

VARIANT NUCLEIC ACID LIBRARIES FOR CORONAVIRUS**CROSS-REFERENCE**

[0001] This application claims the benefit of U.S. Provisional Patent Application No. 63/115,568 filed on November 18, 2020, U.S. Provisional Patent Application No. 63/104,465 filed on October 22, 2020, U.S. Provisional Patent Application No. 63/073,362 filed on September 1, 2020, U.S. Provisional Patent Application No. 63/069,665 filed on August 24, 2020, U.S. Provisional Patent Application No. 63/034,896 filed on June 4, 2020, U.S. Provisional Patent Application No. 63/016,254 filed on April 27, 2020, each of which is incorporated by reference in its entirety.

BACKGROUND

[0002] Coronaviruses like severe acute respiratory coronavirus 2 (SARS-CoV-2) can cause severe respiratory problems. Therapies are needed for treating and preventing viral infection caused by coronaviruses like SARS-CoV-2. Antibodies possess the capability to bind with high specificity and affinity to biological targets. However, the design of therapeutic antibodies is challenging due to balancing of immunological effects with efficacy. Thus, there is a need to develop compositions and methods for the optimization of antibody properties in order to develop effective therapies for treating coronavirus infections.

INCORPORATION BY REFERENCE

[0003] All publications, patents, and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication, patent, or patent application was specifically and individually indicated to be incorporated by reference.

BRIEF SUMMARY

[0004] Provided herein are nucleic acid libraries comprising: a plurality of sequences that when translated encode for antibodies or antibody fragments that bind to SARS-CoV-2 or ACE2 protein, wherein each of the sequences comprises a predetermined number of variants within a CDR relative to an input sequence that encodes an antibody, and wherein the library comprises at least 50,000 variant sequences. Further provided herein are nucleic acid libraries, wherein the antibodies or antibody fragments bind to a spike glycoprotein, a membrane protein, an envelope protein, a nucleocapsid protein, or combinations thereof of the SARS-CoV-2. Further provided herein are nucleic acid libraries, wherein the antibodies or antibody fragments bind to a spike glycoprotein. Further provided herein are nucleic acid libraries, wherein the antibodies or antibody fragment bind to a receptor binding domain of the spike glycoprotein. Further provided herein are nucleic acid libraries, wherein the library comprises at least 100,000 variant sequences. Further provided herein are nucleic acid libraries, wherein at least some of the sequences encode for an antibody light chain. Further provided herein are nucleic acid libraries, wherein at least some of the sequences encode for an antibody heavy chain. Further provided herein are nucleic acid libraries, wherein

each sequence of the plurality of sequences comprises at least one variant in the CDR of a heavy chain or light chain relative to the input sequence. Further provided herein are nucleic acid libraries, wherein each sequence of the plurality of sequences comprises at least two variants in the CDR of a heavy chain or light chain relative to the input sequence. Further provided herein are nucleic acid libraries, wherein at least one of the variants is present in at least two individuals. Further provided herein are nucleic acid libraries, wherein at least one of the variants is present in at least three individuals. Further provided herein are nucleic acid libraries, wherein at least one sequence when translated encodes for an antibody or antibody fragment having at least 5X higher binding affinity than a binding affinity of the input sequence. Further provided herein are nucleic acid libraries, wherein at least one sequence when translated encodes for an antibody or antibody fragment having at least 25X higher binding affinity than a binding affinity of the input sequence. Further provided herein are nucleic acid libraries, wherein at least one sequence when translated encodes for an antibody or antibody fragment having at least 50X higher binding affinity than a binding affinity of the input sequence. Further provided herein are nucleic acid libraries, wherein each sequence of the plurality of sequences comprises at least one variant in the CDR of a heavy chain or light chain relative to a germline sequence of the input sequence. Further provided herein are nucleic acid libraries, wherein the CDR is a CDR1, CDR2, and CDR3 on a heavy chain. Further provided herein are nucleic acid libraries, wherein the CDR is a CDR1, CDR2, and CDR3 on a light chain. Further provided herein are nucleic acid libraries, wherein the at least one sequence that when translated encodes for an antibody or antibody fragment having at least 70X higher binding affinity than the input sequence. Further provided herein are nucleic acid libraries, wherein the at least one sequence that when translated encodes for an antibody or antibody fragment having a K_D of less than 50 nM. Further provided herein are nucleic acid libraries, wherein the at least one sequence that when translated encodes for an antibody or antibody fragment having a K_D of less than 25 nM. Further provided herein are nucleic acid libraries, wherein the at least one sequence that when translated encodes for an antibody or antibody fragment having a K_D of less than 10 nM. Further provided herein are nucleic acid libraries, wherein the at least one sequence that when translated encodes for an antibody or antibody fragment having a K_D of less than 5 nM. Further provided herein are nucleic acid libraries, wherein the library encodes a CDR sequence of any one of SEQ ID NOs: 1-921, 1047-1208, 1263-1436, 1495-1917, or 2059-2598.

[0005] Provided herein are nucleic acid libraries comprising: a plurality of sequences that when translated encode for antibodies or antibody fragments that bind to a coronavirus or a receptor of the coronavirus, wherein each of the sequences comprises a predetermined number of variants within a CDR relative to an input sequence that encodes an antibody, and wherein the library comprises at least 50,000 variant sequences. Further provided herein are nucleic acid libraries, wherein the coronavirus is SARS-CoV, MERS-CoV, CoV-229E, HCoV-NL63, HCoV-OC43, or HCoV-HKU1. Further provided herein are nucleic acid libraries, wherein the receptor of the coronavirus is ACE2 or dipeptidyl peptidase 4 (DPP4). Further provided herein are nucleic acid libraries, wherein the library comprises at least 100,000 variant sequences. Further provided herein are nucleic acid libraries, wherein at least some of the sequences encode

for an antibody light chain. Further provided herein are nucleic acid libraries, wherein at least some of the sequences encode for an antibody heavy chain. Further provided herein are nucleic acid libraries, wherein each sequence of the plurality of sequences comprises at least one variant in the CDR of a heavy chain or light chain relative to the input sequence. Further provided herein are nucleic acid libraries, wherein each sequence of the plurality of sequences comprises at least two variants in the CDR of a heavy chain or light chain relative to the input sequence. Further provided herein are nucleic acid libraries, wherein at least one of the variants is present in at least two individuals. Further provided herein are nucleic acid libraries, wherein at least one of the variants is present in at least three individuals. Further provided herein are nucleic acid libraries, wherein at least one sequence when translated encodes for an antibody or antibody fragment having at least 5X higher binding affinity than a binding affinity of the input sequence. Further provided herein are nucleic acid libraries, wherein at least one sequence when translated encodes for an antibody or antibody fragment having at least 25X higher binding affinity than a binding affinity of the input sequence. Further provided herein are nucleic acid libraries, wherein at least one sequence when translated encodes for an antibody or antibody fragment having at least 50X higher binding affinity than a binding affinity of the input sequence. Further provided herein are nucleic acid libraries, wherein each sequence of the plurality of sequences comprises at least one variant in the CDR of a heavy chain or light chain relative to a germline sequence of the input sequence. Further provided herein are nucleic acid libraries, wherein the CDR is a CDR1, CDR2, and CDR3 on a heavy chain. Further provided herein are nucleic acid libraries, wherein the CDR is a CDR1, CDR2, and CDR3 on a light chain. Further provided herein are nucleic acid libraries, wherein the at least one sequence that when translated encodes for an antibody or antibody fragment having at least 70X higher binding affinity than the input sequence. Further provided herein are nucleic acid libraries, wherein the at least one sequence that when translated encodes for an antibody or antibody fragment having a K_D of less than 50 nM. Further provided herein are nucleic acid libraries, wherein the at least one sequence that when translated encodes for an antibody or antibody fragment having a K_D of less than 25 nM. Further provided herein are nucleic acid libraries, wherein the at least one sequence that when translated encodes for an antibody or antibody fragment having a K_D of less than 10 nM. Further provided herein are nucleic acid libraries, wherein the at least one sequence that when translated encodes for an antibody or antibody fragment having a K_D of less than 5 nM.

