS-CoV-2 Spike protein was assessed using enzyme-linked immunosorbent assays (ELISA).

Briefly, 96-well plates were coated with SARS-CoV-2 RBD (produced in-house; residues 331-550 of spike from BetaCoV/Wuhan-Hu-1/2019, accession number MN908947), or SARS-CoV (also described herein as SARS-CoV-1) RBD (Sino Biological). Wells were washed and blocked with PBS+1%BSA for 1 hour at room temperature and were then incubated with serially diluted recombinant monoclonal antibodies for 1 hour at room temperature. Bound antibodies were detected by incubating alkaline phosphatase-conjugated goat anti-human IgG (Southern Biotechnology: 2040-04) for 1 hour at room temperature and were developed by 1 mg/ml p-nitrophenylphosphate substrate in 0.1 M glycine buffer (pH 10.4) for 30

minutes 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).

ELISA assay results are shown in Figures 1A-1D. In each figure, binding to RBD of SARS-CoV-2 is shown in the top panel and binding to RBD of SARS-CoV-1 is shown in the bottom panel. Calculated EC50 values (in ng/ml) are shown in the boxes on the right side of the figures and in Table 3.

Table 3. Binding (EC50 ng/ml) of Antibodies to SARS RBDs (ELISA)

Antibody	EC50: SARS-CoV-2 RBD	EC50: SARS-CoV-1 RBD
S2X11	18.70	-
S2X14	26.57	-
S2X16	17.02	-
S2X19	19.44	-
S2X21	20.38	-
S2X25	25.69	-
S2X28	-	-
S2X30	37.94	-
S2X33	34.01	-
S2X35	48.26	84.64
S2X41	20.01	-
S2X42	23.45	26.08
S2X47	92.02	-
S2X52	14.18	-
S2X55	13.75	-
S2X56	12.73	-
S2X58	22.91	-
S2X59	12.56	-
S2X67	17.91	-
S2X71	11.53	-
S2X73	12.03	-

Antibody	EC50: SARS-CoV-2 RBD	EC50: SARS-CoV-1 RBD
S2X76	11.73	-
S2X78	14.34	-

Further assays using the same procedure were carried out with additional antibodies. Results are shown in Figures 8A and 8B. In each of these figures, binding to SARS-CoV-2 RBD is shown in the left panel and binding to SARS-CoV-1 RBD is shown in the right panel. Calculated EC50 values (in ng/ml) are shown in the boxes on the right side of each panel.

The same procedures were carried out with other antibodies. Results are shown in Figures 10A-10E. In each of these figures, binding to SARS-CoV-2 RBD is shown in the top panel and binding to SARSRBD of SARS-CoV-1 is shown in the bottom panel. Calculated EC50 values (in ng/ml), where available, are shown in the boxes on the right side of each panel. In this assay, antibody S2E12 (VH amino acid sequence of SEQ ID NO.:399; VL amino acid sequence of SEQ ID NO.:403) bound SARS-CoV-2 RBD with an EC50 of 43.40 ng/ml.

Binding of additional antibodies to SARS-CoV-2 RBD was determined using similar methods. Results are shown in Figures 22A and 22B. Calculated EC50 values are shown in the boxes to the right of each graph.

EXAMPLE 3

BINDING OF ANTIBODIES TO SARS-COV-1 AND SARS-COV-2 SPIKE PROTEIN AND TO SARS-COV-1 AND SARS-COV-2 RBD

Binding of certain human monoclonal antibodies isolated from patients who recovered from SARS-CoV-2 infection to the Spike protein of SARS-CoV-2, and to the RBD of SARS-CoV-1 and SARS-CoV-2 Spike protein, was assessed by enzyme-linked immunosorbent assays (ELISA).

Briefly, 96-well plates were coated with SARS-CoV Spike S1 Subunit Protein (Sino Biological), SARS-CoV-2 RBD (produced in house; residues 331-550 of spike

from BetaCoV/Wuhan-Hu-1/2019, accession number MN908947), or SARS-CoV RBD (Sino Biological). Wells were washed and blocked with PBS+1%BSA for 1 hour at room temperature and were then incubated with serially diluted recombinant monoclonal antibodies for 1 hour at room temperature. Bound antibodies were detected by incubating alkaline phosphatase-conjugated goat anti-human IgG (Southern Biotechnology: 2040-04) for 1 hour at room temperature and were developed by 1 mg/ml p-nitrophenylphosphate substrate in 0.1 M glycine buffer (pH 10.4) for 30 minutes 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).

ELISA assay results are shown in Figures 4A-4N. Calculated EC50 values (in ng/ml) are shown in the boxes on the right side of each figure.

Binding of additional monoclonal antibodies to Spike protein of SARS-CoV-1 and SARS-CoV-2 and to Spike protein RBD of SARS-CoV-1 and SARS-CoV-2 was assessed using similar methods. Results are shown in Figures 18A-18E. Calculated EC50 values (ng/ml) are shown in the boxes on the right side of each figure.

Binding of additional monoclonal antibodies to SARS-CoV-1 Spike protein, SARS-CoV-1 Spike RBD, and SARS-CoV-2 Spike RBD was determined by similar methods. Results are shown in Figures 20A, 20B, 21A, and 21B. Boxes to the right of the graphs show calculated EC50 values (ng/ml).

EXAMPLE 4

COMPETITIVE BINDING OF ANTIBODIES WITH HUMAN ACE2 FOR BINDING RBD

Competitive binding of recombinant monoclonal antibodies and human ACE2 to RBD was measured by competition ELISA. Recombinant antibodies were produced using monoclonal antibodies isolated from patients who recovered from SARS-CoV-2 infection.

Briefly, ELISA plates were coated with recombinant human ACE2 (produced in-house) Coating was carried out with ACE2 at 2ug/ml in PBS. Plates were incubated overnight at 4°C and blocking was performed with blocker Casein (1% Casein from Thermofisher) for 1 hour at room temperature. Serial dilutions of monoclonal antibodies were incubated with SARS-CoV-2 RBD at 20ng/ml (RBD fused with mouse Fc, from Sino Biological) for 30 minutes at 37°C and then transferred onto the ACE2-coated plates for an additional incubation at room temperature. Plates were washed and binding of RBD to ACE2 was detected using a polyclonal goat anti-mouse Fc-AP antibody (Southern Biotech). After an additional wash, AP substrate pNPP (Sigma) was added and plates were incubated at 20 minutes at room temperature before measuring adsorbance at 405nm with a spectrophotometer (Powerwave340 Biotek). Results are shown in Figure 2.

Further assays were carried out using similar methods for additional monoclonal antibodies. Results are shown in Figures 13A, 13B, 23A, and 23B. In these figures, calculated IC50 values are shown to the right of each graph.

EXAMPLE 5

NEUTRALIZATION OF SARS-COV-2 PSEUDOTYPED MLV BY RECOMBINANT HUMAN MONOCLONAL ANTIBODIES

Monoclonal antibodies isolated from patients who recovered from SARS-CoV-2 infection were expressed recombinantly and tested in neutralization assays against SARS-CoV-2 pseudotyped virus.

Briefly, Murine leukemia virus (MLV) pseudotyped with SARS-CoV-2 Spike protein (SARS-CoV-2pp) was used. VeroE6 cells were used as target cells and were seeded one day before addition of virus and antibodies. SARS-CoV-2pp was activated with trypsin TPCK at 10ug/ml. Activated SARS-CoV-2pp was added to a dilution series of antibodies and incubated for 48 hours. Starting concentration for antibodies was 5ug/ml per antibody, 3-fold dilution. Luminescence was measured after aspirating cell culture supernatant and adding Bio-Glo substrate (Promega).

Results are shown in Figures 3A-3F. Calculated IC50 values, in ng/ml, are shown on the right of each of these figures. Table 4 shows the calculated IC50, IC80, and IC90 values, in ng/ml.

Table 4. Neutralization against MLV Pseudotyped with SARS-CoV-2 S Protein

	ng/ml		
Antibody	**IC50**	**IC80**	**IC90**
S2X47	3	12	25
S2X16	6	22	46
S2X56	8	38	94
S2X55	11	31	57
S2X30	15	31	46
S2X58	19	40	62
S2X76	11	37	74
S2X71	12	48	109
S2X11	28	64	103
S2X28*	13	573	5185
S2X19	22	80	169
S2X14	39	127	255
S2X52	37	134	284
S2X41	41	140	285
S2X78	29	122	285
S2X21	42	138	279
S2X35	92	320	661
S2X33	35	412	1734
S2X25	79	532	1624
S2X73	41	229	628
S2X59	52	234	563
S2X67	45	225	573
S2X42	--	--	--

Further monoclonal antibodies isolated from patients who recovered from SARS-CoV-2 infection were expressed recombinantly and tested in neutralization assays against SARS-CoV-2 pseudotyped virus using the same procedure. Results are shown in Figures 5A-5D and Figures 7A-7D. The antibody labeled "S2H58" in Figure 7D comprises the VH amino acid sequence set forth in SEQ ID NO.: 228 and the VL amino acid sequence set forth in SEQ ID NO.: 238. Calculated EC50 values for the antibodies in Figures 5A-5D are shown in the box to the right of each figure.

Calculated EC50 and EC90 values for the antibodies in Figures 7A-7D are shown in Table 5.

Table 5. Neutralization against MLV Pseudotyped with SARS-CoV-2 S Protein

Antibody	EC50 (ng/ml)	EC90 (ng/ml)
SN12	37.22	79.099
S2N19	98.71	516.291
S2N22	36.19	58.835
S2N24	65.53	167.841
S2N25	39.22	88.528
S2N27	55.97	129.421
S2N28	32.72	174.533
S2N41	0.1125	-
S2X11	50.77	245.392
S2X71	19.09	174.137
S2X76	33.19	67.599
S2H58	9.653	54.544
S2H67	60.12	221.856
S309	727.2	1472.870

Additional monoclonal antibodies isolated from patients who recovered from SARS-CoV-2 infection were expressed recombinantly and tested in neutralization assays against SARS-CoV-2 pseudotyped virus using the same procedure. Results are shown in Figures 9A-9F. Calculated IC50, IC80, and IC90 values are shown below the graph in each figure. Antibody S2E12 shown in Figure 9E comprises the VH amino acid sequence of SEQ ID NO.:399 (CDRH1-H3 of SEQ ID NOs.:400, 401, and 766, respectively) and the VL amino acid sequence of SEQ ID NO.:403 (CDRL1-CDRL3 of SEQ ID NOs.:404-406, respectively).

Neutralization of infection by other antibodies was assayed using similar methods. Results are shown in Figures 11A-11D. Calculated IC50, IC80, and IC90 values are shown on the right of each figure.

Other antibodies were tested in neutralization assays against SARS-CoV-2 pseudotyped virus using similar methods. Results are shown in Figures 17A-17C. Calculated IC50, IC80, and IC90 values are shown below each graph.

Other antibodies were tested in neutralization assays against SARS-CoV-2 pseudotyped virus using similar methods. Results are shown in Figures 19A-19E. Calculated IC50, IC80, and IC90 values are shown to the right the graph in each figure.

EXAMPLE 6

ANTIBODY NEUTRALIZATION OF LIVE SARS-COV-2

Monoclonal antibodies isolated from patients who recovered from SARS-CoV-2 infection were expressed recombinantly and were tested in neutralization assays against live SARS-CoV-2 virus.

Briefly, Vero E6 cells cultured in DMEM supplemented with 10% FBS (VWR) and 1x Penicillin/Streptomycin (Thermo Fisher Scientific) were seeded in white 96-well plates at 20,000 cells/well and attached overnight. Serial 1:4 dilutions of the monoclonal antibodies were incubated with 200 pfu of SARS-CoV-2 (isolate USA-WA1/2020, passage 3, passaged in Vero E6 cells) for 30 minutes at 37°C in a BSL-3 facility. Cell supernatant was removed and the virus-antibody mixture was added to the cells. 24 hours post infection, cells were fixed with 4% paraformaldehyde for 30 minutes, followed by two PBS (pH 7.4) washes and permeabilization with 0.25% Triton X-100 in PBS for 30 minutes. After blocking in 5% milk powder/PBS for 30 minutes, cells were incubated with a primary antibody targeting SARS-CoV-2 nucleocapsid protein (Sino Biological, cat. 40143-R001) at a 1:2000 dilution for 1hour. After washing and incubation with a secondary Alexa647-labeled antibody mixed with 1 µg/ml Hoechst33342 for 1 hour, plates were imaged on an automated cell-imaging reader (Cytation 5, Biotek) and nucleocapsid-positive cells were counted using the manufacturer's supplied software. Data were processed using Prism software (GraphPad Prism 8.0).

Results are shown in Figures 6A and 6B, and Tables 6 and 7 (EC50 and EC90 values, ng/ml). Calculated IC50 values (ng/ml) are shown in Table 8.

Table 6.

X (Interpolated)	S309-v2 LS (entered)	S2X71 (entered)	S2X30 (entered)	S2X56 (entered)	S2X76 (entered)	S2X16 (entered)	S2X35 (entered)	S2X28 (entered)	S2X55 (entered)	S2X11 (entered)
287.351	90.000									
81.753	50.000									
37.711		90.000								
7.417		50.000								
24.483			90.000							
6.720			50.000							
72.423				90.000						
15.551				50.000						
18.972					90.000					
5.243					50.000					
34.097						90.000				
7.570						50.000				
376.690							90.000			
94.413							50.000			
53.786								90.000		
7.373								50.000		

X (Interpolated)	S309-v2 LS (entered)	S2X71 (entered)	S2X30 (entered)	S2X56 (entered)	S2X76 (entered)	S2X16 (entered)	S2X35 (entered)	S2X28 (entered)	S2X55 (entered)	S2X11 (entered)
29.826									90.000	
11.470									50.000	
19.539										90.000
6.693										50.000

Table 7.

X (Interpolated)	S309-v2 LS (entered)	S2X71 (entered)	S2X30 (entered)	S2X56 (entered)	S2X58 (entered)	S2X76 (entered)	S2X16 (entered)	S2X35 (entered)	S2X28 (entered)	S2X55 (entered)	S2X11 (entered)
452.707	90.000										
199.976	50.000										
110.659		90.000									
24.449		50.000									
351.094			90.000								
132.514			50.000								
364.145				90.000							
95.154				50.000							
228.754					90.000						

X (Interpolated)	S309-v2 LS (entered)	S2X71 (entered)	S2X30 (entered)	S2X56 (entered)	S2X58 (entered)	S2X76 (entered)	S2X16 (entered)	S2X35 (entered)	S2X28 (entered)	S2X55 (entered)	S2X11 (entered)
58.650					50.000						
108.265						90.000					
34.773						50.000					
156.012							90.000				
36.085							50.000				
840.691								90.000			
243.758								50.000			
159.046									90.000		
35.974									50.000		
101.959										90.000	
34.220										50.000	
86.467											90.000
23.224											50.000

Table 8.

Antibody	IC50 Experiment 1	IC90 Experiment 1	IC50 Experiment 2	IC90 Experiment 2
S309-v2 LS	81.75	297	201.8	452
S2X71	7.417	32	24.59	110
S2X30	6.720	24	134.4	351
S2X56	15.49	72	94.92	364
S2X58	-	-	58.09	228
S2X76	5.243	19	34.56	108
S2X16	7.512	34	35.55	156
S2X35	94.41	377	237.4	840
S2X28	7.140	54	35.75	159
S2X55	11.44	30	35.48	102
S2X11	6.679	20	22.53	86

Twenty-two further antibodies, along with comparator antibody S309-v2 (VH as set forth in SEQ ID NO.: 342, VL as set forth in SEQ ID NO.: 346 (CDRH1-H3 and L1-L3 as set forth in SEQ ID NOs.:343-345 and 347-349, respectively)), were tested in neutralization assays against live SARS-CoV-2 virus using similar methods. Results are shown in Figures 16A-16D. S2H58-v2 comprises the VH amino acid sequence set forth in SEQ ID NO: 228 and the VL amino acid sequence (kappa light chain) set forth in SEQ ID NO: 238. S2E12 comprises the VH amino acid sequence set forth in SEQ ID NO.:399 (CDRH1-H3 as set forth in SEQ ID NOs.:400, 401, and 766, respectively), and the VL amino acid sequence set forth in SEQ ID NO.:403 (CDRL1-L3 as set forth in SEQ ID NOs.:404-406, respectively). Calculated IC50 (ng/ml) values are shown in Tables 9-12. Calculated EC50 and EC90 values (ng/ml) are shown in Tables 13-16.