[0006] Provided herein are antibodies, wherein the antibody comprises a sequence comprising at least 90% sequence identity to any one of SEQ ID NOs: 1-2668.

[0007] Provided herein are antibodies, wherein the antibody comprises a sequence comprising at least 90% sequence identity to SEQ ID NOs: 1-2668; and wherein the antibody is a monoclonal antibody, a polyclonal antibody, a bi-specific antibody, a multispecific antibody, a grafted antibody, a human antibody, a humanized antibody, a synthetic antibody, a chimeric antibody, a camelized antibody, a single-chain Fvs (scFv), a single chain antibody, a Fab fragment, a F(ab')₂ fragment, a Fd fragment, a Fv fragment, a single-domain antibody, an isolated complementarity determining region (CDR), a diabody, a fragment comprised

of only a single monomeric variable domain, disulfide-linked Fvs (sdFv), an intrabody, an anti-idiotypic (anti-Id) antibody, or ab antigen-binding fragments thereof.

[0008] Provided herein are methods of treating a SARS-CoV-2 infection, comprising administering the antibody as described herein. Further provided herein are methods, wherein the antibody is administered prior to exposure to SARS-CoV-2. Further provided herein are methods, wherein the antibody is administered at least about 1 week prior to exposure to SARS-CoV-2. Further provided herein are methods, wherein the antibody is administered at least about 1 month prior to exposure to SARS-CoV-2. Further provided herein are methods, wherein the antibody is administered at least about 5 months prior to exposure to SARS-CoV-2. Further provided herein are methods, wherein the antibody is administered after exposure to SARS-CoV-2. Further provided herein are methods, wherein the antibody is administered at most about 24 hours after exposure to SARS-CoV-2. Further provided herein are methods, wherein the antibody is administered at most about 1 week after exposure to SARS-CoV-2. Further provided herein are methods, wherein the antibody is administered at most about 1 month after exposure to SARS-CoV-2.

[0009] Provided herein are methods of treating an individual with a SARS-CoV-2 infection with the antibody as described herein comprising: (a) obtaining or having obtained a sample from the individual; (b) performing or having performed an expression level assay on the sample to determine expression levels of SARS-CoV-2 antibodies; and (c) if the sample has an expression level of the SARS-CoV-2 antibodies then administering to the individual the antibody as described herein, thereby treating the SARS-CoV-2 infection.

[0010] Provided herein are methods for optimizing an antibody comprising: (a) providing a plurality of polynucleotide sequences encoding for an antibody or antibody fragment, wherein the antibody or antibody fragment is derived from a subject having SARS-CoV-2; (b) generating a nucleic acid library comprising the plurality of sequences that when translated encode for antibodies or antibody fragments that bind SARS-CoV-2 or ACE2 protein, wherein each of the sequences comprises a predetermined number of variants within a CDR relative to an input sequence that encodes an antibody; wherein the library comprises at least 50,000 variant sequences; and (c) synthesizing the at least 50,000 variant sequences. Further provided herein are methods, wherein the antibody library comprises at least 100,000 sequences. Further provided herein are methods, wherein the method further comprises enriching a subset of the variant sequences. Further provided herein are methods, wherein the method further comprises expressing the antibody or antibody fragments corresponding to the variant sequences. Further provided herein are methods, wherein the polynucleotide sequence is a murine, human, or chimeric antibody sequence. Further provided herein are methods, wherein each sequence of the plurality of variant sequences comprises at least one variant in each CDR of a heavy chain or light chain, relative to the input sequence. Further provided herein are methods, wherein each sequence of the plurality of variant sequences comprises at least two variants in each CDR of a heavy chain or light chain relative to the input sequence. Further provided herein are methods, wherein at least one sequence when translated encodes for an antibody or antibody fragment having at least 5X higher binding affinity than a binding affinity of the input sequence. Further provided herein are methods, wherein at least one sequence when translated encodes for an antibody or antibody fragment

having at least 25X higher binding affinity than a binding affinity of the input sequence. Further provided herein are methods, wherein at least one sequence when translated encodes for an antibody or antibody fragment having at least 50X higher binding affinity than a binding affinity of the input sequence. Further provided herein are methods, wherein each sequence comprises at least one variant in each CDR of a heavy chain or light chain relative to a germline sequence of the input sequence. Further provided herein are methods, wherein the nucleic acid library has a theoretical diversity of at least 10^{10} sequences. Further provided herein are methods, wherein the nucleic acid library has a theoretical diversity of at least 10^{12} sequences.

[0011] Provided herein are antibodies or antibody fragments comprising a variable domain, heavy chain region (VH) and a variable domain, light chain region (VL), wherein VH comprises complementarity determining regions CDRH1, CDRH2, and CDRH3, wherein VL comprises complementarity determining regions CDRL1, CDRL2, and CDRL3, and wherein (a) an amino acid sequence of CDRH1 is as set forth in any one of SEQ ID NOs: 151-165, 241-255, 331-357, and 547-575; (b) an amino acid sequence of CDRH2 is as set forth in any one of SEQ ID NOs: 166-180, 256-270, 358-384, and 576-604; (c) an amino acid sequence of CDRH3 is as set forth in any one of SEQ ID NOs: 181-195, 271-285, 385-411, and 605-633; (d) an amino acid sequence of CDRL1 is as set forth in any one of SEQ ID NOs: 196-210, 286-300, 412-438, and 634-662; (e) an amino acid sequence of CDRL2 is as set forth in any one of SEQ ID NOs: 211-225, 301-315, 439-465, and 663-691; and (f) an amino acid sequence of CDRL3 is as set forth in any one of SEQ ID NOs: 226-240, 316-330, 466-492, and 692-720. Further provided herein are antibodies or antibody fragments, wherein (a) an amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 155; (b) an amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 170; (c) an amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 185; (d) an amino acid sequence of CDRL1 is as set forth in SEQ ID NO: 200; (e) an amino acid sequence of CDRL2 is as set forth in SEQ ID NO: 215; and (f) an amino acid sequence of CDRL3 is as set forth in SEQ ID NO: 230. Further provided herein are antibodies or antibody fragments, wherein (a) an amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 152; (b) an amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 167; (c) an amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 182; (d) an amino acid sequence of CDRL1 is as set forth in SEQ ID NO: 197; (e) an amino acid sequence of CDRL2 is as set forth in SEQ ID NO: 212; and (f) an amino acid sequence of CDRL3 is as set forth in SEQ ID NO: 227. Further provided herein are antibodies or antibody fragments, wherein (a) an amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 335; (b) an amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 362; (c) an amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 389; (d) an amino acid sequence of CDRL1 is as set forth in SEQ ID NO: 199; (e) an amino acid sequence of CDRL2 is as set forth in SEQ ID NO: 214; and (f) an amino acid sequence of CDRL3 is as set forth in SEQ ID NO: 229. Further provided herein are antibodies or antibody fragments, wherein (a) an amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 336; (b) an amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 363; (c) an amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 390; (d) an amino acid sequence of CDRL1 is as set forth in SEQ ID NO: 201; (e) an amino acid sequence of CDRL2 is

as set forth in SEQ ID NO: 216; and (f) an amino acid sequence of CDRL3 is as set forth in SEQ ID NO: 231. Further provided herein are antibodies or antibody fragments, wherein (a) an amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 158; (b) an amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 173; (c) an amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 188; (d) an amino acid sequence of CDRL1 is as set forth in SEQ ID NO: 203; (e) an amino acid sequence of CDRL2 is as set forth in SEQ ID NO: 218; and (f) an amino acid sequence of CDRL3 is as set forth in SEQ ID NO: 233. Further provided herein are antibodies or antibody fragments, wherein (a) an amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 551; (b) an amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 580; (c) an amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 609; (d) an amino acid sequence of CDRL1 is as set forth in SEQ ID NO: 290; (e) an amino acid sequence of CDRL2 is as set forth in SEQ ID NO: 305; and (f) an amino acid sequence of CDRL3 is as set forth in SEQ ID NO: 320. Further provided herein are antibodies or antibody fragments, wherein (a) an amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 549; (b) an amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 578; (c) an amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 607; (d) an amino acid sequence of CDRL1 is as set forth in SEQ ID NO: 292; (e) an amino acid sequence of CDRL2 is as set forth in SEQ ID NO: 307; and (f) an amino acid sequence of CDRL3 is as set forth in SEQ ID NO: 322. Further provided herein are antibodies or antibody fragments, wherein (a) an amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 552; (b) an amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 581; (c) an amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 610; (d) an amino acid sequence of CDRL1 is as set forth in SEQ ID NO: 291; (e) an amino acid sequence of CDRL2 is as set forth in SEQ ID NO: 306; and (f) an amino acid sequence of CDRL3 is as set forth in SEQ ID NO: 321. Further provided herein are antibodies or antibody fragments, wherein (a) an amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 554; (b) an amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 583; (c) an amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 612; (d) an amino acid sequence of CDRL1 is as set forth in SEQ ID NO: 288; (e) an amino acid sequence of CDRL2 is as set forth in SEQ ID NO: 303; and (f) an amino acid sequence of CDRL3 is as set forth in SEQ ID NO: 318. Further provided herein are antibodies or antibody fragments, wherein the antibody or antibody fragment binds to a spike glycoprotein. Further provided herein are antibodies or antibody fragments, wherein the antibody or antibody fragment binds to a receptor binding domain of the spike glycoprotein. Further provided herein are antibodies or antibody fragments, wherein the antibody or antibody fragment comprises a K_D of less than 50 nM. Further provided herein are antibodies or antibody fragments, wherein the antibody or antibody fragment comprises a K_D of less than 25 nM. Further provided herein are antibodies or antibody fragments, wherein the antibody or antibody fragment comprises a K_D of less than 10 nM. Further provided herein are antibodies or antibody fragments, wherein the antibody or antibody fragment comprises a K_D of less than 5 nM.

[0012] Provided herein are antibodies or antibody fragments comprising a variable domain, heavy chain region (VH) wherein VH comprises complementarity determining regions CDRH1, CDRH2, and CDRH3, wherein (a) an amino acid sequence of CDRH1 is as set forth in any one of SEQ ID NOs: 1-50,

779-919, 1344-1523, and 2381-2452; (b) an amino acid sequence of CDRH2 is as set forth in any one of SEQ ID NOs: 51-100, 920-1061, 1524-1703, and 2453-2524; and (c) an amino acid sequence of CDRH3 is as set forth in any one of SEQ ID NOs: 101-150, 1062-1202, 1704-1883, and 2525-2596. Further provided herein are antibodies or antibody fragments, wherein (a) the amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 1414; (b) the amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 1594; and (c) the amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 1774. Further provided herein are antibodies or antibody fragments, wherein (a) the amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 1447; (b) the amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 1627; and (c) the amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 1807. Further provided herein are antibodies or antibody fragments, wherein (a) the amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 1474; (b) the amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 1654; and (c) the amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 1834. Further provided herein are antibodies or antibody fragments, wherein (a) the amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 1344; (b) the amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 1524; and (c) the amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 1704. Further provided herein are antibodies or antibody fragments, wherein (a) the amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 1363; (b) the amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 1543; and (c) the amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 1723. Further provided herein are antibodies or antibody fragments, wherein (a) the amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 1487; (b) the amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 1667; and (c) the amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 1847. Further provided herein are antibodies or antibody fragments, wherein (a) the amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 780; (b) the amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 921; and (c) the amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 1063. Further provided herein are antibodies or antibody fragments, wherein (a) the amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 782; (b) the amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 923; and (c) the amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 1065. Further provided herein are antibodies or antibody fragments, wherein (a) the amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 39; (b) the amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 89; and (c) the amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 139. Further provided herein are antibodies or antibody fragments, wherein (a) the amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 832; (b) the amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 973; and (c) the amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 1115. Further provided herein are antibodies or antibody fragments, wherein (a) the amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 869; (b) the amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 1010; and (c) the amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 1152. Further provided herein are antibodies or antibody fragments, wherein (a) the amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 889; (b) the amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 1030; and (c) the amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 1172.

Further provided herein are antibodies or antibody fragments, wherein (a) the amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 908; (b) the amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 1049; and (c) the amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 1191.

[0013] Provided herein are antibodies or antibody fragments comprising a variable domain, heavy chain region (VH) and a variable domain, light chain region (VL), wherein the VH comprises an amino acid sequence at least about 90% identical to a sequence as set forth in any one of SEQ ID NOs: 493-519 and 721-749, and wherein the VL comprises an amino acid sequence at least about 90% identical to a sequence as set forth in any one of SEQ ID NOs: 520-546 and 750-778.

[0014] Provided herein are antibodies or antibody fragments comprising a variable domain, heavy chain region (VH) comprising an amino acid sequence at least about 90% identical to a sequence as set forth in any one of SEQ ID NOs: 1884-2063, 2302-2380, and 2597-2668. Further provided herein are antibodies or antibody fragments, wherein the VH comprises an amino acid sequence at least about 90% identical to SEQ ID NO: 1954. Further provided herein are antibodies or antibody fragments, wherein the VH comprises an amino acid sequence at least about 90% identical to SEQ ID NO: 1987. Further provided herein are antibodies or antibody fragments, wherein the VH comprises an amino acid sequence at least about 90% identical to SEQ ID NO: 2014.