Table 9.

Antibody	**IC50**
S309-v2	123.8
S2N22	13.58

Antibody	IC50
S2N12	23.68
S2N28	17.59
S2N25	13.64
S2H58-v2	6.337

Table 10.

Antibody	IC50
S309-v2	145.7
S2E9	24.93
S2E6	13.52
S2E13	approx. 14.02
S2K4	26.36
S2E14	8.300
S2E7	24.43
S2E12	5.409

Table 11.

Antibody	IC50
S309-v2	146.0
S2H37	48.67
S2H73	12.72
S2H40	18.63
S2H70	52.69
S2H71	5.580

5

Table 12.

Antibody	IC50
S309-v2	173.7
S2X30	11.42
S2H58-v1	8.362

Antibody	IC50
S2H66	633.0
S2H62	24.17
S2H30	28.80

Table 13.

Antibody	EC50	EC90
S309-v2	126	438
S2N22	13	46
S2N12	25	77
S2N28	18	44
S2N25	13	49
S2H58-v2	6	19

Table 14.

Antibody	EC50	EC90
S309-v2	145	342
S2E6	16	70
S2E9	25	66
S2E13	14	17
S2K4	13	49
S2E14	9	41
S2E12	5	16

5

Table 15.

Antibody	EC50	EC90
S309-v2 (with M428L and N434S Fc mutations)	151	461
S2H37	49	169
S2H73	13	65
S2H40	20	65

S2H70	52	234
S2H71	6	20

Table 16.

Antibody	**EC50**	**EC90**
S309-v2 (with M428L and N434S Fc mutations)	174	588
S2X30	12	34
S2H58	8	23
S2H66	584	5000
S2H62	24	82
S2H30	27	121

Neutralization assays were carried out using additional monoclonal antibodies using similar methods. Results are shown in Figures 25A and 25B. Figure 25A shows results for four antibodies, along with comparator antibodies S309 N55Q LS and S2X193. S309 N55Q LS (also referred-to herein as S309-v2) comprises the VH sequence as set forth in SEQ ID NO:342 and the VL sequence as set forth in SEQ ID NO: 346, and comprises M428L and N434S mutations in the Fc region. Figure 25B shows results for antibodies S2X129 and S2X132, along with four comparator antibodies. IC50 and interpolated EC50 and EC90 values (ng/ml) are shown in Table 17.

Table 17.

Antibody	**IC50**	**EC50**	**EC90**
S309 N55Q_MLNS (2 measurements)	268.4; 205.4	256; 194	635; 634
S2X127	17.18	17	54
S2X129 (2 measurements)	5.379; 4.104	5; 4	12; 12
S2X132	16.50; 9.265	16; 9	38; 24

Antibody	IC50	EC50	EC90
(2 measurements)			
S2X190	24.18	23	64
S2X193	26.69	26	61
S2X195	17.85	17	47
S2X219	20.63	20	69
S2X246	7.894	8	22

Neutralization by other antibodies (expressed as recombinant IgG1 with wild-type or M428L/N434S ("LS")-modified Fc) was assessed using VSV-luc(spike D19) pseudovirus. Plots are shown in Figure 26; IC50 values and interpolated EC50 and EC90 values (ng/ml) are shown in Table 18.

Table 18.

Antibody	IC50	EC50	EC90
S309 (wt)	25.69	25.8	121
S2E12-LS	1.401	1.4	11.9
S2M11-v1-LS	0.9143	1.1	14.4
S2D106-LS	3.376	3.6	15.4
409_11_3_v1-LS	4.085	5.3	40.9
S2X227-v2-LS	4.446	5.3	27.5
409_11_2_v1-LS	2.327	2.4	9.3

These antibodies were also tested for neutralization of live SARS-CoV-2. Plots are shown in Figure 27; data are from triplicate wells SARS-CoV-2-luc, MOI 0.1, 6h infection. IC50 values and interpolated EC50 and EC90 values (ng/ml) are shown in Table 19.

Table 19.

Antibody	IC50	EC50	EC90
S2E12-LS	4.844	5	30
S2M11-v1-LS	3.214	4	11

Antibody	IC50	EC50	EC90
S2D106-LS	4.485	6	22
409_11_3_v1-LS	8.233	10	39
S2X227-v2-LS	7.061	10	44
409_11_2_v1-LS	5.073	5	20
S309	84.30	79	289

EXAMPLE 7

PRODUCTION OF S2X16, S2X30, S2X35, AND S2X47 VARIANT ANTIBODIES

Recombinant IgG1 antibodies are produced using the VH and VL sequences of antibodies S2X16, S2X30, S2X35, and S2X47, or engineered variants thereof. The combinations are produced as indicated in Table 20. Each of the antibodies is produced by transient transfection and expression of a plasmid vector encoding the recombinant antibody in HD 293F cells (GenScript). Cells are harvested on day 4 and IgG expression is validated by Western blot and protein A titer analysis.

Table 20.

Antibody	VH (WT/Variant)	VH amino acid SEQ ID NO.	VL (WT/Variant)	VL amino acid SEQ ID NO.
S2X16-11	WT	22	WT	26
S2X16-21	W50F	150	WT	26
S2X16-12	WT	22	N33Q	154
S2X13-23	W50F	150	G34A	157
S2X30-11	WT	42	WT	46
S2X30-21	D112E	163	WT	46
S2X30-12	WT	42	W94F	168
S2X35-11	WT	129	WT	133
S2X35-21	W50F	173	WT	133
S2X35-31	W109F	175	WT	133

S2X35-41	W50F-W109F-I110A	178	WT	133
S2X47-11	WT	52	WT	56
S2X47-21	W111F	186	WT	56
S2X47-12	WT	52	W92F-W99F	194
S2X47-33	W36F	189	W92F	196
S2X47-42	W36F-W111F	191	W92F-W99F	194

EXAMPLE 8

S2H58 AND S2N22 VARIANT ANTIBODIES

Recombinant IgG1 antibodies are produced using the VH and VL sequences of monoclonal antibodies S2H58 and S2N22, or engineered variants thereof. The combinations are produced as indicated in Table 21. Each of the antibodies is produced by transient transfection and expression of a plasmid vector encoding the recombinant antibody in HD 293F cells (GenScript). Cells are harvested on day 4 and IgG expression is validated by Western blot and protein A titer analysis.

Table 21.

Antibody	**VH (WT/Variant)**	**VH amino acid SEQ ID NO.**	**VL (WT/Variant)**	**VL amino acid SEQ ID NO.**
S2H58-11	WT	228	WT	238
S2H58-21	W50F	350	WT	238
S2H58-31	W50F-S55A	351	WT	238
S2H58-32	W50F-S55A	351	V34G	355
S2H58-43	W50F-S55A-L102A	353	M94I	357
S2N22-11	WT	312	WT	316
S2N22-21	N56Q	359	WT	316
S2N22-31	N56G	361	WT	316

Antibody	VH (WT/Variant)	VH amino acid SEQ ID NO.	VL (WT/Variant)	VL amino acid SEQ ID NO.
S2N22-41	T58A	363	WT	316
S2N22-51	Y57P	365	WT	316
S2N22-61	T58A-S63A	367	WT	316
S2N22-71	T58A-S63A-M34I	368	WT	316

EXAMPLE 9

S2E12 VARIANT ANTIBODIES

Recombinant IgG1 antibodies were produced using the VH and VL sequences of monoclonal antibody S2E12 and engineered variants thereof. V-region amino acid sequences of S2E12 and certain engineered S2E12 variants are summarized in Table 22.

Table 22.

Antibody	VH amino acid SEQ ID NO.	VL amino acid SEQ ID NO.
S2E12	399	403
409_11_4_v2	399	738
409_11_4_v3	399	744
409_11_4_v4	399	746
409_11_4_v5	748	403
409_11_4_v6	749	403
409_11_4_v7	750	403
409_11_4_v8	752	403
409_11_4_v9	754	403
409_11_4_v10	756	403
409_11_4_v11	758	403
409_11_4_v12	759	403
409_11_4_v13	761	403

EXAMPLE 10

NEUTRALIZATION OF SARS-COV-2 BY RECOMBINANT ANTIBODIES

Human monoclonal antibodies isolated from patients who recovered from SARS-CoV-2 infection were expressed recombinantly and tested in neutralization assays against SARS-CoV-2 pseudotyped virus (VSV).

Recombinant monoclonal antibodies were serially diluted and incubated with a constant amount of VSV-deltaG-luc pseudotyped with SARS-CoV-2 (strain BetaCoV/Wuhan-Hu-1/2019, accession number MN908947) for 1.5 hours at 37 °C. VeroE6 cells were then added in complete DMEM medium and plates were incubated for 24 hours at 37 °C. To measure the amount of luciferase expressed in infected cells, culture medium was aspirated and luciferase substrate Bio-Glo Luciferase assay system (Promega AG) warmed to room temperature was added. After 10 minutes incubation in the dark on a shaker, signals were measured in a luminometer using 1 second integration time.

Results for certain monoclonal antibodies are shown in Figures 12A-12D. Calculated IC50 and IC90 values (ng/ml) are shown below each graph.

EXAMPLE 11

BINDING OF ANTIBODIES TO RBD USING OCTET

Binding affinity and avidity of antibodies S2X193, S2X195, S2X219, S2X244, S2X246, S2X256, S2X269, and S2X278 for SARS-CoV-2 RBD was measured by Octet. Antibody was loaded on Protein A pins at 2.7 µg/ml. SARS-CoV-2 RBD was loaded for 5 minutes at 6 µg/ml, 1.5 µg/ml, or 0.4 µg/ml. Dissociation was measured for 7 minutes. Results are shown in Figures 14A-14H. In each graph, the vertical dashed line indicates the start of the dissociation phase.

Binding affinity and avidity of antibodies S2X193, S2X195, S2X219, S2X244, S2X246, S2X256, S2X269, and S2X278, along with four comparator antibodies, to SARS-CoV-1 RBD was also measured by Octet. Antibody was loaded on Protein A

pins at 2.7 μg/ml. SARS-CoV-1 RBD was loaded for 5 minutes at 6 μg/ml. Dissociation was measured for 7 minutes. Results are shown in Figure 15. In each graph, the vertical dashed line indicates the start of the dissociation phase.

EXAMPLE 12

QUANTITATIVE EPITOPE-SPECIFIC SEROLOGY OF SARS-COV-2 SPIKE PROTEIN

SARS-CoV-2 Spike protein antibody binding was analyzed by antibody competition assays, cryo-EM data, and crystallography data. From this analysis, Spike RBD antigenic Sites Ia, Ib, Ic, Id, II, and IV were identified. A map showing these sites and antibodies that bind within each site is shown in Figure 24.

EXAMPLE 13

BINDING OF S2E12 ANTIBODIES TO SARS-COV-2 RBD

Binding of S2E12 and S2E12 variant antibodies to SARS-CoV-2 RBD was measured by surface plasmon resonance (SPR). SPR experiments were carried out with a Biacore T200 instrument using a single-cycle kinetics approach. Antibodies were captured on the surface and increasing concentrations of purified SARS-CoV-2 RBD were injected. Association and dissociation kinetics were monitored and fit to a binding model to determine affinity.

Results are shown in Tables 23 and 24. Antibody "S2E12-11" was obtained from the supernatant of CHO cells transformed to express S2E12 antibody. Antibody S2E12 WT (VH of SEQ ID NO.:399, VL of SEQ ID NO.:403) was generated using purified antibody produced in transformed HEK cells. KD/KD_WT lists the KD value for the indicated antibody divided by the KD value for S2E12 WT. KD_WT/KD lists the KD value for S2E12 WT divided by the KD value for the indicated antibody. Blank cells indicate that no binding was measured using this assay.

Table 23.

Antibody	Ka (1/Ms)	Kd (1/s)	KD (M)	KD/KD_WT
S2E12 WT	1.98E+06	0.002335	1.18E-09	1.0
S2E12-11	2.42E+06	0.003174	1.31E-09	1.1
409_11_4_v5	2.68E+06	0.03576	1.33E-08	0.098
409_11_4_v3	1.18E+06	0.01527	1.30E-08	0.100
409_11_4_v7	1.86E+06	0.009129	4.90E-09	0.267
409_11_4_v8				
409_11_4_v9				
409_11_4_v10				
409_11_4_v11				

Table 24.

Antibody	KD (M) [first phase]	KD_WT/KD
S2E12 WT	2.28E-09	1.00
409_11_4_v4	2.59E-08	0.09
409_11_4_v2	7.88E-10	2.89
409_11_4_v6	2.04E-08	0.11
409_11_4_v12	4.53E-08	0.05
409_11_4_v13	5.14E-08	0.04

EXAMPLE 14

ACE2-INDEPENDENT MECHANISM OF SARS-COV-2 NEUTRALIZATION BY ANTIBODIES

Mechanisms of antibody neutralization of SARS-CoV-2 infection were investigated. In the following experiments, unless otherwise indicated, S309 antibody (VH of SEQ ID NO.:139, VL of SEQ ID NO.:143) was expressed as recombinant IgG1

with M428L and N434S mutations. The effect of ACE2 overexpression on S309 antibody neutralization of infection was investigated. Vero E6 or Vero E6-TMPRSS2 cells were infected with SARS-CoV-2 (isolate USA-WA1/2020) at MOI 0.01 in the presence of S309 (10 μg/ml). Cells were fixed 24h post infection, viral nucleocapsid protein was immunostained and quantified. Nucleocapsid staining was effectively absent in antibody-treated cells. S309 had an IC50 (ng/mL) in Vero E6 cells of 65 and in Vero E6-TMPRSS2 of 91 (data not shown).

A panel of seven cell lines (HeLa, 293T (wt), Vero E6, Huh7, 293T ACE2, MRC 5-ACE2-TMPRSS2, A549-ACE2-TMPRSS2 clone 5, A549-ACE2-TMPRSS2 clone 10) were infected with SARS-CoV-2-Nluc or VSV pseudotyped with the SARS-CoV-2 spike protein in the presence of S309. Luciferase signal was quantified 24h post infection. S309 maximum neutralization values were as shown in Table 25.

Table 25. Maximum Neutralization Values of S309

Cell Type	Virus/Pseudotype	
	SARS-CoV-2-Nluc	VSV Pseudotype
Vero E6	>99%	>99%
Vero E6-TMPRSS2	>99%	96%
Huh7	98%	78%
293T ACE2	26%	34%
MRC5-ACE2-TMPRSS2	87%	45%
A549-ACE2-TMPRSS2 clone 5	89%	65%
A549-ACE2-TMPRSS2 clone 10	81%	42%

S2E12 neutralization data are shown in Figure 53 (SARS-CoV-2-Nluc) and Figure 54 (pseudotyped VSV). Notably, S2E12 showed comparable neutralizing activity on all target cells.

Binding of purified, fluorescently-labeled SARS-CoV-2 spike protein binding to these cell lines was quantified by flow cytometry. HeLa and 239T WT cells had he lowest MFIs, followed by Huh7 and VeroE6 cells. 293T ACE2 cells (highest), MRC 5-

ACE2-TMPRSS2 (third-highest), A549-ACE2-TMPRSS2 clone 5 (fourth-highest), and A549-ACE2-TMPRSS2 clone 10 (second-highest) had higher MFIs. Correlation analysis between spike binding maximum neutralization potential of S309 was determined; S309 Spearman correlation values were: r = -0.94 for both viral models. p = 0.017. See Figure 55.

To further characterize SARS-CoV-2-susceptible cell lines, the seven cell lines described above were incubated with purified, fluorescently-labeled SARS-CoV-2 spike protein or RBD protein and protein binding was quantified by flow cytometry. In descending order of MFI, the cell lines were: A549-ACE2-TMPRSS2 clone 10; 293T ACE2; MRC 5-ACE2-TMPRSS2; A549-ACE2-TMPRSS2 clone 5; Vero E6; Huh7; 293T (wt); and HeLa.

Selected lectins and published receptor candidates were screened using HEK293T cells infected with SARS-CoV-2 VSV pseudoviruses. ACE2, DC-SIGN, L-SIGN, and SIGLEC-1 gave the highest signals. ACE2 provided a signal of approximately 10^5 relative luminescence units (RLUs), and DC-SIGN, SIGLEC-1, and L-SIGN had signals of approximately 10^4 RLUs. All other lectins/candidates tested gave signals of approximately $10^2 - 10^3$ RLUs.

HEK 293T, HeLa and MRC5 cells were transiently transduced to overexpress DC-SIGN, L-SIGN, SIGLEC1 or ACE2 and infected with SARS-CoV-2 VSV pseudoviruses. Uninfected cells and untransduced cells were included as controls. In HEK293T cells, ACE2, DC-SIGN, SIGLEC-1, and L-SIGN all provided substantial increases in infection. In HeLa and MRC5 cells, only ACE2 increased infection.

Stable HEK293T cell lines overexpressing DC-SIGN, L-SIGN, SIGLEC-1 or ACE2 were infected with authentic SARS-CoV-2 (MOI 0.1), fixed and immunostained at 24 hours for the SARS-CoV-2 nucleoprotein. Wild-type cells (infected and uninfected) were used as controls. Increased staining was observed in cells overexpressing DC-SIGN, L-SIGN, or SIGLEC-1, and staining was significantly increased in cells overexpressing ACE2.

Stable cell lines were infected with SARS-CoV-2-Nluc and luciferase levels were quantified at 24 hours. In ascending order of RLUs: uninfected (approx. 10^2-10^3

RLUs); parental 293T (approx. 10^4 RLUs); DC-SIGN (approx. 10^5 RLUs); L-SIGN (approx. 10^5 RLUs); SIGLEC-1 (approx. 10^5-10^6 RLUs); ACE2 (>10^7 RLUs).

Stable cell lines were incubated with different concentration of anti-SIGLEC1 mAb (clone 7-239) and infected with SARS-CoV-2-Nluc. Infection as a percentage of untreated cells remained near to exceeded 100% in 293T cells expressing DC-SIGN, L-SIGN, or ACE2, but dropped to below 50% (0.2 μg/mL anti-SIGLEC) to close to 0 (1 μg/mL or 5 μg/mL anti-SIGLEC) in 293T cells expressing SIGLEC-1.

Single cell expression levels of selected potential SARS-CoV-2 (co)receptor candidates were determined in different lung cell types derived from the Human Lung Cell Atlas (nature.com/articles/s41586-020-2922-4). DC-SIGN, L-SIGN and SIGLEC-1 are expressed in a variety of cell types in the lung at levels similar to or even higher than ACE2.

Binding of antibodies targeting DC-/L-SIGN, DC-SIGN, SIGLEC1 or ACE2 on HEK293T cells stably over-expressing the respective attachment receptor was analyzed by flow cytometry and immunofluorescence analysis. HEK 293T cells over-expressing the respective attachment receptors were infected with VSV pseudotyped with SARS-COV-2 wildtype spike or spike bearing mutations of the B1.1.7 lineage. Luminescence was analyzed one day post infection. Infection was increased in cells expressing the attachment receptors. Infection by VSV pseudotyped with either spike was similar for each test group. Cells expressing ACE2 gave the highest luminescence signal.

Vero E6 cells, *in vitro* differentiated moDCs or PBMCs were infected with SARS-CoV-2 at MOI 0.01. At 24h post infection, cells were fixed, immunostained for viral nucleocapsid protein and infected cells were quantified. Only VeroE6 cells showed infection (approximately 7% of cells). Supernatant of the infected cells was taken at 24, 48 and 72h and infectious viral titer was quantified by FFU assay on Vero E6 cells.

Major cell types with detectable SARS-CoV-2 genome in bronchoalveolar lavage fluid (BALF) and sputum of severe COVID-19 patients were assessed. A t-SNE plot was generated, and the count of each SARS-CoV-2+ cell type was determined (total n=3,085 cells from 8 subjects in Ren et al. Cell 2021). Cell types were T, NK,

plasma, neutrophil, macrophage, ciliated, squamous, and secretory. Expression of ACE2, DC-SIGN, L-SIGN, SIGLEC-1, and combinations of these was assessed for each cell type. Figures 65-66.

ACE2, DC-SIGN (CD209), L-SIGN (CLEC4M), SIGLEC1 transcript counts were correlated with SARS-CoV-2 RNA counts in macrophages and in secretory cells. Correlation was based on counts (before log transformation), from Ren et al. Cell 2021.

Representative data showing expression of receptors in stable HEK293T cell lines are shown in Figure 41.

Representative data showing the ability of VSV pseudovirus expressing SARS-CoV-2 S protein with luciferase reporter to infect the HEK293T cells was assessed using a luminescence assay are shown in Figure 42 (*see also* Figure 57); expression of DC-SIGN or L-SIGN increased pseudovirus infection levels by over 10-fold compared to infection of WT HEK293T cells, and expression of ACE2 increased pseudovirus infection levels by over 100-fold compared to infection of WT HEK293T cells.

Neutralizing activity of mAb S309 against the VSV pseudovirus was assessed in the engineered HEK293T cells. Data are shown in Figure 43; S309 fully neutralized infection via DC-SIGN and L-SIGN, and to a lesser extent, ACE2.

The ability of live SARS-CoV-2 with luciferase reporter to infect the HEK293T cells was examined using a luminescence assay. Data are shown in Figure 44; expression of DC-SIGN or L-SIGN increased live virus infection levels by over 3-fold compared to infection of WT HEK293T cells, and expression of ACE2 increased live virus infection levels by over 100-fold compared to infection of WT HEK293T cells. See also Figure 58, showing infection as determined by staining for SARS-CoV-2 nucleoprotein.

Neutralizing activity of S309 against the VSV pseudovirus was assessed in the engineered HEK293T cells. Data are shown in Figure 45; S309 fully neutralized infection via DC-SIGN and L-SIGN, and neutralized infection via ACE2 to a lesser extent.

Experiments were performed to investigate whether S309 or S2E12 antibody can neutralize entry of SARS-CoV-2 via SIGLEC-1. In the following experiments,

S309 antibody (VH of SEQ ID NO.:139, VL of SEQ ID NO.:143) and S2E12 antibody (VH of SEQ ID NO.:399, VL of SEQ ID NO.:403) were expressed as recombinant IgG1 with M428L and N434S mutations. Briefly, stable cell HEK293T lines were generated as described above to overexpress DC-SIGN/L-SIGN, DC-SIGN, SIGLEC-1, or ACE2. Expression data are shown in Figure 46. As shown in Figure 47, expression of DC-SIGN, L-SIGN, or SIGLEC increased live virus infection levels by over 10-fold compared to infection of WT HEK293T cells, and expression of ACE2 increased pseudovirus infection levels by over 100-fold compared to infection of WT HEK293T cells. As shown in Figure 48, S309 fully neutralized infection via DC-SIGN, L-SIGN, and SIGLEC-1. As shown in Figure 49, S2E12 fully neutralized infection via SIGLEC-1 and ACE2.

Expression of DC-SIGN (CD209) and other cell surface receptor proteins including SIGLEC-1 and other SIGLECs was determined on a variety of cell types. Data are summarized in Figures 50A and 50B.

Further experiments were performed to investigate the function(s) of DC-SIGN, L-SIGN, and SIGLEC-1 in SARS-CoV-2 infection. In one set of experiments, HEK293T cells stably expressing DC-SIGN, L-SIGN, SIGLEC-1 or ACE2 were infected with live SARS-CoV-2 Nluc at three different multiplicities of infection (MOI): 0.01, 0.1, and 1). Infection was determined using relative luminescence units and compared to infection in HEK293T cells (parental). Data are shown in Figure 51. At the lowest MOI tested, an increase of infection in cells expressing DC-SIGN, L-SIGN, or SIGLEC was observed. At the highest MOI tested, infection was not further increased versus parental by expression of DC-SIGN, L-SIGN, or SIGLEC. These data indicate that the parental 293T cells are susceptible to infection by SARS-CoV-2 and L-SIGN, DC-SIGN, and SIGLEC-1 enhance infection levels but do not function as primary receptors for infection.

In another set of experiments, 293T cells, HeLa cells, and MRC5 cells were transiently transduced with lentivirus encoding DC-SIGN, L-SIGN, SIGLEC-1 or ACE2 and infected with VSV pseudovirus three days after transduction. Data are shown in Figure 52. While the 293T cells showed a low level of susceptibility

(compare uninfected with untransduced), HeLa and MRC5 cells were completely refractory to the virus. The low level of infection in 293T cells can be increased by expression of L-SIGN, DC-SIGN, or SIGLEC-1, consistent with a role for these proteins as as attachment factors. The HeLa and MRC5 cells remained refractory to infection even after expression of L-SIGN, DC-SIGN, or SIGLEC-1, and only become susceptible after expression of ACE2. These data indicate that L-SIGN, DC-SIGN, and SIGLEC-1 are not primary receptors for SARS-CoV-2.

Trans-infection, cell-cell fusion, and further neutralization of infection assays were performed. Figure 71 shows neutralization on Vero E6 cells using antibodies S309, S2E12, and S2X333. Figure 72 shows neutralization on Vero E6-TMPRSS2 cells using the same antibodies. Figures 75 and 76 show neutralization of infection by these antibodies on various cell types. Figures 77-80 show results from cell-cell fusion and fusion inhibition assays. Figures 81-84 show neutralization of infection by antibodies on stable HEK293T cell line overexpressing ACE2, SIGLEC1, DC-SIGN, or L-SIGN.

EXAMPLE 15

IN VIVO EFFICACY OF S309 ANTIBODY AND THE COMBINATION OF S309 AND S2E12 ANTIBODIES

The efficacy of S309 and the combination of S309 and S2E12 was investigated in Syrian hamsters. This animal model represents to-date the most relevant model of SARS-CoV-2 infection that did not require *in vivo* over-expression of ACE2 to support productive infection and disease. Prophylactic administration of S309 induced dose-dependent protection against SARS-CoV-2 infection and tissue damage in hamsters, as demonstrated by the viral RNA levels, the viral load, and the histopathological score in the lungs (Fig. 56A, left column). These data indicate that poor and incomplete neutralization of entry by S309 *in vitro* when using ACE2 over-expressing cells did not compromise *in vivo* efficacy of non-RBM mAbs. Similar results were obtaining using a combination of S309 and S2E12 antibodies (Fig. 56A, right column).

S309 carrying the N297A mutation has a reduced capacity to trigger effector functions as a consequence of diminished engagement to Fcγ receptors. This was further confirmed by the reduced binding of S309-N297A variant to hamster monocytes in the spleen. The *in vivo* efficacy measured with the N297A mAb is similar or just slightly inferior to the wt S309, suggesting that neutralizing capacity of the mAb is prevailing upon its effector function capacity in these conditions. The serum concentration of S309 required to reduce the viral RNA in the lung by 90% was 9 µg/ml (Figure 56B, left column). Similar results were obtained using a combination of S309 and S2E12 antibodies (Figure 56B, right column).

EXAMPLE 16

FURTHER *IN VIVO* STUDIES USING S2E12-V2 ANTIBODY

A preclinical study using non-human primates was conducted to assess pharmacokinetics and potential tissue cross-reactivity safety of S2E12-v2 (shown in Figure 99 as "S2E12") having the VH amino acid sequence of SEQ ID NO:399 and the VL amino acid sequence of SEQ ID NO:738, and comprising M428L and N434S Fc mutations. As shown in Figures 99 and 100, a single 5 mg/kg dose of S2E12-v2 MLNS had a mean $T_{1/2}$ (across 3 animals) of 25.4 days. Tissue cross-reactivity studies (using CHO-CoV2-S spike, CHO-CoV2S-spike:CHO at 1:1, and CHO as controls) did not identify cross-reactive staining by S2E12-v2 in any tissue at 1.25, 0.3125, or 0.078125 μg/ml.

EXAMPLE 17

FURTHER NEUTRALIZATION STUDIES

The potential effect of known SARS-CoV-2 mutations on neutralization potency of S2E12 was investigated. The following individual mutations in SARS-CoV-2 S had less than a 3-fold decrease on neutralization of S2E12 against live SARS-CoV-2 or SARS-CoV-2 pseudovirus: N501Y; S477N; N439K; L452R; E484K; K417N; T478K; S494P; A520S; N501T; A522S; Y453F; P384L.

EXAMPLE 18

MATERIALS AND METHODS

Flow-cytometry based screening for binding to CoV S protein expressed on mammalian cells

ExpiCHO cells were transfected with S protein of SARS-CoV-2. The 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 transfectants.

Transient expression of recombinant SARS-CoV-2 protein

The full-length S gene of SARS-CoV-2 strain (2019-nCoV-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-SARS-CoV-2-S, phCMV1-MERS-CoV-S (London1/2012), SARS-spike_pcDNA.3 (strain SARS) or the empty phCMV1 (Mock) using Expifectamine CHO Enhancer. Two days after transfection, cells were collected, fixed, or fixed and permeabilized with saponin for immunostaining with a panel of 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 (Biorard) 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)

Unless otherwise indicated herein, 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 mins.

Competition experiments using Octet (BLI, biolayer interferometry)

For ACE2 competition experiments, ACE2-His (Bio-Techne AG) was loaded for 30 minutes at 5 μg/ml in KB onto anti-HIS (HIS2) biosensors (Molecular Devices-ForteBio). SARS-CoV-1 RBD-rabbitFc or SARS-CoV-2 RBD-mouseFc (Sino Biological Europe GmbH) at 1 μg/ml was associated for 15 minutes, after a preincubation with or without antibody (30 μg/ml, 30 minutes). Dissociation was monitored for 5 minutes.

Affinity determination using Octet (BLI, biolayer interferometry)

For K_D determination of full-length antibodies, protein A biosensors (Pall ForteBio) were used to immobilize recombinant antibodies at 2.7 μg/ml for 1 minute, after a hydration step for 10 minutes with Kinetics Buffer. Association curves were recorded for 5min by incubating the antibody-coated sensors with different concentration of SARS-CoV-1 RBD (Sino Biological) or SARS-CoV-2 RBD (produced in house; residues 331-550 of spike from BetaCoV/Wuhan-Hu-1/2019, accession number MN908947). Highest RBD concentration tested was 10ug/ml, then 1:2.5 serially diluted. Dissociation was recorded for 9min by moving the sensors to wells containing KB. K_D values were calculated using a global fit model (Octet). Octet Red96 (ForteBio) equipment was used.

For K_D determination of full-length antibodies compared to Fab fragments, His-tagged RBD of SARS-CoV-1 or SARS-CoV-2 were loaded at 3 μg/ml in KB for 15 minutes onto anti-HIS (HIS2) biosensors (Molecular Devices, ForteBio). Association of full-length antibody and Fab was performed in KB at 15 ug/ml and 5 ug/ml respectively for 5 minutes. Dissociation in KB was measured for 10min.

ELISA binding

The reactivities of mAbs with SARS-CoV-2 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-2 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).

Neutralization assay

Unless otherwise indicated, Murine leukemia virus (MLV) pseudotyped with SARS-CoV-2 Spike protein (SARS-CoV-2pp) or SARS-CoV-1 Spike protein (SARS-CoV-1pp) were used. DBT cells stably transfected with ACE2 (DBT-ACE2) were used as target cells. SARS-CoV-2pp or SARS-CoV-1pp was activated with trypsin TPCK at 10ug/ml. Activated SARS-CoV-2pp or SARS-CoV-1pp was added to a dilution series of antibodies (starting 50ug/ml final concentration per antibody, 3-fold dilution). DBT-ACE2 cells were added to the antibody-virus mixtures and incubated for 48h. Luminescence was measured after aspirating cell culture supernatant and adding steady-GLO substrate (Promega).

Unless otherwise indicated, pseudoparticle neutralization assays use a VSV-based luciferase reporter pseudotyping system (Kerafast). VSV pseudoparticles and antibody are mixed in DMEM and allowed to incubate for 30 minutes at 37C. The infection mixture is then allowed to incubate with Vero E6 cells for 1h at 37C, followed by the addition of DMEM with Pen-Strep and 10% FBS (infection mixture is not removed). The cells are incubated at 37C for 18-24 hours. Luciferase is measured using an Ensight Plate Reader (Perkin Elmer) after the addition of Bio-Glo reagent (Promega).

SPR single-cycle kinetics

SPR experiments were carried out with a Biacore T200 instrument using a single-cycle kinetics approach. S309 IgG was captured on the surface and increasing concentrations of purified SARS-CoV-2 RBD, either glycosylated or deglycosylated,

were injected. Association and dissociation kinetics were monitored and fit to a binding model to determine affinity.