[0015] Provided herein are antibodies, wherein the antibody comprises a sequence comprising at least 90% sequence identity to any one of SEQ ID NOs: 1-2668; and wherein the antibody is a monoclonal antibody, a polyclonal antibody, a bi-specific antibody, a multispecific antibody, a grafted antibody, a human antibody, a humanized antibody, a synthetic antibody, a chimeric antibody, a camelized antibody, a single-chain Fvs (scFv), a single chain antibody, a Fab fragment, a F(ab')₂ fragment, a Fd fragment, a Fv fragment, a single-domain antibody, an isolated complementarity determining region (CDR), a diabody, a fragment comprised of only a single monomeric variable domain, disulfide-linked Fvs (sdFv), an intrabody, an anti-idiotypic (anti-Id) antibody, or ab antigen-binding fragments thereof.

[0016] Provided herein are nucleic acid compositions comprising: a) a first nucleic acid encoding a variable domain, heavy chain region (VH) comprising an amino acid sequence at least about 90% identical to a sequence as set forth in any one of SEQ ID NOs: 493-519 and 721-749; b) a second nucleic acid encoding a variable domain, light chain region (VL) comprising at least about 90% identical to a sequence as set forth in any one of SEQ ID NOs: 520-546 and 750-778; and an excipient.

[0017] Provided herein are nucleic acid compositions comprising: a) a first nucleic acid encoding a variable domain, heavy chain region (VH) comprising an amino acid sequence at least about 90% identical to a sequence as set forth in any one of SEQ ID NOs: 1884-2063, 2302-2380, and 2597-2668; and b) an excipient. Further provided herein are nucleic acid compositions, wherein the VH comprises an amino acid sequence at least about 90% identical to SEQ ID NO: 1954. Further provided herein are nucleic acid compositions, wherein the VH comprises an amino acid sequence at least about 90% identical to SEQ ID NO: 1987. Further provided herein are nucleic acid compositions, wherein the VH comprises an amino acid sequence at least about 90% identical to SEQ ID NO: 2014.

[0018] Provided herein are methods of treating a SARS-CoV-2 infection, comprising administering the antibody or antibody fragment described herein. Further provided herein are methods, wherein the antibody is administered prior to exposure to SARS-CoV-2. Further provided herein are methods, wherein the antibody is administered at least about 1 week prior to exposure to SARS-CoV-2. Further provided herein are methods, wherein the antibody is administered at least about 1 month prior to exposure to SARS-CoV-2. Further provided herein are methods, wherein the antibody is administered at least about 5 months prior to exposure to SARS-CoV-2. Further provided herein are methods, wherein the antibody is administered after exposure to SARS-CoV-2. Further provided herein are methods, wherein the antibody is administered at most about 24 hours after exposure to SARS-CoV-2. Further provided herein are methods, wherein the antibody is administered at most about 1 week after exposure to SARS-CoV-2. Further provided herein are methods, wherein the antibody is administered at most about 1 month after exposure to SARS-CoV-2. Further provided herein are methods of treating an individual with a SARS-CoV-2 infection with the antibody or antibody fragment described herein comprising: a) obtaining or having obtained a sample from the individual; b) performing or having performed an expression level assay on the sample to determine expression levels of SARS-CoV-2 antibodies; and if the sample has an expression level of the SARS-CoV-2 antibodies then administering to the individual the antibody or antibody fragment described herein, thereby treating the SARS-CoV-2 infection. Further provided herein are methods for optimizing an antibody comprising: a) providing a plurality of polynucleotide sequences encoding for an antibody or antibody fragment, wherein the antibody or antibody fragment is derived from a subject having SARS-CoV-2; b) generating a nucleic acid library comprising the plurality of sequences that when translated encode for antibodies or antibody fragments that bind SARS-CoV-2 or ACE2 protein, wherein each of the sequences comprises a predetermined number of variants within a CDR relative to an input sequence that encodes an antibody; wherein the library comprises at least 50,000 variant sequences; and c) synthesizing the at least 50,000 variant sequences. Further provided herein are methods, wherein the antibody library comprises at least 100,000 sequences. Further provided herein are methods, wherein the method further comprises enriching a subset of the variant sequences. Further provided herein are methods, wherein the method further comprises expressing the antibody or antibody fragments corresponding to the variant sequences. Further provided herein are methods, wherein the polynucleotide sequence is a murine, human, or chimeric antibody sequence. Further provided herein are methods, wherein each sequence of the plurality of variant sequences comprises at least one variant in each CDR of a heavy chain or light chain, relative to the input sequence. Further provided herein are methods, wherein each sequence of the plurality of variant sequences comprises at least two variants in each CDR of a heavy chain or light chain relative to the input sequence. Further provided herein are methods, wherein at least one sequence when translated encodes for an antibody or antibody fragment having at least 5X higher binding affinity than a binding affinity of the input sequence. Further provided herein are methods, wherein at least one sequence when translated encodes for an antibody or antibody fragment having at least 25X higher binding affinity than a binding affinity of the input sequence. Further provided herein are methods, wherein at least one sequence when translated encodes for

an antibody or antibody fragment having at least 50X higher binding affinity than a binding affinity of the input sequence. Further provided herein are methods, wherein each sequence comprises at least one variant in each CDR of a heavy chain or light chain relative to a germline sequence of the input sequence. Further provided herein are methods, wherein the nucleic acid library has a theoretical diversity of at least 10^{10} sequences. Further provided herein are methods, wherein the nucleic acid library has a theoretical diversity of at least 10^{12} sequences.

BRIEF DESCRIPTION OF THE DRAWINGS

- [0019] **Figure 1** depicts a workflow for antibody optimization.
- [0020] **Figure 2** presents a diagram of steps demonstrating an exemplary process workflow for gene synthesis as disclosed herein.
- [0021] **Figure 3** illustrates an example of a computer system.
- [0022] **Figure 4** is a block diagram illustrating an architecture of a computer system.
- [0023] **Figure 5** is a diagram demonstrating a network configured to incorporate a plurality of computer systems, a plurality of cell phones and personal data assistants, and Network Attached Storage (NAS).
- [0024] **Figure 6** is a block diagram of a multiprocessor computer system using a shared virtual address memory space.
- [0025] **Figure 7** is a schema of a panning workflow.
- [0026] **Figures 8A-8B** are graphs of panning data from round 4 for antibody 1.
- [0027] **Figures 8C-8D** are graphs of panning data from round 4 for antibody 2.
- [0028] **Figures 9A-9B** are graphs of panning data from round 4 for antibody 3.
- [0029] **Figures 9C-9D** are graphs of panning data from round 4 for antibody 4.
- [0030] **Figure 10** shows graphs of ACE2 binding to SARS-CoV-2 variant antibodies.
- [0031] **Figures 11A-11B** are graphs of affinity data for SARS-CoV-2 variant antibodies.
- [0032] **Figures 12A-12C** are graphs of affinity data for ACE2 variant antibodies.
- [0033] **Figure 13** is a graph of binding of SARS-CoV-2 variant antibodies to S1 protein.
- [0034] **Figures 14** is a graph of variant 4-23 binding in VERO E6 cells.
- [0035] **Figures 15A-15C** are graphs of variant antibody binding in VERO E6 cells.
- [0036] **Figure 15D** is a graph of data from S1 RBD ACE2 inhibitor ELISA.
- [0037] **Figure 16A-16B** are graphs of SARS-CoV-2 and ACE2 competition ELISAs.
- [0038] **Figure 17A** is a graph of SARS-CoV-2 and ACE2 competition ELISAs from a first set.
- [0039] **Figure 17B** is a graph of SARS-CoV-2 and ACE2 competition ELISAs from a first set showing SARS-CoV-2 variant antibodies.
- [0040] **Figures 18A-18B** are graphs from a first set (**FIG. 18A**) and second set (**FIG. 18B**) showing ACE2 variant antibodies.
- [0041] **Figures 18C-18D** are graphs of SARS-CoV-2 variant antibodies in neutralization assays.