Expression of recombinant antibodies

Recombinant antibodies were expressed in ExpiCHO cells transiently co-transfected with plasmids expressing the heavy and light chain as previously described. (Stettler *et al.* (2016) Specificity, cross-reactivity, and function of antibodies elicited by Zika virus infection. Science, 353(6301), 823–826) Monoclonal antibodies S303, S304, S306, S309, S310, and S315 were expressed as rIgG-LS antibodies. The LS mutation confers a longer half-life in vivo. (Zalevsky *et al.* (2010) Enhanced antibody half-life improves in vivo activity. Nature Biotechnology, 28(2), 157–159)

Sequence alignment

SARS-CoV-2 genomics sequences were downloaded from GISAID on March 29th 2020, using the "complete (>29,000 bp)" and "low coverage exclusion" filters. Bat and pangolin sequences were removed to yield human-only sequences. The spike ORF was localized by performing reference protein (YP_009724390.1)-genome alignments with GeneWise2. Incomplete matches and indel-containing ORFs were rescued and included in downstream analysis. Nucleotide sequences were translated *in silico* using seqkit. Sequences with more than 10% undetermined aminoacids (due to N basecalls) were removed. Multiple sequence alignment was performed using MAFFT. Variants were determined by comparison of aligned sequences (n=2,229) to the reference sequence using the R/Bioconductor package Biostrings. A similar strategy was used to extract and translate spike protein sequences from SARS-CoV genomes sourced from ViPR (search criteria: SARS-related coronavirus, full-length genomes, human host, deposited before December 2019 to exclude SARS-CoV-2, n=53). Sourced SARS-CoV genome sequences comprised all the major published strains, such as Urbani, Tor2, TW1, P2, Frankfurt1, among others. Pangolin sequences as shown by Tsan-Yuk Lam *et al* were sourced from GISAID. Bat sequences from the three clades of Sarbecoviruses as shown by Lu *et al* (Lancet 2020) were sourced from Genbank. Civet and racoon dog sequences were similarly sourced from Genbank.

Generation of stable overexpression cell lines

Lentiviruses were generated by co-transfection of Lenti-X 293T cells (Takara) with lentiviral expression plasmids encoding DC-SIGN (CD209), L-SIGN (CLEC4M), SIGLEC1, TMPRSS2 or ACE2 (all obtained from Genecopoeia) and the respective lentiviral helper plasmids. Forty-eight hours post transfection, lentivirus in the supernatant was harvested and concentrated by ultracentrifugation for 2 h at 20,000 rpm. Lenti-X 293T (Takara), Vero E6 (ATCC), MRC5 (Sigma-Aldrich), A549 (ATCC) were transduced in the presence of 6 ug/mL polybrene (Millipore) for 24 h. Cell lines overexpressing two transgenes were transduced subsequently. Selection with puromycin and/or blasticidin (Gibco) was started two days after transduction and selection reagent was kept in the growth medium for all subsequent culturing. Single cell clones were derived from the A549-ACE2-TMPRSS2 cell line, all other cell lines represent cell pools.

SARS-CoV-2 neutralization

Vero E6 or Vero E6-TMPRSS2 cells cultured in DMEM supplemented with 10% FBS (VWR) and 1x Penicillin/Streptomycin (Thermo Fisher Scientific) were seeded in black 96-well plates at 20,000 cells/well. Serial 1:4 dilutions of the monoclonal antibodies were incubated with 200 pfu of SARS-CoV-2 (isolate USA-WA1/2020, passage 3, passaged in Vero E6 cells) for 30 min at 37°C in a BSL-3 facility. Cell supernatant was removed and the virus-antibody mixture was added to the cells. 24 h post infection, cells were fixed with 4% paraformaldehyde for 30 min, followed by two PBS (pH 7.4) washes and permeabilization with 0.25% Triton X-100 in PBS for 30 min. After blocking in 5% milk powder/PBS for 30 min, cells were incubated with a primary antibody targeting SARS-CoV-2 nucleocapsid protein (Sino Biological, cat. 40143-R001) at a 1:2000 dilution for 1h. After washing and incubation with a secondary Alexa647-labeled antibody mixed with 1 ug/ml Hoechst33342 for 1 hour, plates were imaged on an automated cell-imaging reader (Cytation 5, Biotek) and nucleocapsid-positive cells were counted using the manufacturer's supplied software.

SARS-CoV-2-Nluc neutralization

Neutralization was determined using SARS-CoV-2-Nluc, an infectious clone of SARS-CoV-2 (based on strain 2019-nCoV/USA_WA1/2020) encoding nanoluciferase

in place of the viral ORF7, which demonstrates comparable growth kinetics to wild type virus (Xie et al., Nat Comm, 2020, https://doi.org/10.1038/s41467-020-19055-7). Cells were seeded into black-walled, clear-bottom 96-well plates at 20,000 cells/well (293T cells were seeded into poly-L-lysine-coated wells at 35,000 cells/well) and cultured overnight at 37°C. The next day, 9-point 4-fold serial dilutions of antibodies were prepared in infection media (DMEM + 10% FBS). SARS-CoV-2-Nluc was diluted in infection media at the indicated MOI, added to the antibody dilutions and incubated for 30 min at 37°C. Media was removed from the cells, mAb-virus complexes were added, and cells were incubated at 37°C for 24 h. Media was removed from the cells, Nano-Glo luciferase substrate (Promega) was added according to the manufacturer's recommendations, incubated for 10 min at RT and luciferase signal was quantified on a VICTOR Nivo plate reader (Perkin Elmer).

SARS-CoV-2 pseudotyped VSV production and neutralization

To generate SARS-CoV-2 pseudotyped vesicular stomatitis virus, Lenti-X 293T cells (Takara) were seeded in 10-cm dishes for 80% next day confluency. The next day, cells were transfected with a plasmid encoding for SARS-CoV-2 S-glycoprotein (YP_009724390.1) harboring a C-terminal 19 aa truncation using TransIT-Lenti (Mirus Bio) according to the manufacturer's instructions. One day post-transfection, cells were infected with VSV(G*ΔG-luciferase) (Kerafast) at an MOI of 3 infectious units/cell. Viral inoculum was washed off after one hour and cells were incubated for another day at 37°C. The cell supernatant containing SARS-CoV-2 pseudotyped VSV was collected at day 2 post-transfection, centrifuged at 1000 x g for 5 minutes to remove cellular debris, aliquoted, and frozen at -80°C.

For viral neutralization, Cells were seeded into black-walled, clear-bottom 96-well plates at 20,000 cells/well (293T cells were seeded into poly-L-lysine-coated wells at 35,000 cells/well) and cultured overnight at 37°C. The next day, 9-point 4-fold serial dilutions of antibodies were prepared in media. SARS-CoV-2 pseudotyped VSV was diluted 1:30 in media in the presence of 100 ng/mL anti-VSV-G antibody (clone 8G5F11, Absolute Antibody) and added 1:1 to each antibody dilution. Virus:antibody mixtures were incubated for 1 hour at 37°C. Media was removed from the cells and 50

μL of virus:antibody mixtures were added to the cells. One hour post-infection, 100 μL of media was added to all wells and incubated for 17-20 hours at 37°C. Media was removed and 50 μL of Bio-Glo reagent (Promega) was added to each well. The plate was shaken on a plate shaker at 300 RPM at room temperature for 15 minutes and RLUs were read on an EnSight plate reader (Perkin-Elmer).

Transfection-based attachment receptor screen

Lenti-X 293T cells (Takara) were transfected with plasmids encoding the following receptor candidates (all purchased from Genecopoeia): ACE2 (NM_021804), DC-SIGN (NM_021155), L-SIGN (BC110614), LGALS3 (NM_002306), SIGLEC1 (NM_023068), SIGLEC3 (XM_057602), SIGLEC9 (BC035365), SIGLEC10 (NM_033130), MGL (NM_182906), MINCLE (NM_014358), CD147 (NM_198589), ASGR1 (NM_001671.4), ASGR2 (NM_080913), NRP1 (NM_003873). One day post transfection, cells were infected with SARS-CoV-2 pseudotyped VSV at 1:20 dilution in the presence of 100 ng/mL anti-VSV-G antibody (clone 8G5F11, Absolute Antibody) at 37°C. One hour post-infection, 100 μL of media was added to all wells and incubated for 17-20 hours at 37°C. Media was removed and 50 μL of Bio-Glo reagent (Promega) was added to each well. The plate was shaken on a plate shaker at 300 RPM at room temperature for 15 minutes and RLUs were read on an EnSight plate reader (Perkin-Elmer).

Trans-infection

Parental HeLa cells or HeLa cells stably expressing DC-SIGN, L-SIGN or SIGLEC1 were seeded at 5,000 cells per well in black-walled clear-bottom 96-well plates. One day later, cells reached about 50% confluency and were inoculated with SARS-CoV-2 pseudotyped VSV at 1:10 dilution in the presence of 100 ng/mL anti-VSV-G antibody (clone 8G5F11, Absolute Antibody) at 37°C for 2 h. For antibody-mediated inhibition of trans-infection, cells were pre-incubated with 10 ug/mL anti-SIGLEC1 antibody (Biolegend, clone 7-239) for 30 min. After 2 h inoculation, cells were washed four times with complete medium and 10,000 VeroE6-TMPRSS2 cells per well were added and incubated 17-20 h at 37°C for trans-infection. Media was removed and 50 μL of Bio-Glo reagent (Promega) was added to each well. The plate was shaken

on a plate shaker at 300 RPM at room temperature for 15 minutes and RLUs were read on an EnSight plate reader (Perkin-Elmer).

Cell-cell fusion of CHO-S cells

CHO cells stably expressing SARS-CoV-2 S-glycoprotein were seeded in 96 well plates for microscopy (Thermo Fisher Scientific) at 12'500 cells/well and the following day, different concentrations of mAbs and nuclei marker Hoechst (final dilution 1:1000) were added to the cells and incubated for additional 24h hours. Fusion degree was established using the Cytation 5 Imager (BioTek) and an object detection protocol was used to detect nuclei as objects and measure their size. The nuclei of fused cells (i.e., syncytia) are found aggregated at the center of the syncitia and are recognized as a unique large object that is gated according to its size. The area of the objects in fused cells divided by the total area of all the object multiplied by 100 provides the percentage of fused cells

Immunofluorescence analysis

HEK 293T cells were seeded onto poly-D-Lysine-coated 96-well plates (Sigma-Aldrich) and fixed 24 h after seeding with 4% paraformaldehyde for 30 min, followed by two PBS (pH 7.4) washes and permeabilization with 0.25% Triton X-100 in PBS for 30 min. Cells were incubated with primary antibodies anti-DC-SIGN/L-SIGN (Biolegend, cat. 845002, 1:500 dilution), anti-DC-SIGN (Cell Signaling, cat. 13193S, 1:500 dilution), anti-SIGLEC1 (Biolegend, cat. 346002, 1:500 dilution) or anti-ACE2 (R&D Systems, cat. AF933, 1:200 dilution) diluted in 3% milk powder/PBS for 2 h at room temperature. After washing and incubation with a secondary Alexa647-labeled antibody mixed with 1 ug/ml Hoechst33342 for 1 hour, plates were imaged on an inverted fluorescence microscope (Echo Revolve).

ACE2/TMPRSS2 RT-qPCR

RNA was extracted from the cells using the NucleoSpin RNA Plus kit (Macherey-Nagel) according to the manufacturer's protocol. RNA was reverse transcribed using the High Capacity cDNA Reverse Transcription kit (Applied Biosystems) according to the manufacturer's instructions. Intracellular levels of ACE2 (Forward Primer: CAAGAGCAAACGGTTGAACAC, Reverse Primer:

CCAGAGCCTCTCATTGTAGTCT), HPRT (Forward Primer: CCTGGCGTCGTGATTAGTG, Reverse Primer: ACACCCTTTCCAAATCCTCAG), and TMPRSS2 (Forward Primer: CAAGTGCTCCRACTCTGGGAT, Reverse Primer: AACACACCGRTTCTCGTCCTC) were quantified using the Luna Universal qPCR Master Mix (New England Biolabs) according to the manufacturer's protocol. Levels of ACE2 and TMPRSS2 were normalized to HPRT. Hela cells were used as the reference sample. All qPCRs were run on a QuantStudio 3 Real-Time PCR System (Applied Biosystems).

SARS2 D614G Spike Production and biotinylation

Prefusion-stabilized SARS2 D614G spike (comprising amino acid sequence Q14 to K1211) with a C-terminal TEV cleavage site, T4 bacteriophage fibritin foldon, 8x His-, Avi- and EPEA-tag was transfected into HEK293 Freestyle cells, using 293fectin as a transfection reagent. Cells were left to produce protein for three days at 37°C. Afterwards, supernatant was harvested by centrifuging cells for 30 minutes at 500 xg, followed by another spin for 30 minutes at 4000 xg. Cell culture supernatant was filtered through a 0.2 um filter and loaded onto a 5 mL C-tag affinity matrix column, pre-equilibrated with 50 mM Tris pH 8 and 200 mM NaCl. SARS2 D614G spike was eluted, using 10 column volumes of 100 mM Tris, 200 mM NaCl and 3.8 mM SEPEA peptide. Elution peak was concentrated and injected on a Superose 6 increase 10/300 GL gel filtration column, using 50 mM Tris pH 8 and 200 mM NaCl as a running buffer. SEC fractions corresponding to monodisperse SARS2 D614G spike were collected and flash frozen in liquid nitrogen for storage at -80°C. Purified SARS2 D614G spike protein was biotinylated using BirA500 biotinylation kit from Avidity. To 50 ug of spike protein, 5 ug of BirA, and 11 uL of BiomixA and BiomixB was added. Final spike protein concentration during the biotinylation reaction was ~1 uM. The reaction was left to proceed for 16 hours at 4°C. Then, protein was desalted using two Zeba spin columns pre-equilibrated with 1x PBS pH 7.4.

Flow cytometry analysis for DC-SIGN, L-SIGN, SIGLEC1 and ACE-2

HEK 293T cells expressing DC-SIGN, L-SIGN, SIGLEC1 or ACE2 were resuspended at $4x10^6$ cells/mL and 100 µL per well were seeded onto V-bottom 96-well

plates (Corning, 3894). The plate was centrifuged at 2,000 rpm for 5 minutes and washed with PBS (pH 7.4). The cells were resuspended in 200 µL of PBS containing Ghost violet 510 viability dye (Cell Signaling, cat. 13-0870-T100, 1:1,000 dilution), incubated for 15 minutes on ice and then washed. The cells were resuspended in 100 µL of FACS buffer prepared with 0.5% BSA (Sigma-Aldrich) in PBS containing the primary antibodies at a 1:100 dilution: mouse anti-DC/L-SIGN (Biolegend, cat. 845002), rabbit anti-DC-SIGN (Cell Signaling, cat. 13193), mouse anti-SIGLEC1 (Biologend, cat. 346002) or goat anti-ACE2 (R&D Systems, cat. AF933). After 1 h incubation on ice, the cells were washed two times and resuspended in FACS buffer containing the Alexa Fluor-488-labeled secondary antibodies at a 1:200 dilution: goat anti-mouse (Invitrogen cat. A11001), goat anti-rabbit (Invitrogen cat. A11008) or donkey anti-goat (Invitrogen cat. A11055). After incubation for 45 min on ice, the cells were washed three times with 200µL of FACS buffer and fixed with 200µL of 4% PFA (Alfa Aesar) for 15 mins at room temperature. Cells were washed three times, resuspended in 200µL of FACS buffer and analyzed by flow cytometry using the CytoFLEX flow cytometer (Beckman Coulter).

Flow cytometry of SARS-CoV-2 Spike and RBD binding to cells

Biotinylated SARS-CoV-2 Spike D614G protein (Spikebiotin, in-house generated) or the biotinylated SARS-CoV-2 Spike receptor-binding domain (RBDbiotin, Sino Biological, 40592-V08B) were incubated with Alexa Fluor® 647 streptavidin (AF647-strep, Invitrogen, S21374) at a 1:20 ratio by volume for 20 min at room temperature. The labeled proteins were then stored at 4°C until further use. Cells were dissociated with TrpLE Express (Gibco, 12605-010) and 10^5 cells were transferred to each well of a 96-well V bottom plate (Corning, 3894). Cells were washed twice in flow cytometry buffer (2% FBS in PBS (w/o Ca/Mg)) and stained with Spikebiotin-AF647-strep at a final concentration of 20 µg/ml or RBDbiotin-AF647-strep at a final concentration of 7.5 µg/ml for 1h on ice. Stained cells were washed twice with flow cytometry buffer, resuspended in 1% PFA (Electron Microscopy Sciences, 15714-S) and analyzed with the Cytoflex LX (Beckman Coulter).

Recombinant expression of SARS-CoV-2-specific mAbs.