- [0042] **Figure 19** is a graph of anti-ACE2 inhibitors.
- [0043] **Figure 20** is a graph of SARS-CoV-2 and ACE2 inhibition.
- [0044] **Figures 21A-21D** are graphs of SARS-CoV-2 variant antibodies on VERO E6 inhibition measured by FACS.
- [0045] **Figures 22A-22B** are graphs of SARS-CoV-2 variant antibodies on VERO E6 inhibition measured by FACS as compared to CR3022.
- [0046] **Figures 22C-22D** are graphs of affinity of SARS-CoV-2 variant antibodies determined by coating ELISA plates with SARS-CoV-2 Spike Glycoprotein S1 (**FIG. 22C**) or S protein trimer (**Fig. 22D**).
- [0047] **Figure 22E** is a graph of mean fluorescent intensity (MFI) plotted for each SARS-CoV-2 variant antibody dilution.
- [0048] **Figure 23** are images from bluDiagnostics assay of CR3022 and variant 2-6.
- [0049] **Figures 24A-24B** are graphs of phage ELISA data from panning data for antibody 5 (**FIG. 24A**) and antibody 6 (**FIG. 24B**).
- [0050] **Figures 25A-25H** are graphs of phage ELISA for antibody 5 variants.
- [0051] **Figures 26A-26J** are graphs of phage ELISA for antibody 6 variants.
- [0052] **Figures 27A-27B** are graphs of phage ELISA for select antibody 6 variants.
- [0053] **Figures 28A-28F** are graphs of phage ELISA for antibody 5 variants using 1 nM and 0.1 nM concentrations of antibodies.
- [0054] **Figures 29A-29J** are graphs of phage ELISA for antibody 6 variants using 1 nM and 0.1 nM concentrations of antibodies.
- [0055] **Figures 30A-30C** are graphs of mean fluorescent intensity (MFI) plotted for each SARS-CoV-2 variant antibody dilution.
- [0056] **Figures 31A-31B** are graphs of antibody kinetics for variants 2-5, 2-2, and 2-6 (**FIG. 31A**) and variants 1-12, 1-42, 1-20, and 1-19 (**FIG. 31B**).
- [0057] **Figure 31C** is a graph of percent neutralization for variants 1-12, 1-42 and 1-20.
- [0058] **Figure 31D** is a graph of percent neutralization for variants 1-12, 1-42 and 1-20 using live virus.
- [0059] **Figure 32** is a graph of ACE Activity in the presence of variant ACE2 antibodies.
- [0060] **Figures 33A-33D** are graphs of variant antibodies neutralizing live virus.
- [0061] **Figure 33E** is a graph of variant antibodies neutralizing live virus FRNT.
- [0062] **Figure 33F-33I** show data of variant antibodies neutralizing live virus PRNT.
- [0063] **Figure 34A** shows a graph of percent weight change (y-axis) versus day post injection (PI, x-axis) for positive control convalescent plasma and negative control Mab c7d11.
- [0064] **Figure 34B** shows a graph of percent weight change (y-axis) versus day post injection (PI, x-axis) for variant antibody 6-63.
- [0065] **Figure 34C** shows a graph of percent weight change (y-axis) versus day post injection (PI, x-axis) for variant antibody 6-3.

- [0066] **Figure 34D** shows a graph of percent weight change (y-axis) versus day post injection (PI, x-axis) for variant antibody 6-36.
- [0067] **Figure 34E** shows graphs of percent weight change (y-axis) versus day post injection (PI, x-axis) based on dose.
- [0068] **Figure 34F** shows graphs of percent weight change (y-axis) versus day post injection (PI, x-axis) based on dose for variant antibodies 2-3, 2-63, and 1-20.
- [0069] **Figure 34G** shows a graph of data from a plaque assay to detect infectious virus in Day 9 lungs. The indicated antibodies were administered Day -1. Lungs were collected on Day 9, the right lobe was homogenized, clarified and supernatants were quantified by plaque titration. Individual hamster values are shown as symbols. White symbols indicate no infectious virus detected. The geometric mean PFU/gram is shown as bars. Limit of assay shown as dotted line.
- [0070] **Figure 34H** shows a graph of data from *in situ* hybridization (ISH) to detect infected cells in Day 9 lungs. The indicated antibodies were administered Day -1. Three animals per group were analyzed. Individual hamster values are shown as symbols. Median ISH scores are shown as bars.
- [0071] **Figure 34I** shows a graph of data from cumulative inflammation and edema scores for Day 9 lungs. The indicated antibodies were administered Day -1. Three animals per group were analyzed. Individual hamster cumulative pathology scores are shown as symbols. Median scores are shown as bars.
- [0072] **Figure 35** shows an exemplary sequence of a SARS-CoV-2 membrane glycoprotein construct.
- [0073] **Figures 36A-36D** show graphs of membrane glycoprotein variant antibodies binding.
- [0074] **Figure 37A-37B** show graphs of ELISA assays of membrane glycoprotein variant antibodies.
- [0075] **Figures 38A-38J** show graphs of FACS titration data for membrane glycoprotein variant antibodies.
- [0076] **Figures 39A-39B** show graphs of binding affinity and binding for membrane glycoprotein variant antibodies.
- [0077] **Figures 40A-40D** show graphs of flow titrations for pool and single pool HEK for membrane protein antibodies.
- [0078] **Figure 41A** shows a graph of the positive control pAb in a neutralization assay.
- [0079] **Figure 41B** shows a graph of neutralization of antibodies 6-63, 6-3, and 1-12 in VSV-SARS B.135 strain.
- [0080] **Figure 42A** shows a graph of the positive control in a neutralization assay.
- [0081] **Figures 42B-42C** show graphs of neutralization by antibodies described herein.
- [0082] **Figure 43A** shows graphs weight change. Animals were immunosuppressed and then exposed to SARS-CoV-2 virus, WA1 strain, on Day 0. Top graph indicates data from the control group that received the cocktail on Day -1 (D-1, Group A). A group was immunosuppressed but not exposed to virus (CYP Control, Group I). Negative control is an IgG monoclonal (Group H). The cocktail was administered on the indicated day post-exposure (Groups B-G; middle and bottom graphs). Arrows indicate day of antibody

administration. Symbols are mean $\pm$ SEM. Statistical differences in the area under the curve (AOC) are shown to the right of each line. * indicates p value <0.05 , ns= not significant.

[0083] **Figure 43B** shows a graph of data from **FIG. 43A** plotted on one graph.

[0084] **Figure 43C** shows a graph of infectious virus in lungs on Day 14. Plaque assays were run on Day 14 lung homogenates. Plaque forming units (PFU) per gram of tissue were calculated and plotted. The limit of the assay is shown as a dotted line. Bars are the geometric means for each group. Group ID are in parentheses. White symbols indicated no infectious virus was detected. CYP= cyclophosphamide; Neg= Negative; Cont= control.