Human mAbs were isolated from plasma cells or memory B cells of SARS-CoV-2 immune donors, as previously described. Recombinant antibodies were expressed in ExpiCHO cells at 37°C and 8% CO_2. Cells were transfected using ExpiFectamine. Transfected cells were supplemented 1 day after transfection with ExpiCHO Feed and ExpiFectamine CHO Enhancer. Cell culture supernatant was collected eight days after transfection and filtered through a 0.2 μm filter. Recombinant antibodies were affinity purified on an ÄKTA xpress FPLC device using 5 mL HiTrap™ MabSelect™ PrismA columns followed by buffer exchange to Histidine buffer (20 mM Histidine, 8% sucrose, pH 6) using HiPrep 26/10 desalting columns

SARS-CoV-2 infection model in hamster

Virus preparation

The SARS-CoV-2 strain used in this study, BetaCov/Belgium/GHB-03021/2020 (EPI ISL 109 407976|2020-02-03), was recovered from a nasopharyngeal swab taken from an RT-qPCR confirmed asymptomatic patient who returned from Wuhan, China in February 2020. A close relation with the prototypic Wuhan-Hu-1 2019-nCoV (GenBank accession 112 number MN908947.3) strain was confirmed by phylogenetic analysis. Infectious virus was isolated by serial passaging on HuH7 and Vero E6 cells; passage 6 virus was used for the study described here. The titer of the virus stock was determined by end-point dilution on Vero E6 cells by the Reed and Muench method.

Cells

Vero E6 cells (African green monkey kidney, ATCC CRL-1586) were cultured in minimal essential medium (Gibco) supplemented with 10% fetal bovine serum (Integro), 1% L- glutamine (Gibco) and 1% bicarbonate (Gibco). End-point titrations were performed with medium containing 2% fetal bovine serum instead of 10%.

SARS-CoV-2 infection model in hamsters

The hamster infection model of SARS-CoV-2 has been described before. The specific study design is shown in the schematic below. In brief, wild-type Syrian Golden hamsters (*Mesocricetus auratus*) were purchased from Janvier Laboratories and were housed per two in ventilated isolator cages (IsoCage N Biocontainment System, Tecniplast) with *ad libitum* access to food and water and cage enrichment (wood block).

The animals were acclimated for 4 days prior to study start. Housing conditions and experimental procedures were approved by the ethics committee of animal experimentation of KU Leuven (license P065- 2020). Female 6-8 week old hamsters were anesthetized with ketamine/xylazine/atropine and inoculated intranasally with 50 µL containing 2×10^6 TCID50 SARS-CoV-2 (day 0).

Treatment regimen

Animals were prophylactically treated 48h before infection by intraperitoneal administration (i.p.) and monitored for appearance, behavior, and weight. At day 4 post infection (p.i.), hamsters were euthanized by i.p. injection of 500 µL Dolethal (200 mg/mL sodium pentobarbital, Vétoquinol SA). Lungs were collected and viral RNA and infectious virus were quantified by RT-qPCR and end-point virus titration, respectively. Blood samples were collected before infection for PK analysis.

SARS-CoV-2 RT-qPCR

Collected lung tissues were homogenized using bead disruption (Precellys) in 350µL RLT buffer (RNeasyMinikit, Qiagen)and centrifuged (10.000 rpm, 5 min) to pellet the cell debris. RNA was extracted according to the manufacturer's instructions. Of 50 µL eluate, 4 µL was used as a template in RT-qPCR reactions. RT-qPCR was performed on a LightCycler96 platform (Roche) using the iTaq Universal Probes One-Step RT-qPCR kit (BioRad) with N2 primers and probes targeting the nucleocapsid. Standards of SARS-CoV-2 cDNA (IDT) were used to express viral genome copies per mg tissue or per mL serum.

End-point virus titrations

Lung tissues were homogenized using bead disruption (Precellys) in 350 µL minimal essential medium and centrifuged (10,000 rpm, 5min, 4°C) to pellet the cell debris. To quantify infectious SARS-CoV-2 particles, endpoint titrations were performed on confluent Vero E6 cells in 96- well plates. Viral titers were calculated by the Reed and Muench method using the Lindenbach calculator and were expressed as 50% tissue culture infectious dose (TCID50) per mg tissue.

Histology

For histological examination, the lungs were fixed overnight in 4% formaldehyde and embedded in paraffin. Tissue sections (5 μm) were analyzed after staining with hematoxylin and eosin and scored blindly for lung damage by an expert pathologist. The scored parameters, to which a cumulative score of 1 to 3 was attributed, were the following: congestion, intra-alveolar hemorrhagic, apoptotic bodies in bronchus wall, necrotizing bronchiolitis, perivascular edema, bronchopneumonia, perivascular inflammation, peribronchial inflammation and vasculitis.

Binding of immunocomplexes to hamster monocytes

Immunocomplexes (IC) were generated by complexing S309 mAb (hamster IgG, either wt or N297A) with a biotinylated anti-idiotype fab fragment and Alexa-488-streptavidin, using a precise molar ratio (4:8:1, respectively). Pre-generated fluorescent IC were serially diluted incubated at 4°C for 3 hrs with freshly revitalized hamster splenocytes, obtained from a naïve animal. Cellular binding was then evaluated by cytometry upon exclusion of dead cells and physical gating on monocyte population. Results are expressed as Alexa-488 mean florescent intensity of the entire monocyte population.

Bioinformatic analyses

Processed Human Lung Cell Atlas (HLCA) data and cell-type annotations were downloaded from Github (github.com/krasnowlab/HLCA). Processed single-cell transcriptome data and annotation of lung epithelial and immune cells from SARS-CoV-2 infected individuals were downloaded from NCBI GEO database (ID: GSE158055) and Github (github.com/zhangzlab/covid_balf). Available sequence data from the second single-cell transcriptomics study by Liao et al. were downloaded from NCBI SRA (ID: PRJNA608742) for inspection of reads corresponding to viral RNA. The proportion of sgRNA relative to genomic RNA was estimated by counting TRS-containing reads supporting a leader-TRS junction. Criteria and methods for detection of leader-TRS junction reads were adapted from Alexandersen et al. The viral genome reference and TRS annotation was based on Wuhan-Hu-1 NC_045512.2/MN908947[49].

Only 2 samples from individuals with severe COVID-19 had detectable leader-TRS junction reads (SRR11181958, SRR11181959).

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. 63/022,392, filed May 8, 2020, U.S. Patent Application No. 63/024,372, filed May 13, 2020, U.S. Patent Application No. 63/027,814, filed May 20, 2020, U.S. Patent Application No. 63/029,338, filed May 22, 2020, U.S. Patent Application No. 63/031,286, filed May 28, 2020, U.S. Patent Application No. 63/033,045, filed June 1, 2020, U.S. Patent Application No. 63/036,683, filed June 9, 2020, U.S. Patent Application No. 63/039,939, filed June 16, 2020, U.S. Patent Application No. 63/046,465, filed June 30, 2020, U.S. Patent Application No. 63/057,767, filed July 28, 2020, U.S. Patent Application No. 63/090,667, filed October 12, 2020, U.S. Patent Application No. 63/113,450, filed November 13, 2020, U.S. Patent Application No. 63/153,784, filed February 25, 2021, and U.S. Patent Application No. 63/170, 368, filed April 2, 2021, 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.

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.

CLAIMS

What is claimed is:

1. 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.: 400, 23, 33, 43, 53, 63, 75, 85, 97, 107, 120, 130, 140, 147, 160, 170, 174, 183, 190, 199, 209, 219, 229, 241, 255, 265, 275, 285, 299, 313, 323, 333, 370, 380, 390, 410, 420, 430, 435, 445, 455, 465, 475, 485, 495, 505, 515, 525, 535, 545, 555, 565, 575, 585, 595, 605, 615, 631, and 693, 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.: 401, 24, 34, 44, 54, 64, 76, 86, 98, 108, 121, 131, 141, 148, 151, 161, 171, 184, 200, 210, 220, 230, 242, 256, 266, 276, 286, 300, 314, 324, 334, 352, 360, 362, 364, 366, 371, 381, 391, 411, 421, 431, 436, 446, 456, 466, 476, 486, 496, 506, 516, 526, 536, 546, 556, 566, 576, 586, 596, 606, 616, 625, 632, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 675, 677, 679, 681, 683, 685, and 694, 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.: 766, 25, 35, 45, 55, 65, 77, 87, 99, 109, 122, 132, 142, 149, 162, 164, 165, 172, 176, 177, 179, 180, 185, 187, 188, 201, 211, 221, 231, 243, 257, 267, 277, 287, 301, 315, 325, 335, 354, 372, 382, 392, 412, 422, 432, 437, 447, 457, 467, 477, 487, 497, 507, 517, 527, 537, 547, 557, 567, 577, 587, 597, 607, 617, 627,

633, 695, 751, 753, 755, 757, 760, 763, 765, and 402, 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.: 404, 27, 37, 47, 57, 67, 79, 89, 101, 111, 124, 134, 144, 152, 155, 156, 158, 159, 166, 181, 192, 203, 213, 223, 233, 245, 259, 269, 279, 289, 303, 317, 327, 337, 356, 374, 384, 394, 414, 424, 439, 449, 459, 469, 479, 489, 499, 509, 519, 529, 539, 549, 559, 569, 579, 589, 599, 609, 619, 687, and 697, 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.: 405, 28, 38, 48, 58, 68, 80, 90, 102, 112, 125, 135, 145, 153, 167, 182, 193, 204, 214, 224, 234, 246, 260, 270, 280, 290, 304, 318, 328, 338, 375, 385, 395, 415, 425, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 688, and 698, 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.: 406, 29, 39, 49, 59, 69, 81, 91, 103, 113, 126, 136, 146, 169, 195, 197, 205, 215, 225, 235, 247, 261, 271, 281, 291, 305, 319, 329, 339, 358, 376, 386, 396, 416, 426, 441, 451, 461, 471, 481, 491, 501, 511, 521, 531, 541, 551, 561, 571, 581, 591, 601, 611, 621, 689, 699, 745 and 747, 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.

2. 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.

3. The antibody or antigen-binding fragment of any one of claims 1-2, comprising CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 amino acid sequences of SEQ ID NOs.:

(i) 400, 401, 766, and 404-406, respectively;

(ii)400-402 and 404-406, respectively;

(iii) 43-45 and 47-49, respectively;

(iv) 53-55 and 57-59, respectively;

(v) 63-65 and 67-69, respectively;

(vi) 75-77 and 79-81, respectively;

(vii) 85-87 and 89-91, respectively;

(viii) 97-99 and 101-103, respectively;

(ix) 107-109 and 111-113, respectively;

(x) 120-122 and 124-126, respectively;

(xi) 130-132 and 134-136, respectively;

(xii) 23 or 147, any one of 24, 148 or 151, 25 or 149, any one of 27, 152, 155, 156, 158, or 159, 28 or 153, and 29, respectively;

(xiii) 43 or 160, 44 or 161, any one of 45, 162, 164, or 165, 47 or 166, 48 or 167, and 49 or 169, respectively;

(xiv) any one of 130, 170, or 174, 130, 131, 132, 134 or 181, 135 or 182, and 136, respectively;

(xv) any one of 53, 183, or 190, 54 or 184, any one of 55, 185, 187, or 188, 57 or 192, 58 or 193, and any one of 59, 195, or 197, respectively;

(xvi) 199-201 and 203-205, respectively;

(xvii) 209-211 and 213-215, respectively;

(xviii) 219-221 and 223-225, respectively;

(xix) 229-231 and 233-235, respectively;

(xx) 241-243 and 245-247, respectively;

(xxi) 255-257 and 259-261, respectively;

(xxii) 265-267 and 269-271, respectively;

(xxiii) 275-277 and 279-281, respectively;

(xxiv) 285-287 and 289-291, respectively;

(xxv) 299-301 and 303-305, respectively;

(xxvi) 313-315 and 317-319, respectively;

(xxvii) 323-325 and 327-329, respectively;

(xxviii) 333-335 and 337-339, respectively;

(xxix) 229, 230 or 352, 231 or 354, and 233 or 356, 234, and 235 or 358, respectively;

(xxx) 313, any one of 314, 360, 362, 364, or 366, 315 and 317-319, respectively;

(xxxi) 370-372 and 374-376, respectively;

(xxxii) 380-382 and 384-386, respectively;

(xxxiii) 390-392 and 394-396, respectively;

(xxxiv)23-25 and 27-29, respectively;

(xxxv) 410-412 and 414-416, respectively;

(xxxvi) 420-422 and 424-426, respectively;

(xxxvii) 435-437 and 439-441, respectively;

(xxxviii) 445-447 and 449-451, respectively;

(xxxix) 455-457 and 459-461, respectively;

(xxxx) 465-467 and 469-471, respectively;

(xxxxi) 475-477 and 479-481, respectively;

(xxxxii) 485-487 and 489-491, respectively;

(xxxxiii) 494-497 and 499-501, respectively;

(xxxxiv) 505-507 and 509-511, respectively;

(xxxxv) 515-517 and 519-521, respectively;

(xxxxvi) 525-527 and 529-531, respectively;

(xxxxvii) 535-537 and 539-541, respectively;

(xxxxviii) 545-547 and 549-551, respectively;

(xxxxix) 555-557 and 559-561, respectively;

(xxxxx) 565-567 and 569-571, respectively;

(xxxxxi) 575-577 and 579-581, respectively;

(xxxxxii) 585, 586 or 625, 587 or 627, and 589-591, respectively;

(xxxxxiii) 595-597 and 599-601, respectively;

(xxxxxiv) 605-607 and 609-611, respectively;

(xxxxxv) 615-617 and 619-621, respectively;

(xxxxxvi) 631, 632 or 635 or 637 or 639 or 641 or 643 or 645 or 647 or 649 or 651 or 653 or 655 or 657 or 659 or 661 or 663 or 665 or 667 or 669 or 671 or 673 or 675 or 677 or 679 or 681 or 683 or 685, 633, and 697-699, respectively;

(xxxxxvii) 693-695 and 697-699, respectively;

(xxxxxviii) 400, 401 and any one of 751, 753, 755, 757, or 760 and 404, 405, and any one of 745 or 747, respectively;

(xxxxxxix) 585, 586, and 762 or 764 and 589-591, respectively;

(xxxxxxx) 33-35 and 37-39, respectively; or

(xxxxxxxi) 400, 401, 766, 404, 405 or variant of 405 comprising one, two, or three amino acid substiutions, wherein each of the one, two, or three amino acid substitutions is optionally a conservative amino acid substitution, and 406, respectively.

4. An antibody, or antigen-binding fragment thereof, comprising the CDRH1, the CDRH2, and the CDRH3 of the VH amino acid sequence set forth in SEQ ID NO.:399, and the CDRL1, the CDRL2 or a variant of the CDRL2 comprising one, two, or three amino acid substiutions, wherein each of the one, two, or three amino acid substitutions is optionally a conservative amino acid substitution, and the CDRL3 of the

VL amino acid sequence set forth in SEQ ID NO.:738, wherein the CDRs are according to IMGT,

and 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. An antibody, or an antigen-binding fragment thereof, comprising a heavy chain variable domain (VH) comprising complementarity determining region (CDR)H1, CDRH2, and CDRH3, and a light chain variable domain (VL) comprising CDRL1, CDRL2, and CDRL3, wherein CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 comprise the amino acid sequences set forth in: (a) SEQ ID NOs.:400, 401, 766, 404, 405, and 406, respectively; (b) SEQ ID NOs.:400, 401, 769, 404, 405, and 406, respectively; (c) SEQ ID NOs.:400, 401, 770, 404, 405, and 406, respectively; (d) SEQ ID NOs.:400, 401, 771, 404, 405, and 406, respectively; (e) SEQ ID NOs.:400, 401, 772, 404, 405, and 406, respectively; (f) SEQ ID NOs.:400, 401, 773, 404, 405, and 406, respectively; (g) SEQ ID NOs.:400, 401, 766, 404, 405, and 745, respectively; (h) SEQ ID NOs.:400, 401, 769, 404, 405, and 745, respectively; (i) SEQ ID NOs.:400, 401, 770, 404, 405, and 745, respectively; (j) SEQ ID NOs.:400, 401, 771, 404, 405, and 745, respectively; (k) SEQ ID NOs.:400, 401, 772, 404, 405, and 745, respectively; (l) SEQ ID NOs.: 400, 401, 773, 405, 405, and 745, respectively; (m) SEQ ID NOs.:400, 401, 766, 404, 405, and 747, respectively; (n) SEQ ID NOs.:400, 401, 769, 404, 405, and 747, respectively; (o) SEQ ID NOs.:400, 401, 770, 404, 405, and 747, respectively; (p) SEQ ID NOs.:400, 401, 771, 404, 405, and 747, respectively; (q) SEQ ID NOs.:400, 401, 772, 404, 405, and 747, respectively; or (r) SEQ ID NOs.:400, 401, 773, 404, 405, and 747, respectively,

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.

6. The antibody or antigen-binding fragment thereof of claim 5, 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 CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 comprise the amino acid sequences set forth in: (a) SEQ ID NOs.:400, 401, 766, 404, 405, and 406, respectively.

7. The antibody or antigen-binding fragment of any one of claims 4-6, comprising the amino acid sequences set forth in: (a) SEQ ID NOs.:400, 401, 402, 404, 405, and 406; (b) SEQ ID NOs.:400, 401, 751, 404, 405, and 406; (c) SEQ ID NOs.:400, 401, 753, 404, 405, and 406; (d) SEQ ID NOs.:400, 401, 755, 404, 405, and 406; (e) SEQ ID NOs.:400, 401, 757, 404, 405, and 406; (f) SEQ ID NOs.:400, 401, 760, 404, 405, and 406; (g) SEQ ID NOs.:400, 401, 402, 404, 405, and 745; (h) SEQ ID NOs.:400, 401, 751, 404, 405, and 745; (i) SEQ ID NOs.:400, 401, 753, 404, 405, and 745; (j) SEQ ID NOs.:400, 401, 755, 404, 405, and 745; (k) SEQ ID NOs.:400, 401, 757, 404, 405, and 745; (l) SEQ ID NOs.: 400, 401, 760, 404, 405, and 745; (m) SEQ ID NOs.:400, 401, 402, 404, 405, and 747; (n) SEQ ID NOs.:400, 401, 751, 404, 405, and 747; (o) SEQ ID NOs.:400, 401, 753, 404, 405, and 747; (p) SEQ ID NOs.:400, 401, 755, 404, 405, and 747; (q) SEQ ID NOs.:400, 401, 757, 404, 405, and 747; or (r) SEQ ID NOs.:400, 401, 760, 404, 405, and 747.

8. The antibody or antigen-binding fragment of any one of claims 4-7, comprising, in VH, the amino acid sequence set forth in SEQ ID NO.: 400, the amino acid sequence set forth in SEQ ID NO.:401, and the amino acid sequence set forth in SEQ ID NO.:402, and in VL, the amino acid sequence set forth in SEQ ID NO.:404, the amino acid sequence set forth in SEQ ID NO.:405, and the amino acid sequence set forth in SEQ ID NO.:406.

9. An antibody, or an antigen-binding fragment thereof, comprising a heavy chain variable domain (VH) comprising complementarity determining region

(CDR)H1, CDRH2, and CDRH3, and a light chain variable domain (VL) comprising CDRL1, CDRL2, and CDRL3, wherein CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 comprise the amino acid sequences set forth in SEQ ID NOs.:525, 526, 527, 529, 530, and 531, respectively,

and 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.

10. An antibody, or an antigen-binding fragment thereof, comprising a heavy chain variable domain (VH) comprising complementarity determining region (CDR)H1, CDRH2, and CDRH3, and a light chain variable domain (VL) comprising CDRL1, CDRL2, and CDRL3, wherein CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 comprise the amino acid sequences set forth in SEQ ID NOs.:585, 586 or 625, 587 or 627, 589, 590, and 591, respectively,

and 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.

11. An antibody, or an antigen-binding fragment thereof, comprising a heavy chain variable domain (VH) comprising complementarity determining region (CDR)H1, CDRH2, and CDRH3, and a light chain variable domain (VL) comprising CDRL1, CDRL2, and CDRL3, wherein CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 comprise the amino acid sequences set forth in SEQ ID NOs.:229, 230, 231, 233, 234, and 235, respectively,

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.

12. The antibody or antigen-binding fragment of any one of claims 1-11, wherein:

(i) the VH comprises or consists of an amino acid sequence having at least 85% (*e.g.,* 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.: 399, 22, 32, 42, 52, 62, 72, 74, 84, 96, 106, 119, 129, 139, 150, 163, 173, 175, 178, 186, 189, 191, 198, 208, 218, 228, 240, 254, 264, 274, 284, 298, 312, 322, 332, 350, 351, 353, 359, 361, 363, 365, 367, 368, 369, 379, 389, 409, 419, 429, 434, 444, 454, 464, 474, 484, 494, 504, 514, 524, 534, 544, 554, 564, 574, 584, 594, 604, 614, 624, 626, 628, 630, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, 684, 692, 740, 741, 742, 743, 748, 749, 750, 752, 754, 756, 758, 759, 761, 762, and 764, wherein the variation is optionally limited to one or more framework regions and/or the variation 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% (*e.g.,* 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.: 738, 26, 36, 46, 56, 66, 78, 88, 94, 100, 110, 123, 133, 143, 154, 157, 168, 194, 196, 202, 212, 222, 232, 238, 244, 250, 252, 258, 268, 278, 288, 294, 296, 302, 308, 310, 316, 326, 336, 355, 357, 373, 383, 393, 403, 413, 423, 438, 448, 458, 468, 478, 488, 498, 508, 518, 528, 538, 548, 558, 568, 578, 588, 598, 608, 618, 686, 696, 744, and 746, wherein the variation is optionally limited to one or more framework regions and/or the variation comprises one or more substitution to a germline-encoded amino acid.

13. The antibody or antigen-binding fragment of any one of claims 1-12, wherein the VH comprises or consists of an amino acid sequence having at least 85% identity to the amino acid sequence set forth in SEQ ID NO.:399 and the VL comprises or consists of an amino acid sequence having at least 85% identity to the amino acid sequence set forth in SEQ ID NO.:403 or SEQ ID NO.:738.

14. The antibody or antigen-binding fragment of any one of claims 1-13, wherein the VH comprises or consists of an amino acid sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO.:399 and the VL comprises or consists of an amino acid sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO.:403 or SEQ ID NO.:738.

15. The antibody or antigen-binding fragment of any one of claims 1-14, wherein the VH comprises or consists of an amino acid sequence having at least 95% identity to the amino acid sequence set forth in SEQ ID NO.:399 and the VL comprises or consists of an amino acid sequence having at least 95% identity to the amino acid sequence set forth in SEQ ID NO.:403 or SEQ ID NO.:738.

16. The antibody or antigen-binding fragment of any one of claims 1-15, wherein the VH comprises or consists of an amino acid sequence having at least 97% identity to the amino acid sequence set forth in SEQ ID NO.:399 and the VL comprises or consists of an amino acid sequence having at least 97% identity to the amino acid sequence set forth in SEQ ID NO.:403 or SEQ ID NO.:738.

17. The antibody or antigen-binding fragment of any one of claims 1-16, wherein the VH comprises or consists of an amino acid sequence having at least 99% identity to the amino acid sequence set forth in SEQ ID NO.:399 and the VL comprises or consists of an amino acid sequence having at least 99% identity to the amino acid sequence set forth in SEQ ID NO.:403 or SEQ ID NO.:738.

18. The antibody or antigen-binding fragment of any one of claims 1-12, wherein the VH and the VL have at least 85% identity (*e.g.,* 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%) to the amino acid sequences set forth in:

(i) SEQ ID NOs.:524 and 528, respectively;

(ii) SEQ ID NOs.:584 or 624 or 626 or 628 and 588, respectively;

(iii) SEQ ID NOs.:228 or 740 or 741 or 742 or 743 and 232, respectively; or

(iv) SEQ ID NOs.:228 or 740 or 741 or 742 or 743 and 238, respectively.

19. The antibody or antigen-binding fragment of any one of claims 1-18, wherein the VH comprises or consists of any VH amino acid sequence set forth in Table 2, and wherein the VL comprises or consists of any VL amino acid sequence set forth in Table 2, wherein, optionally, the VH and the VL comprise or consist of the amino acid sequences according to SEQ ID NOs.:

(i) 399 and 403 or 738, respectively;

(ii) 32 and 36, respectively;

(iii) 42 and 46, respectively;

(iv) 52 and 56, respectively;

(v) 62 and 66, respectively;

(vi) 72 and 66, respectively;

(vii) 74 and 78, respectively;

(viii) 84 and 88, respectively;

(ix) 84 and 88, respectively;

(x) 96 and 100, respectively;

(xi) 106 and 110, respectively;

(xii) 119 and 123, respectively; or

(xiii) 129 and 133, respectively;

(xiv) 22 or 150 and 26, 154, or 157, respectively;

(xv) 42 or 163 and 46 or 168, respectively;

(xvi) any one of 129, 173, 175, or 178 and 133, respectively;

(xvii) any one of 52, 186, 189, or 191 and any one of 56, 194, or 196, respectively;

(xviii) 198 and 202, respectively;

(xix) 208 and 212, respectively;

(xx) 218 and 222, respectively;

(xxi) 228 and 232 or 238, respectively;

(xxii) 240 and any one of 244, 250, or 252, respectively;

(xxiii) 254 and 258, respectively;

(xxiv) 264 and 268, respectively;

(xxv) 274 and 278, respectively; or

(xxvi) 284 and any one of 288, 294, or 296, respectively;

(xxvii) 298 and any one of 302, 308, or 310, respectively;

(xxviii) 312 and 316, respectively;

(xxix) 322 and 326, respectively;

(xxx) 332 and 336, respectively;

(xxxi) any one of 228, 350, 351, or 353 and 232, 238, 355, or 357, respectively;

(xxxii) any one of 312, 359, 361, 363, 365, 367, or 368 and 316, respectively;

(xxxiii) 369 and 373, respectively;

(xxxiv) 379 and 383, respectively;

(xxxv) 389 and 393, respectively;

(xxxvi) 22 and 26, respectively;

(xxxvii) 409 and 413, respectively;

(xxxviii) 419 and 423, respectively;

(xxxix) 434 and 438, respectively;

(xxxx) 444 and 448, respectively;

(xxxxi) 454 and 458, respectively;

(xxxxii) 464 and 468, respectively;

(xxxxiii) 474 and 478, respectively;

(xxxxiv) 484 and 488, respectively;

(xxxxv) 494 and 498, respectively;

(xxxxvi) 504 and 508, respectively;

(xxxxvii) 514 and 518, respectively;

(xxxxviii) 524 and 528, respectively;

(xxxxix) 534 and 538, respectively;

(xxxxx) 544 and 548, respectively;

(xxxxxi) 554 and 558, respectively;

(xxxxxii) 564 and 568, respectively;

(xxxxxiii) 574 and 578, respectively;

(xxxxxiv) 584 and 588, respectively;

(xxxxxv) 594 and 598, respectively;

(xxxxxvi) 604 and 608, respectively;

(xxxxxvii) 614 and 618, respectively;

(xxxxxviii) 624, 626, or 628 and 588, respectively;

(xxxxxix) 630, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, or 684, and 686, respectively;

(xxxxxx) 692 and 696, respectively;

(xxxxxxi) any one of 740-743 and 238, respectively;

(xxxxxxii) any one of 399, 748, 749, 750, 752, 754, 756, 758, 759, and 761 and any one of 403, 744, and 746, respectively; or

(xxxxxxiii) 762 or 764 and 588, respectively.

20. An antibody, or an antigen-binding fragment thereof, comprising a heavy chain variable domain (VH) and a light chain variable domain (VL), wherein the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO:399 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO:738,

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.

21. An antibody, or an antigen-binding fragment thereof, comprising a heavy chain variable domain (VH) and a light chain variable domain (VL), wherein the

VH comprises or consists of the amino acid sequence set forth in SEQ ID NO:399 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO:403,

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.

22. An antibody, or an antigen-binding fragment thereof, comprising a heavy chain variable domain (VH) and a light chain variable domain (VL), wherein the VH comprises or consists of the amino acid sequence set forth in any one of SEQ ID NOs:399, 748, 749, 750, 752, 754, 756, 758, 759, and 761, the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO:403,

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.

23. An antibody, or an antigen-binding fragment thereof, comprising a heavy chain variable domain (VH) and a light chain variable domain (VL), wherein the VH comprises or consists of the amino acid sequence set forth in any one of SEQ ID NOs:399, 748, 749, 750, 752, 754, 756, 758, 759, and 761, the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO:738,

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.

24. An antibody, or an antigen-binding fragment thereof, comprising a heavy chain variable domain (VH) and a light chain variable domain (VL), wherein the VH comprises or consists of the amino acid sequence set forth in any one of SEQ ID NOs:399, 748, 749, 750, 752, 754, 756, 758, 759, and 761, the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO:744,

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.

25. An antibody, or an antigen-binding fragment thereof, comprising a heavy chain variable domain (VH) and a light chain variable domain (VL), wherein the VH comprises or consists of the amino acid sequence set forth in any one of SEQ ID NOs:399, 748, 749, 750, 752, 754, 756, 758, 759, and 761, the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO:746,

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.

26. An antibody, or an antigen-binding fragment thereof, comprising a heavy chain variable domain (VH) and a light chain variable domain (VL), wherein the VH comprises or consists of the amino acid sequence set forth in SEQ ID NO:524 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO:528,

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.

27. An antibody, or an antigen-binding fragment thereof, comprising a heavy chain variable domain (VH) and a light chain variable domain (VL), wherein the VH comprises or consists of the amino acid sequence set forth in any one of SEQ ID NOs.:584, 624, 626, and 628 and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO:588,

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.

28. An antibody, or an antigen-binding fragment thereof, comprising a heavy chain variable domain (VH) and a light chain variable domain (VL), wherein the VH comprises or consists of the amino acid sequence set forth in any one of SEQ ID NOs.:228, 740, 741, 742, and 743, and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO:232,

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.

29. An antibody, or an antigen-binding fragment thereof, comprising a heavy chain variable domain (VH) and a light chain variable domain (VL), wherein the VH comprises or consists of the amino acid sequence set forth in any one of SEQ ID NOs.:228, 740, 741, 742, and 743, and the VL comprises or consists of the amino acid sequence set forth in SEQ ID NO:238,

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.

30. An antibody, or an antigen-binding fragment thereof, comprising a heavy chain variable domain (VH) and a light chain variable domain (VL), wherein the VH comprises or consists of the amino acid sequence as set forth in SEQ ID NO: 32 and the VL comprises or consists of the amino acid sequence as set forth in SEQ ID NO: 36.

31. 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 CDRH1, CDRH2, and CDRH3 comprise or consist of the amino acid sequences set forth in SEQ ID NOs: 33-35, respectively, and the CDRL1, CDRL2, and

CDRL3 comprise or consist of the amino acid sequences set forth in SEQ ID NOs: 37-39, respectively.

32. The antibody or antigen-binding fragment of any one of claims 3-31, 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.

33. The antibody or antigen-binding fragment of any one of claims 1-32, which:

(i) recognizes an epitope in the ACE2 receptor binding motif (RBM, SEQ ID NO.:5) of SARS-CoV-2;

(ii) is capable of blocking an interaction between SARS-CoV-2 (*e.g.*, SARS-CoV-2 RBM) and human ACE2;

(iii) is capable of binding to SARS-CoV-2S protein;

(iv) recognizes an epitope that is conserved in the ACE2 RBM of SARS-CoV-2 and in an ACE2 RBM of SARS-CoV-1;

(v) is cross-reactive against SARS-CoV-2 and SARS-CoV-1 coronavirus;

(vii) recognizes an epitope in the SARS-CoV-2 surface glycoprotein that is not in the ACE2 RBM;

(viii) is capable of binding to a SARS-CoV-2 S protein trimer in a prefusion conformation;

or

(ix) any combination of (i)-(viii).

34. The antibody or antigen-binding fragment of any one of claims 1-33, which is a IgG, IgA, IgM, IgE, or IgD isotype.

35. The antibody or antigen-binding fragment of any one of claims 1-34, which is an IgG isotype selected from IgG1, IgG2, IgG3, and IgG4.

36. The antibody or antigen-binding fragment of any one of claims 1-35, which is human, humanized, or chimeric.

37. The antibody or antigen-binding fragment of any one of claims 1-36, 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, a scFv, or a scFab.

38. The antibody or antigen-binding fragment of claim 37, wherein the scFv comprises more than one VH domain and more than one VL domain.

39. The antibody or antigen-binding fragment of any one of claims 1-38, wherein the antibody or antigen-binding fragment is a multi-specific antibody or antigen binding fragment.

40. The antibody or antigen-binding fragment of claim 39, wherein the antibody or antigen binding fragment is a bispecific antibody or antigen-binding fragment.