[0085] **Figure 43D** shows a graph infectious virus in lungs of untreated control hamsters. CYP-treated animals were exposed to 1,000 pfu of virus by intranasal route on Day 0. Groups of four animals were euthanized and lungs were collected on the indicated days. Lung homogenates were assayed for infectious virus by plaque assay. Plaque forming units (PFU) per gram lung tissue are plotted. Geometric mean titers and SD are shown.

DETAILED DESCRIPTION

[0086] The present disclosure employs, unless otherwise indicated, conventional molecular biology techniques, which are within the skill of the art. Unless defined otherwise, all technical and scientific terms used herein have the same meaning as is commonly understood by one of ordinary skill in the art.

[0087] **Definitions**

[0088] Throughout this disclosure, various embodiments are presented in a range format. It should be understood that the description in range format is merely for convenience and brevity and should not be construed as an inflexible limitation on the scope of any embodiments. Accordingly, the description of a range should be considered to have specifically disclosed all the possible subranges as well as individual numerical values within that range to the tenth of the unit of the lower limit unless the context clearly dictates otherwise. For example, description of a range such as from 1 to 6 should be considered to have specifically disclosed subranges such as from 1 to 3, from 1 to 4, from 1 to 5, from 2 to 4, from 2 to 6, from 3 to 6 etc., as well as individual values within that range, for example, 1.1, 2, 2.3, 5, and 5.9. This applies regardless of the breadth of the range. The upper and lower limits of these intervening ranges may independently be included in the smaller ranges, and are also encompassed within the disclosure, subject to any specifically excluded limit in the stated range. Where the stated range includes one or both of the limits, ranges excluding either or both of those included limits are also included in the disclosure, unless the context clearly dictates otherwise.

[0089] The terminology used herein is for the purpose of describing particular embodiments only and is not intended to be limiting of any embodiment. As used herein, the singular forms “a,” “an” and “the” are intended to include the plural forms as well, unless the context clearly indicates otherwise. It will be further understood that the terms “comprises” and/or “comprising,” when used in this specification, specify the presence of stated features, integers, steps, operations, elements, and/or components, but do not preclude the presence or addition of one or more other features, integers, steps, operations, elements, components, and/or

groups thereof. As used herein, the term “and/or” includes any and all combinations of one or more of the associated listed items.

[0090] Unless specifically stated or obvious from context, as used herein, the term “about” in reference to a number or range of numbers is understood to mean the stated number and numbers +/- 10% thereof, or 10% below the lower listed limit and 10% above the higher listed limit for the values listed for a range.

[0091] Unless specifically stated, as used herein, the term “nucleic acid” encompasses double- or triple-stranded nucleic acids, as well as single-stranded molecules. In double- or triple-stranded nucleic acids, the nucleic acid strands need not be coextensive (i.e., a double-stranded nucleic acid need not be double-stranded along the entire length of both strands). Nucleic acid sequences, when provided, are listed in the 5' to 3' direction, unless stated otherwise. Methods described herein provide for the generation of isolated nucleic acids. Methods described herein additionally provide for the generation of isolated and purified nucleic acids. A “nucleic acid” as referred to herein can comprise at least 5, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000, or more bases in length. Moreover, provided herein are methods for the synthesis of any number of polypeptide-segments encoding nucleotide sequences, including sequences encoding non-ribosomal peptides (NRPs), sequences encoding non-ribosomal peptide-synthetase (NRPS) modules and synthetic variants, polypeptide segments of other modular proteins, such as antibodies, polypeptide segments from other protein families, including non-coding DNA or RNA, such as regulatory sequences e.g. promoters, transcription factors, enhancers, siRNA, shRNA, RNAi, miRNA, small nucleolar RNA derived from microRNA, or any functional or structural DNA or RNA unit of interest. The following are non-limiting examples of polynucleotides: coding or non-coding regions of a gene or gene fragment, intergenic DNA, loci (locus) defined from linkage analysis, exons, introns, messenger RNA (mRNA), transfer RNA, ribosomal RNA, short interfering RNA (siRNA), short-hairpin RNA (shRNA), micro-RNA (miRNA), small nucleolar RNA, ribozymes, complementary DNA (cDNA), which is a DNA representation of mRNA, usually obtained by reverse transcription of messenger RNA (mRNA) or by amplification; DNA molecules produced synthetically or by amplification, genomic DNA, recombinant polynucleotides, branched polynucleotides, plasmids, vectors, isolated DNA of any sequence, isolated RNA of any sequence, nucleic acid probes, and primers. cDNA encoding for a gene or gene fragment referred herein may comprise at least one region encoding for exon sequences without an intervening intron sequence in the genomic equivalent sequence. cDNA described herein may be generated by de novo synthesis.

[0092] Antibody Optimization Library for Coronavirus

[0093] Provided herein are methods, compositions, and systems for the optimization of antibodies for coronavirus. In some embodiments, the antibodies are optimized for SARS-CoV, MERS-CoV, CoV-229E, HCoV-NL63, HCoV-OC43, or HCoV-HKU1. In some embodiments, the antibodies are optimized for SARS-CoV-2. In some embodiments, the antibodies are optimized for a receptor that binds to the coronavirus. In some embodiments, the receptor of the coronavirus is ACE2 or dipeptidyl peptidase 4

(DPP4). In some embodiments, the antibodies are optimized based on interactions between the coronavirus and the receptor that binds the coronavirus. In some embodiments, the antibodies are optimized for angiotensin-converting enzyme 2 (ACE2). In some embodiments, the antibodies are optimized based on interactions between SARS-CoV-2 and ACE2.

[0094] Antibodies are in some instances optimized by the design of in-silico libraries comprising variant sequences of an input antibody sequence (**FIG. 1**). Input sequences **100** are in some instances modified in-silico **102** with one or more mutations or variants to generate libraries of optimized sequences **103**. In some instances, such libraries are synthesized, cloned into expression vectors, and translation products (antibodies) evaluated for activity. In some instances, fragments of sequences are synthesized and subsequently assembled. In some instances, expression vectors are used to display and enrich desired antibodies, such as phage display. Selection pressures used during enrichment in some instances includes, but is not limited to, binding affinity, toxicity, immunological tolerance, stability, receptor-ligand competition, or developability. Such expression vectors allow antibodies with specific properties to be selected ("panning"), and subsequent propagation or amplification of such sequences enriches the library with these sequences. Panning rounds can be repeated any number of times, such as 1, 2, 3, 4, 5, 6, 7, or more than 7 rounds. Sequencing at one or more rounds is in some instances used to identify which sequences **105** have been enriched in the library.

[0095] Described herein are methods and systems of in-silico library design. For example, an antibody or antibody fragment sequence is used as input. In some instances, the antibody sequence used as input is an antibody or antibody fragment sequence that binds SARS-CoV-2. In some instances, the input is an antibody or antibody fragment sequence that binds a protein of SARS-CoV-2. In some instances, the protein is a spike glycoprotein, a membrane protein, an envelope protein, a nucleocapsid protein, or combinations thereof. In some instances, the protein is a spike glycoprotein of SARS-CoV-2. In some instances, the protein is a receptor binding domain of SARS-CoV-2. In some instances, the input sequence is an antibody or antibody fragment sequence that binds angiotensin-converting enzyme 2 (ACE2). In some instances, the input sequence is an antibody or antibody fragment sequence that binds an extracellular domain of the angiotensin-converting enzyme 2 (ACE2).