41. The antibody or antigen-binding fragment of claim 39 or 40, 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% (*e.g.,* 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.: 22, 32, 42, 52, 62, 72, 74, 84, 96, 106, 119, 129, 139, 150, 163, 173, 175, 178, 186, 189, 191, 198, 208, 218, 228, 240, 254, 264, 274, 284, 298, 312, 322, 332, 350, 351, 353, 359, 361, 363, 365, 367, 368, 369, 379, 389, 399, 409, 419, 429, 434, 444, 454, 464, 474, 484, 494, 504, 514, 524, 534, 544, 554, 564, 574, 584, 594, 604, 614, 624, 626, 628, 630, 634, 636, 638,

640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, 684, 692, 740, 741, 742, 743, 748, 749, 750, 752, 754, 756, 758, 759, 761, 762, and 764, and

wherein the first VL and the second VL are different and each independently comprise an amino acid sequence having at least 85% (*e.g.,* 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.: 26, 36, 46, 56, 66, 78, 88, 94, 100, 110, 123, 133, 143, 154, 157, 168, 194, 196, 202, 212, 222, 232, 238, 244, 250, 252, 258, 268, 278, 288, 294, 296, 302, 308, 310, 316, 326, 336, 355, 357, 373, 383, 393, 403, 413, 423, 438, 448, 458, 468, 478, 488, 498, 508, 518, 528, 538, 548, 558, 568, 578, 588, 598, 608, 618, 686, 696 738, 744, and 746;

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.

42. The antibody or antigen-binding fragment of claim 40 or 41, comprising:

(i) a first VH and a first VL; and

(ii) a second VH and a second VL,

wherein the first VH comprises an amino acid sequence having at least 85% (*e.g.,* 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.: 139 and 342 and the first VL comprises 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.:143 and 346 and wherein the second VH comprises an amino acid sequence having at least 85% (*e.g.,* 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.: 399, 748, 749, 750, 752, 754, 756, 758, 759, and 761 and the second VL comprises 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.:403, 744, and 746.

43. The antibody or antigen-binding fragment of claim 39 or 40, comprising a first antigen-binding portion having a first specificity and a second antigen-binding portion having a second specificity, wherein the first antigen-binding portion comprises a VH that comprises or consists of the amino acid sequence set forth in SEQ ID NO:399 and a VL that comprises or consists of the amino acid sequence set forth in SEQ ID NO.:738 or SEQ ID NO.:403.

44. The antibody or antigen-binding fragment of claim 43, wherein the second antigen-binding portion comprises a VH that comprises or consists of the amino acid sequence set forth in SEQ ID NO.:139 and a VL that comprises or consists of the amino acid sequence set forth in SEQ ID NO.:143.

45. The antibody or antigen-binding fragment of claim 43, wherein the second antigen-binding portion comprises a VH that comprises or consists of the amino acid sequence set forth in SEQ ID NO.:342 and a VL that comprises or consists of the amino acid sequence set forth in SEQ ID NO.:346.

46. The antibody or antigen-binding fragment of any one of claims 1-45, wherein the antibody or antigen-binding fragment further comprises a Fc polypeptide or a fragment thereof.

47. The antibody or antigen-binding fragment of claim 46, 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.

48. The antibody or antigen-binding fragment of claim 47, 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.

49. The antibody or antigen-binding fragment of claim 47 or 48, 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).

50. The antibody or antigen-binding fragment of any one of claims 47-49, wherein the mutation that enhances binding to FcRn comprises M428L/N434S.

51. The antibody or antigen-binding fragment of any one of claims 47-50, wherein the mutation that enhances binding to a FcγR comprises S239D; I332E; A330L; G236A; or any combination thereof.

52. The antibody or antigen-binding fragment of any one of claims 47-51, 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.

53. The antibody or antigen-binding fragment of any one of claims 47-52, wherein the Fc polypeptide comprises a L234A mutation and a L235A mutation.

54. The antibody or antigen-binding fragment of any one of claims 1-53, 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.

55. The antibody or antigen-binding fragment of any one of claims 1-54, which is capable of binding to a SARS-CoV-2 surface glycoprotein with an EC50 of less than 500 ng/ml, less than 250 ng/ml, less than 100 ng/ml, less than 90 ng/ml, less than 80 ng/ml, less than 70 ng/ml, less than 60 ng/ml, less than 50 ng/ml, less than 40 ng/ml, less than 30 ng/ml, less than 25 ng/ml, less than 20 ng/ml, less than 16 ng/ml, less than 15 ng/ml, less than 14 ng/ml, less than 13 ng/ml, less than 12 ng/ml, less than 10 ng/ml, less than 9 ng/ml, less than 8 ng/ml, less than 7 ng/ml, less than 6 ng/ml, less than 5 ng/ml, less than 4 ng/ml, or less than 2 mg/ml, as measured by ELISA (optionally, indirect ELISA and/or sandwich ELISA) and/or by flow cytometry, wherein the SARS CoV-2 surface glycoprotein is expressed at a cell surface of a host cell.

56. The antibody or antigen-binding fragment of any one of claims 1-55, which is capable of binding to a SARS-CoV-2 surface glycoprotein RBD with an EC50 of less than 500 ng/ml, less than 250 ng/ml, less than 100 ng/ml, less than 90 ng/ml, less than 80 ng/ml, less than 70 ng/ml, less than 60 ng/ml, less than 50 ng/ml, less than 40 ng/ml, less than 30 ng/ml, less than 25 ng/ml, less than 20 ng/ml, less than 16 ng/ml, less than 15 ng/ml, less than 14 ng/ml, less than 13 ng/ml, less than 12 ng/ml, less than 10 ng/ml, less than 9 ng/ml, less than 8 ng/ml, less than 7 ng/ml, less than 6 ng/ml, less than 5 ng/ml, less than 4 ng/ml, or less than 2 mg/ml, as measured by ELISA (optionally, indirect ELISA and/or sandwich ELISA) and/or by flow cytometry,

wherein the SARS CoV-2 surface glycoprotein is expressed at a cell surface of a host cell.

57. The antibody or antigen-binding fragment of any one of claims 1-56, which is capable of binding to a SARS-CoV-2 RBD with a KD of less than 5×10^{-8} M, less than 4×10^{-8} M, less than 3×10^{-8} M, less than 2×10^{-8} M, less than 1×10^{-8} M, less than 5×10^{-9} M, less than 1×10^{-9} M, less than 5×10^{-10} M, less than 1×10^{-10} M, less than 5×10^{-11} M, less than 1×10^{-11} M, less than 5×10^{-12} M, or less than 1×10^{-12} M, as determined using biolayer interferometry (BLI), optionally using an Octet instrument with antibody or antigen-binding fragment loaded on Protein A pins, optionally at 2.7 µg/ml, and SARS-CoV-2 RBD loaded for 5 minutes at 6 µg/ml, 1.5 µg/ml, or 0.4 µg/ml, further optionally with dissociation measured for 7 minutes.

58. The antibody or antigen-binding fragment of any one of claims 1-57, which is capable of binding to a SARS-CoV-2 RBD with a KD of less than 6×10^{-8} M, less than 5×10^{-8} M, less than 4×10^{-8} M, less than 3×10^{-8} M, less than 2×10^{-8} M, less than 1×10^{-8} M, less than 5×10^{-9} M, less than 4×10^{-9} M, less than 3×10^{-9} M, less than 2×10^{-9} M, less than 1×10^{-9} M, or less than 8×10^{-10} M, as determined using surface plasmon resonance (SPR), optionally using a Biacore T200 instrument using a single-cycle kinetics approach.

59. The antibody or antigen-binding fragment of any one of claims 1-58, which is capable of binding to a SARS-CoV-2 RBD and inhibiting an interaction between (i) the RBD and (ii) a human ACE2 and/or a human SIGLEC-1.

60. The antibody or antigen-binding fragment of any one of claims 1-59, which is capable of neutralizing:

(i) infection by a SARS-CoV-2 pseudovirus, optionally:

(i)(a) with a neutralization IC50 of less than 100 ng/ml, less than 90 ng/ml, less than 80 ng/ml, less than 70 ng/ml, less than 60 ng/ml, less than 50

ng/ml, less than 40 ng/ml, less than 30 ng/ml, less than 25 ng/ml, less than 20 ng/ml, less than 15 ng/ml, less than 10 ng/ml, less than 9 ng/ml, less than 8 ng/ml, less than 7 ng/ml, less than 6 ng/ml, less than 5 ng/ml, less than 4 ng/ml, less than 3 ng/ml, less than 2 ng/ml, or less than 1 ng/ml, preferably less than 10 ng/ml, less than 9 ng/ml, less than 8 ng/ml, less than 7 ng/ml, less than 6 ng/ml, less than 5 ng/ml, less than 4 ng/ml, less than 3 ng/ml, less than 2 ng/ml, or less than 1 ng/ml, and/or

(i)(b) with a neutralization IC80 of less than 100 ng/ml, less than 90 ng/ml, less than 80 ng/ml, less than 70 ng/ml, less than 60 ng/ml, less than 50 ng/ml, less than 40 ng/ml, less than 30 ng/ml, or less than 25 ng/ml, preferably less than 50 ng/ml, less than 40 ng/ml, less than 30 ng/ml, or less than 25 ng/ml, and/or

(i)(c) with a neutralization EC90 of less than 300 ng/ml, less than 200 ng/ml, less than 100 ng/ml, less than 90 ng/ml, less than 80 ng/ml, less than 70 ng/ml, less than 60 ng/ml 50 ng/ml, less than 40 ng/ml, less than 30 ng/ml, less than 25 ng/ml, less than 20 ng/ml, less than 15 ng/ml, or less than 10 ng/ml, wherein, further optionally, the SARS-CoV-2 pseudovirus comprises a VSV pseudovirus and/or a MLV pseudovirus, and/or

(i)(d) the SARS-CoV-2 pseudovirus comprises a VSV pseudovirus and/or a MLV pseudovirus; and/or

(ii) infection by live SARS-CoV-2, optionally

(ii)(a) with a EC50 of less than 60 ng/ml, less than 50 ng/ml, less than 40 ng/ml, less than 30 ng/ml, less than 25 ng/ml, less than 20 ng/ml, less than 15 ng/ml, less than 12 ng/ml, less than 11 ng/ml, less than 10 ng/ml, less than 9 ng/ml, less than 8 ng/ml, less than 7 ng/ml, less 6 ng/ml, less than 5/ng ml, or less than 4 ng/ml, preferably less than 15 ng/ml, less than 12 ng/ml, less than 11 ng/ml, less than 10 ng/ml, less than 9 ng/ml, less than 8 ng/ml, less than 7 ng/ml, less 6 ng/ml, less than 5/ng ml, or less than 4 ng/ml, and/or

(ii)(b) with a EC90 of less than 50 ng/ml, less than 40 ng/ml, less than 35 ng/ml, less than 30 ng/ml, less than 25 ng/ml, less than 20 ng/ml, less than 15

ng/ml, less than 12 ng/ml, less than 11 ng/ml, less than 10 ng/ml, less than 9 ng/ml, less than 8 ng/ml, less than 7 ng/ml, less 6 ng/ml, less than 5/ng ml, or less than 4 ng/ml, preferably less than 30 ng/ml, less than 25 ng/ml, less than 20 ng/ml, less than 15 ng/ml, or less than 12 ng/ml, and/or

(ii)(c) over a 6-hour period, with a multiplicity of infection of 0.1; and/or

(iii) infection by live SARS-CoV-2 in a host cell (*e.g.* a HEK293T cell) that expresses, optionally is engineered to overexpress, DC-SIGN, L-SIGN, SIGLEC, or ACE2; and/or

(iv) infection by live SARS-CoV-2 in a host cell (*e.g.* a HEK293T cell) that expresses, optionally is engineered to overexpress, SIGLEC-1 or ACE2, wherein neutralizing infection comprises fully neutralizing infection.

61. The antibody or antigen-binding fragment of any one of claims 1-60, which is capable of neutralizing infection by a SARS-CoV-2 variant that comprises any one of the following mutations in the surface glycoprotein as compared to a SARS-CoV-2 surface glycoprotein comprising SEQ ID NO.:3: N501Y; S477N; N439K; L452R; E484K; K417N; T478K; S494P; A520S; N501T; A522S; Y453F; P384L.

62. The antibody or antigen-binding fragment of claim 61, which is capable of neutralizing infection by the SARS-CoV-2 variant with a potency that is less than 3-fold lower than the potency with which the antibody or antigen-binding fragment neutralizes infection by a SARS-CoV-2 comprising the surface glycoprotein amino acid sequence set forth in SEQ ID NO.:3.

63. The antibody or antigen-binding fragment of any one of claims 1-62, which is capable of activating a FcγRIIa, a FcγRIIIa, or both, wherein, optionally:(i) the FcγRIIa comprises a H131 allele; and/or

(ii) the FcγRIIIa comprises a V158 allele; and/or

(iii) activation is determined using a SARS-CoV-2 S-expressing target cell, such as a CHO cell, and a reporter cell expressing a NFAT-driven reporter, such as luciferase.

64. The antibody or antigen-binding fragment of any one of claims 1-63, comprising:

(a) the CH1-CH3 amino acid sequence set forth in SEQ ID NO.:6 and the CL amino acid sequence set forth in SEQ ID NO.:8;

(b) The CH1-CH3 amino acid sequence set forth in SEQ ID NO.:6 and the CL amino acid sequence set forth in SEQ ID NO.:9;

(c) the CH1-CH3 amino acid sequence set forth in SEQ ID NO.:7 and the CL amino acid sequence set forth in SEQ ID NO.:8; or

(d) The CH1-CH3 amino acid sequence set forth in SEQ ID NO.:7 and the CL amino acid sequence set forth in SEQ ID NO.:9.

65. An isolated antibody comprising:

(i) the heavy chain amino acid sequence set forth in SEQ ID NO.:767; and

(ii) the light chain amino acid sequence set forth in SEQ ID NO.:768.

66. The antibody or antigen-binding fragment of any one of claims 1-65, which has an *in vivo* half-life in a non-human primate of between 20 and 30 days, or between 22 and 28 days, or between 23 and 27 days, or between 24 and 26 days, or of about 25 days.

67. The antibody or antigen-binding fragment of any one of claims 1-66, wherein the antibody or antigen-binding fragment is capable of neutralizing a SARS-CoV-2 infection and/or of neutralizing an infection of a target cell with an IC50 of about 20 to about 30 ng/ml.

68. The antibody or antigen-binding fragment of any one of claims 1-66, wherein the antibody or antigen-binding fragment is capable of neutralizing a SARS-CoV-2 infection and/or of neutralizing an infection of a target cell with an IC50 of about 10 to about 20 ng/ml.

69. The antibody or antigen-binding fragment of any one of claims 1-66, wherein the antibody or antigen-binding fragment is capable of neutralizing a SARS-CoV-2 infection and/or of neutralizing an infection of a target cell with an IC50 of about 5 to about 10 ng/ml.

70. The antibody or antigen-binding fragment of any one of claims 1-66, wherein the antibody or antigen-binding fragment is capable of neutralizing a SARS-CoV-2 infection and/or of neutralizing an infection of a target cell with an IC50 of about 1 to about 5 ng/ml.

71. The antibody or antigen-binding fragment of any one of claims 1-70, wherein the antibody or antigen-binding fragment is capable of neutralizing infection by SARS-CoV-2 and does not compete with a human ACE2 for binding to the SARS-CoV-2S protein,

wherein, optionally, the neutralizing comprises neutralizing infection in an in vitro model of infection.

72. An antibody, or an antigen-binding fragment thereof, that competes for binding to a SARS-CoV-2 surface glycoprotein with the antibody or antigen-binding fragment of any one of claims 1-71.

73. An isolated polynucleotide encoding the antibody or antigen-binding fragment of any one of claims 1-72, or encoding a VH, a heavy chain, a VL, and/or a light chain of the antibody or the antigen-binding fragment.

74. The polynucleotide of claim 73, wherein the polynucleotide comprises deoxyribonucleic acid (DNA) or ribonucleic acid (RNA), wherein the RNA optionally comprises messenger RNA (mRNA).