[0096] A database **102** comprising known mutations or variants of one or more viruses is queried **101**, and a library **103** of sequences comprising combinations of these mutations or variants are generated. In some instances, the database comprises known mutations or variants of SARS-CoV-like coronaviruses, SARS-CoV-2, SARS-CoV, or combinations thereof. In some instances, the database comprises known mutations or variants of the spike protein of SARS-CoV-like coronaviruses, SARS-CoV-2, SARS-CoV, or combinations thereof. In some instances, the database comprises known mutations or variants of the receptor binding domain of SARS-CoV-like coronaviruses, SARS-CoV-2, SARS-CoV, or combinations thereof. In some instances, the database comprises mutations or variants of a protein of SARS-CoV-like coronaviruses, SARS-CoV-2, SARS-CoV, or combinations thereof that binds to ACE2.

[0097] In some instances, the input sequence is a heavy chain sequence of an antibody or antibody fragment that binds SARS-CoV-like coronaviruses, SARS-CoV-2, SARS-CoV, or combinations thereof. In some instances, the input sequence is a light chain sequence of an antibody or antibody fragment that binds SARS-CoV-like coronaviruses, SARS-CoV-2, SARS-CoV, or combinations thereof. In some instances, the heavy chain sequence comprises varied CDR regions. In some instances, the light chain sequence comprises varied CDR regions. In some instances, known mutations or variants from CDRs are used to build the sequence library. Filters 104, or exclusion criteria, are in some instances used to select specific types of variants for members of the sequence library. For example, sequences having a mutation or variant are added if a minimum number of organisms in the database have the mutation or variant. In some instances, additional CDRs are specified for inclusion in the database. In some instances, specific mutations or variants or combinations of mutations or variants are excluded from the library (e.g., known immunogenic sites, structure sites, etc.). In some instances, specific sites in the input sequence are systematically replaced with histidine, aspartic acid, glutamic acid, or combinations thereof. In some instances, the maximum or minimum number of mutations or variants allowed for each region of an antibody are specified. Mutations or variants in some instances are described relative to the input sequence or the input sequence's corresponding germline sequence. For example, sequences generated by the optimization comprise at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or more than 16 mutations or variants from the input sequence. In some instances, sequences generated by the optimization comprise no more than 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or no more than 18 mutations or variants from the input sequence. In some instances, sequences generated by the optimization comprise about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or about 18 mutations or variants relative to the input sequence. In some instances, sequences generated by the optimization comprise about 1, 2, 3, 4, 5, 6, or 7 mutations or variants from the input sequence in a first CDR region. In some instances, sequences generated by the optimization comprise about 1, 2, 3, 4, 5, 6, or 7 mutations or variants from the input sequence in a second CDR region. In some instances, sequences generated by the optimization comprise about 1, 2, 3, 4, 5, 6, or 7 mutations or variants from the input sequence in a third CDR region. In some instances, sequences generated by the optimization comprise about 1, 2, 3, 4, 5, 6, or 7 mutations or variants from the input sequence in a first CDR region of a heavy chain. In some instances, sequences generated by the optimization comprise about 1, 2, 3, 4, 5, 6, or 7 mutations or variants from the input sequence in a second CDR region of a heavy chain. In some instances, sequences generated by the optimization comprise about 1, 2, 3, 4, 5, 6, or 7 mutations or variants from the input sequence in a third CDR region of a heavy chain. In some instances, sequences generated by the optimization comprise about 1, 2, 3, 4, 5, 6, or 7 mutations or variants from the input sequence in a first CDR region of a light chain. In some instances, sequences generated by the optimization comprise about 1, 2, 3, 4, 5, 6, or 7 mutations or variants from the input sequence in a second CDR region of a light chain. In some instances, sequences generated by the optimization comprise about 1, 2, 3, 4, 5, 6, or 7 mutations or variants from the input sequence in a third CDR region of a light chain. In some instances, a first CDR region is CDR1. In some instances, a second CDR region is CDR2. In some instances, a third CDR region is

CDR3. In-silico antibodies libraries are in some instances synthesized, assembled, and enriched for desired sequences.

[0098] The germline sequences corresponding to an input sequence may also be modified to generate sequences in a library. For example, sequences generated by the optimization methods described herein comprise at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or more than 16 mutations or variants from the germline sequence. In some instances, sequences generated by the optimization comprise no more than 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or no more than 18 mutations or variants from the germline sequence. In some instances, sequences generated by the optimization comprise about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or about 18 mutations or variants relative to the germline sequence.

[0099] Provided herein are methods, systems, and compositions for antibody optimization, wherein the input sequence comprises mutations or variants in an antibody region. Exemplary regions of the antibody include, but are not limited to, a complementarity-determining region (CDR), a variable domain, or a constant domain. In some instances, the CDR is CDR1, CDR2, or CDR3. In some instances, the CDR is a heavy domain including, but not limited to, CDRH1, CDRH2, and CDRH3. In some instances, the CDR is a light domain including, but not limited to, CDRL1, CDRL2, and CDRL3. In some instances, the variable domain is variable domain, light chain (VL) or variable domain, heavy chain (VH). In some instances, the VL domain comprises kappa or lambda chains. In some instances, the constant domain is constant domain, light chain (CL) or constant domain, heavy chain (CH). In some instances, sequences generated by the optimization comprise about 1, 2, 3, 4, 5, 6, or 7 mutations or variants from the germline sequence in a first CDR region. In some instances, sequences generated by the optimization comprise about 1, 2, 3, 4, 5, 6, or 7 mutations or variants from the germline sequence in a second CDR region. In some instances, sequences generated by the optimization comprise about 1, 2, 3, 4, 5, 6, or 7 mutations or variants from the germline sequence in a third CDR region. In some instances, sequences generated by the optimization comprise about 1, 2, 3, 4, 5, 6, or 7 mutations or variants from the germline sequence in a first CDR region of a heavy chain. In some instances, sequences generated by the optimization comprise about 1, 2, 3, 4, 5, 6, or 7 mutations or variants from the germline sequence in a second CDR region of a heavy chain. In some instances, sequences generated by the optimization comprise about 1, 2, 3, 4, 5, 6, or 7 mutations or variants from the germline sequence in a third CDR region of a heavy chain. In some instances, sequences generated by the optimization comprise about 1, 2, 3, 4, 5, 6, or 7 mutations or variants from the germline sequence in a first CDR region of a light chain. In some instances, sequences generated by the optimization comprise about 1, 2, 3, 4, 5, 6, or 7 mutations or variants from the germline sequence in a second CDR region of a light chain. In some instances, sequences generated by the optimization comprise about 1, 2, 3, 4, 5, 6, or 7 mutations or variants from the germline sequence in a third CDR region of a light chain. In some instances, a first CDR region is CDR1. In some instances, a second CDR region is CDR2. In some instances, a third CDR region is CDR3.