75. The polynucleotide of claim 73 or 74, which is codon-optimized for expression in a host cell.

76. The polynucleotide of any one of claims 73-75, comprising a polynucleotide having at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or at least 99% identity to, or comprises or consists of, the polynucleotide sequence according to any one or more of SEQ ID NOs.: 30, 31, 40, 41, 50, 51, 60, 61, 70, 71, 73, 82, 83, 92, 93, 95, 104, 105, 114, 115, 116, 117, 118, 127, 128, 137, 138, 206, 207, 216, 217, 226, 227, 236, 237, 239, 248, 249, 251, 253, 262, 263, 272, 273, 282, 283, 292, 293, 295, 297, 306, 307, 309, 311, 320, 321, 330, 331, 340, 341, 377, 378, 387, 388, 397, 398, 407, 408, 417, 418, 427, 428, 433, 442, 443, 452, 453, 462, 463, 472, 473, 482, 483, 492, 493, 502, 503, 512, 513, 552, 523, 532, 533, 542, 543, 552, 553, 562, 563, 572, 573, 582, 583, 592, 593, 602, 603, 612, 613, 622, 623, 690, 691, 700-737 and 739.

77. The polynucleotide of any one of claims 73-76, comprising:

(i) a polynucleotide having at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or at least 99% identity to, or that comprises or consists of, the nucleotide sequence set forth in SEQ ID NO.:407; and

(ii) a polynucleotide having at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or at least 99% identity to, or that comprises or consists of, the nucleotide sequence set forth in SEQ ID NO.:408, 737, or 739.

78. A recombinant vector comprising the polynucleotide of any one of claims 73-77.

79. A host cell comprising the polynucleotide of any one of claims 77 and/or the vector of claim 78, wherein the polynucleotide is heterologous to the host cell.

80. A human B cell comprising the polynucleotide of any one of claims 73-77, wherein polynucleotide is heterologous to the human B cell and/or wherein the human B cell is immortalized.

81. A composition comprising:

(i) the antibody or antigen-binding fragment of any one of claims 1-72;

(ii) the polynucleotide of any one of claims 73-77;

(iii) the recombinant vector of claim 78;

(iv) the host cell of claim 79; and/or

(v) the human B cell of claim 80,

and a pharmaceutically acceptable excipient, carrier, or diluent.

82. The composition of claim 81, comprising two or more antibodies or antigen-binding fragments of any of claims 1-72.

83. The composition of claim 82, comprising:

(i) a first antibody or antigen-binding fragment, comprising a VH comprising or consisting of the amino acid sequence as set forth in SEQ ID NO: 32 and a VL comprising or consisting of the amino acid sequence as set forth in SEQ ID NO: 36; and

(ii) a second antibody or antigen-binding fragment comprising, a VH comprising or consisting of the amino acid sequence as set forth in SEQ ID NO: 139 and a VL comprising of consisting of the amino acid sequence as set forth in SEQ ID NO: 143.

84. The composition of claim 82, comprising:

(i) a first antibody or antigen-binding fragment 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 CDRH1, CDRH2, and CDRH3 comprise or consist of the amino acid sequences set forth in SEQ ID NOs: 33-35, respectively, and the CDRL1, CDRL2, and CDRL3 comprise or consist of the amino acid sequences set forth in SEQ ID NOs: 37-39, respectively; and

(ii) a second antibody or antigen-binding fragment 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 CDRH1, CDRH2, and CDRH3 comprise or consist of the amino acid sequences set forth in SEQ ID NOs: 140-142, respectively, and the CDRL1, CDRL2, and CDRL3 comprise or consist of the amino acid sequences set forth in SEQ ID NOs: 144-146, respectively.

85. The composition of claim 82, comprising:

(i) a first antibody or antigen-binding fragment, comprising a VH comprising or consisting of the amino acid sequence as set forth in SEQ ID NO: 139 or 342 and a VL comprising or consisting of the amino acid sequence as set forth in SEQ ID NO: 143 or 346; and

(ii) a second antibody or antigen-binding fragment comprising a VH comprising or consisting of the amino acid sequence as set forth in SEQ ID NO: 399, 748, 749, 750, 752, 754, 756, 758, 759, or 761, and a VL comprising or consisting of the amino acid sequence as set forth in SEQ ID NO: 403, 744, or 746.

86. The composition of claim 82, comprising:

(i) a first antibody or antigen-binding fragment 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 CDRH1, CDRH2, and CDRH3 comprise or consist of the amino acid sequences set forth in SEQ ID NOs: 140-142, respectively, or 343-345, respectively, and the CDRL1, CDRL2, and CDRL3 comprise or consist of the amino acid sequences set forth in SEQ ID NOs: 144-146, respectively; and

(ii) a second antibody or antigen-binding fragment 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 CDRH1, CDRH2, and CDRH3 comprise or consist of the amino acid sequences set forth in SEQ ID NOs: 400, 401, and any one of 751, 753, 755, 757, 760, respectively, and the CDRL1, CDRL2, and CDRL3 comprise or consist of the amino acid sequences set forth in SEQ ID NOs: 404, 405, and any one of 406, 745, and 747, respectively.

87. A composition comprising:

(i) a first antibody or antigen-binding fragment, comprising

(i)(a) a VH comprising or consisting of the amino acid sequence as set forth in SEQ ID NO: 32, and

(i)(b) a VL comprising or consisting of the amino acid sequence as set forth in SEQ ID NO: 36; and

(ii) a second antibody or antigen-binding fragment comprising

(ii)(a) a VH comprising or consisting of the amino acid sequence as set forth in SEQ ID NO: 139 and

(ii)(b) a VL comprising of consisting of the amino acid sequence as set forth in SEQ ID NO: 143.

88. A composition comprising:

(i) a first antibody or antigen-binding fragment that is capable of binding to a SARS-CoV-2 surface glycoprotein and comprises

(i)(a) a VH comprising the CDRH1, CDRH2, and CDRH3 amino acid sequences set forth in SEQ ID NOs.:400, 402, and 766, respectively, and

(i)(b) a VL comprising the CDRL1, CDRL2, and CDRL3 amino acid sequences set forth in SEQ ID NOs.:404, 405, and 406, respectively; and

(ii) a second antibody or antigen-binding fragment that is capable of binding to a SARS-CoV-2 surface glycoprotein and comprises

(ii)(a) a VH comprising the CDRH1, CDRH2, and CDRH3 amino acid sequences set forth in SEQ ID NOs.:140, 141 or 343, and 142, respectively, and

(ii)(b) a VL comprising CDRL1, CDRL2, and CDRL3 amino acid sequences as set forth in SEQ ID NOs.:144, 145, and 146, respectively.

89. A composition comprising:

(i) a first antibody or antigen-binding fragment that is capable of binding to a SARS-CoV-2 surface glycoprotein and comprises

(i)(a) a VH comprising the amino acid sequence set forth in SEQ ID NO.:399 and

(i)(b) a VL comprising the amino acid sequence set forth in SEQ ID NOs.:403 or SEQ ID NO.:738; and

(ii) a second antibody or antigen-binding fragment that is capable of binding to a SARS-CoV-2 surface glycoprotein and comprises

(ii)(a) a VH comprising the amino acid sequence set forth in SEQ ID NOs.:139 or 342, and

(ii)(b) a VL comprising the amino acid sequence set forth in SEQ ID NO.:143.

90. The composition of any one of claims 82-89, wherein the first antibody or antigen-binding fragment and the second antibody or antigen-binding fragment each comprise an IgG1 Fc polypeptide comprising a M428L mutation and a N434S mutation.

91. The composition of any one of claims 82-90, wherein the first antibody or antigen-binding fragment and the second antibody or antigen-binding fragment each comprise an IgG1 Fc polypeptide comprising a G236A mutation, a A330L mutation, and a I332E mutation.

92. A composition comprising the polynucleotide of any one of claims 73-77 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.

93. A composition comprising:

(i) a first antibody or antigen-binding fragment that is capable of binding to a SARS-CoV-2 surface glycoprotein and inhibiting an interaction between the SARS-CoV-2 surface glycoprotein and a first cell surface receptor selected from ACE2, DC-SIGN, L-SIGN, and SIGLEC-1; and

(ii) a second antibody or antigen-binding fragment that is capable of binding to a SARS-CoV-2 surface glycoprotein and inhibiting an interaction between the SARS-CoV-2 surface glycoprotein and a second cell surface receptor selected from ACE2, DC-SIGN, L-SIGN, and SIGLEC-1,

wherein the first cell surface receptor and the second cell surface receptor are different.

94. A method of treating a coronavirus infection, *e.g.* a SARS-CoV-2 infection, in a subject, the method comprising administering to the subject an effective amount of:

(i) the antibody or antigen-binding fragment of any one of claims 1-72;

(ii) the polynucleotide of any one of claims 73-77;

(iii) the recombinant vector of claim 78;

(iv) the host cell of claim 79;

(v) the human B cell of claim 80; and/or

(vi) the composition of any one of claims 81-93.

95. A method of treating a coronavirus infection, *e.g.* a SARS-CoV-2 infection, in a subject, the method comprising administering to the subject:

(i) a first antibody or antigen-binding fragment that is capable of binding to a SARS-CoV-2 surface glycoprotein and comprises

(i)(a) a VH comprising the CDRH1, CDRH2, and CDRH3 amino acid sequences set forth in SEQ ID NOs.:400, 402, and 766, respectively, and

(i)(b) a VL comprising the CDRL1, CDRL2, and CDRL3 amino acid sequences set forth in SEQ ID NOs.:404, 405, and 406, respectively; and

(ii) a second antibody or antigen-binding fragment that is capable of binding to a SARS-CoV-2 surface glycoprotein and comprises

(ii)(a) a VH comprising the CDRH1, CDRH2, and CDRH3 amino acid sequences set forth in SEQ ID NOs.:140, 141 or 343, and 142, respectively, and

(ii)(b) a VL comprising CDRL1, CDRL2, and CDRL3 amino acid sequences as set forth in SEQ ID NOs.:144, 145, and 146, respectively.

96. A method of treating a coronavirus infection, *e.g.* a SARS-CoV-2 infection, in a subject, the method comprising administering to the subject:

(i) a first antibody or antigen-binding fragment that is capable of binding to a SARS-CoV-2 surface glycoprotein and comprises

(i)(a) a VH comprising the amino acid sequence set forth in SEQ ID NO.:399 and

(i)(b) a VL comprising the amino acid sequence set forth in SEQ ID NOs.:403 or SEQ ID NO.:738; and

(ii) a second antibody or antigen-binding fragment that is capable of binding to a SARS-CoV-2 surface glycoprotein and comprises

(ii)(a) a VH comprising the amino acid sequence set forth in SEQ ID NOs.:139 or 342, and

(ii)(b) a VL comprising the amino acid sequence set forth in SEQ ID NO.:143.

97. A method of preventing or treating or neutralizing a coronavirus infection in a subject, the method comprising administering to a subject who has received a first antibody or antigen binding fragment comprising:

(i)(a) VH and VL amino acid sequences according to SEQ ID NOs.:32 and 36 respectively; or

(i)(b) CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 amino acid sequences according to SEQ ID NOS.:33-35 and 37-39, respectively;

a second antibody or antigen binding fragment comprising:

(ii)(a) a VH amino acid sequence according to SEQ ID NO.: 139, and a VL amino acid sequence according to SEQ ID NO: 143; or

(ii)(b) CDRH1, CDRH2, and CDRH3 amino acids according to SEQ ID NOs: 140-142, respectively, and CDRL1, CDRL2, and CDRL3 amino acid sequences according to SEQ ID NOs: 144-146.

98. A method of preventing or treating or neutralizing a coronavirus infection in a subject, the method comprising administering to a subject who has received a first antibody or antigen binding fragment comprising:

(i)(a) a VH amino acid sequence according to SEQ ID NO.: 139, and a VL amino acid sequence according to SEQ ID NO: 143; or

(i)(b) CDRH1, CDRH2, and CDRH3 amino acid sequences according to SEQ ID NOs: 140-142, respectively; and CDRL1, CDRL2, and CDRL3 amino acid sequences according to SEQ ID NOs: 144-146, respectively;

a second antibody or antigen binding fragment comprising:

(ii)(a) VH and VL amino acid sequences according to SEQ ID NOs.:32 and 36 respectively; or

(ii)(b) CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3 amino acid sequences according to SEQ ID NOS.:33-35 and 37-39, respectively.

99. A method of preventing or treating or neutralizing a coronavirus infection in a subject, the method comprising administering to a subject who has received a first antibody or antigen binding fragment comprising:

(i)(a) a VH amino acid sequence according to SEQ ID NO.: 139 or 342 and a VL amino acid sequence according to SEQ ID NO: 143 or 346; or

(i)(b) CDRH1, CDRH2, and CDRH3 amino acid sequences according to SEQ ID NOs: 140-142, respectively, or 343-345, respectively and CDRL1, CDRL2, and CDRL3 amino acid sequences according to SEQ ID NOs: 144-146, respectively;

a second antibody or antigen binding fragment comprising:

(ii)(a) a VH amino acid sequence according to SEQ ID NO: 399, 748, 749, 750, 752, 754, 756, 758, 759, or 761 and a VL amino acid sequence according to SEQ ID NO: 403, 744, or 746; or

(ii)(b) CDRH1, CDRH2, and CDRH3 amino acid sequences according to SEQ ID NOs: 400, 401, and any one of 751, 753, 755, 757, 760, respectively and CDRL1, CDRL2, and CDRL3 amino acid sequences according to SEQ ID NOs: 404, 405, and any one of 406, 745, and 747, respectively.

100. A method of preventing or treating or neutralizing a coronavirus infection in a subject, the method comprising administering to a subject who has received a first antibody or antigen binding fragment comprising:

(i)(a) a VH amino acid sequence according to SEQ ID NO: 399, 748, 749, 750, 752, 754, 756, 758, 759, or 761 and a VL amino acid sequence according to SEQ ID NO: 403, 744, or 746; or

(i)(b) CDRH1, CDRH2, and CDRH3 amino acid sequences according to SEQ ID NOs: 400, 401, and any one of 751, 753, 755, 757, 760, respectively and CDRL1, CDRL2, and CDRL3 amino acid sequences according to SEQ ID NOs: 404, 405, and any one of 406, 745, and 747, respectively;

a second antibody or antigen binding fragment comprising:

(ii)(a) a VH amino acid sequence according to SEQ ID NO.: 139 or 342 and a VL amino acid sequence according to SEQ ID NO: 143 or 346; or

(ii)(b) CDRH1, CDRH2, and CDRH3 amino acid sequences according to SEQ ID NOs: 140-142, respectively, or 343-345, respectively and CDRL1, CDRL2, and CDRL3 amino acid sequences according to SEQ ID NOs: 144-146, respectively.

101. The method of any one of claims 95-100, wherein the first antibody or antigen-binding fragment and the second antibody or antigen-binding fragment each comprise an IgG1 Fc polypeptide comprising a M428L mutation and a N434S mutation.

102. The method of any one of claims 95-101, wherein the first antibody or antigen-binding fragment and the second antibody or antigen-binding fragment each comprise an IgG1 Fc polypeptide comprising a G236A mutation, a A330L mutation, and a I332E mutation.

103. A method of treating a SARS-CoV-2 infection in a subject, the method comprising administering to the subject:

(i) a first antibody or antigen-binding fragment that is capable of binding to a SARS-CoV-2 surface glycoprotein and inhibiting an interaction between the SARS-CoV-2 surface glycoprotein and a first cell surface receptor selected from ACE2, DC-SIGN, L-SIGN, and SIGLEC-1; and

(ii) a second antibody or antigen-binding fragment that is capable of binding to a SARS-CoV-2 surface glycoprotein and inhibiting an interaction between the SARS-CoV-2 surface glycoprotein and a second cell surface receptor selected from ACE2, DC-SIGN, L-SIGN, and SIGLEC-1,

wherein the first cell surface receptor and the second cell surface receptor are different.

104. The antibody or antigen-binding fragment of any one of claims 1-72, the polynucleotide of any one of claims 73-77, the recombinant vector of claim 78, the host cell of claim 79, the human B cell of claim 80, and/or the composition of any one of claims 81-93 for use in a method of treating a SARS-CoV-2 infection in a subject.

105. The antibody or antigen-binding fragment of any one of claims 1-72, the polynucleotide of any one of claims 73-77, the recombinant vector of claim 78, the host cell of claim 79, the human B cell of claim 80, and/or the composition of any one of claims 81-93 for use in the preparation of a medicament for the treatment of a SARS-CoV-2 infection in a subject.

106. A method for *in vitro* diagnosis of a SARS-CoV-2 infection, the method comprising:

(i) contacting a sample from a subject with an antibody or antigen-binding fragment of any one of claims 1-72; and

(ii) detecting a complex comprising an antigen and the antibody, or comprising an antigen and the antigen-binding fragment.

107. The method of claim 106, wherein the sample comprises blood isolated from the subject.