[00100] *VHH Libraries*

[00101] Provided herein are methods, compositions, and systems for generation of antibodies or antibody fragments. In some instances, the antibodies or antibody fragments are single domain antibodies. Methods, compositions, and systems described herein for the optimization of antibodies comprise a ratio-variant approach that mirror the natural diversity of antibody sequences. In some instances, libraries of optimized antibodies comprise variant antibody sequences. In some instances, the variant antibody sequences are designed comprising variant CDR regions. In some instances, the variant antibody sequences comprising variant CDR regions are generated by shuffling the natural CDR sequences in a llama, humanized, or chimeric framework. In some instances, such libraries are synthesized, cloned into expression vectors, and translation products (antibodies) evaluated for activity. In some instances, fragments of sequences are synthesized and subsequently assembled. In some instances, expression vectors are used to display and enrich desired antibodies, such as phage display. In some instances, the phage vector is a Fab phagemid vector. Selection pressures used during enrichment in some instances includes, but is not limited to, binding affinity, toxicity, immunological tolerance, stability, receptor-ligand competition, or developability. Such expression vectors allow antibodies with specific properties to be selected (“panning”), and subsequent propagation or amplification of such sequences enriches the library with these sequences. Panning rounds can be repeated any number of times, such as 1, 2, 3, 4, 5, 6, 7, or more than 7 rounds. In some instances, each round of panning involves a number of washes. In some instances, each round of panning involves at least or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or more than 16 washes.

[00102] Described herein are methods and systems of in-silico library design. Libraries as described herein, in some instances, are designed based on a database comprising a variety of antibody sequences. In some instances, the database comprises a plurality of variant antibody sequences against various targets. In some instances, the database comprises at least 100, 500, 1000, 1500, 2000, 2500, 3000, 3500, 4000, 4500, 5000, or more than 5000 antibody sequences. An exemplary database is an iCAN database. In some instances, the database comprises naïve and memory B-cell receptor sequences. In some instances, the naïve and memory B-cell receptor sequences are human, mouse, or primate sequences. In some instances, the naïve and memory B-cell receptor sequences are human sequences. In some instances, the database is analyzed for position specific variation. In some instances, antibodies described herein comprise position specific variations in CDR regions. In some instances, the CDR regions comprise multiple sites for variation.

[00103] Described herein are libraries comprising variation in a CDR region. In some instances, the CDR is CDR1, CDR2, or CDR3 of a variable heavy chain. In some instances, the CDR is CDR1, CDR2, or CDR3 of a variable light chain. In some instances, the libraries comprise multiple variants encoding for CDR1, CDR2, or CDR3. In some instances, the libraries as described herein encode for at least 50, 100, 200, 300, 400, 500, 1000, 1200, 1500, 1700, 2000, 2500, 3000, 3500, 4000, 4500, 5000, or more than 5000 CDR1 sequences. In some instances, the libraries as described herein encode for at least 50, 100, 200, 300, 400, 500, 1000, 1200, 1500, 1700, 2000, 2500, 3000, 3500, 4000, 4500, 5000, or more than 5000 CDR2 sequences. In some instances, the libraries as described herein encode for at least 50, 100, 200, 300, 400,

500, 1000, 1200, 1500, 1700, 2000, 2500, 3000, 3500, 4000, 4500, 5000, or more than 5000 CDR3 sequences. In-silico antibodies libraries are in some instances synthesized, assembled, and enriched for desired sequences.

[00104] Following synthesis of CDR1 variants, CDR2 variants, and CDR3 variants, in some instances, the CDR1 variants, the CDR2 variants, and the CDR3 variants are shuffled to generate a diverse library. In some instances, the diversity of the libraries generated by methods described herein have a theoretical diversity of at least or about 10^7 , 10^8 , 10^9 , 10^{10} , 10^{11} , 10^{12} , 10^{13} , 10^{14} , 10^{15} , 10^{16} , 10^{17} , 10^{18} , or more than 10^{18} sequences. In some instances, the library has a final library diversity of at least or about 10^7 , 10^8 , 10^9 , 10^{10} , 10^{11} , 10^{12} , 10^{13} , 10^{14} , 10^{15} , 10^{16} , 10^{17} , 10^{18} , or more than 10^{18} sequences.

[00105] The germline sequences corresponding to a variant sequence may also be modified to generate sequences in a library. For example, sequences generated by methods described herein comprise at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or more than 16 mutations or variants from the germline sequence. In some instances, sequences generated comprise no more than 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or no more than 18 mutations or variants from the germline sequence. In some instances, sequences generated comprise about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or about 18 mutations or variants relative to the germline sequence.

[00106] *Coronavirus Antibody Libraries*

[00107] Provided herein are libraries generated from antibody optimization methods described herein. Antibodies described herein result in improved functional activity, structural stability, expression, specificity, or a combination thereof.

[00108] Provided herein are methods and compositions relating to SARS-CoV-2 binding libraries comprising nucleic acids encoding for a SARS-CoV-2 antibody. Further provided herein are methods and compositions relating to ACE2 binding libraries comprising nucleic acids encoding for an ACE2 antibody. Such methods and compositions in some instances are generated by the antibody optimization methods and systems described herein. Libraries as described herein may be further variegated to provide for variant libraries comprising nucleic acids each encoding for a predetermined variant of at least one predetermined reference nucleic acid sequence. Further described herein are protein libraries that may be generated when the nucleic acid libraries are translated. In some instances, nucleic acid libraries as described herein are transferred into cells to generate a cell library. Also provided herein are downstream applications for the libraries synthesized using methods described herein. Downstream applications include identification of variant nucleic acids or protein sequences with enhanced biologically relevant functions, e.g., improved stability, affinity, binding, functional activity, and for the treatment or prevention of an infection caused by a coronavirus such as SARS-CoV-2.

[00109] In some instances, an antibody or antibody fragment described herein comprises a sequence of any one of SEQ ID NOs: 1-2668. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 80% identical to a sequence of any one of SEQ ID NOs: 1-2668. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 85%

identical to a sequence of any one of SEQ ID NOs: 1-2668. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-2668. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 95% identical to a sequence of any one of SEQ ID NOs: 1-2668.

[00110] In some instances, an antibody or antibody fragment described herein comprises a CDRH1 sequence of any one of SEQ ID NOs: 151-165, 241-255, 331-357, and 547-575. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 80% identical to a CDRH1 sequence of any one of SEQ ID NOs: 151-165, 241-255, 331-357, and 547-575. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 85% identical to a CDRH1 sequence of any one of SEQ ID NOs: 151-165, 241-255, 331-357, and 547-575. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 90% identical to a CDRH1 sequence of any one of SEQ ID NOs: 151-165, 241-255, 331-357, and 547-575. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 95% identical to a CDRH1 sequence of any one of SEQ ID NOs: 151-165, 241-255, 331-357, and 547-575. In some instances, an antibody or antibody fragment described herein comprises a CDRH2 sequence of any one of SEQ ID NOs: 166-180, 256-270, 358-384, and 576-604. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 80% identical to a CDRH2 sequence of any one of SEQ ID NOs: 166-180, 256-270, 358-384, and 576-604. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 85% identical to a CDRH2 sequence of any one of SEQ ID NOs: 166-180, 256-270, 358-384, and 576-604. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 90% identical to a CDRH2 sequence of any one of SEQ ID NOs: 166-180, 256-270, 358-384, and 576-604. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 95% identical to a CDRH2 sequence of any one of SEQ ID NOs: 166-180, 256-270, 358-384, and 576-604. In some instances, an antibody or antibody fragment described herein comprises a CDRH3 sequence of any one of SEQ ID NOs: 181-195, 271-285, 385-411, and 605-633. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 80% identical to a CDRH3 sequence of any one of SEQ ID NOs: 181-195, 271-285, 385-411, and 605-633. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 85% identical to a CDRH3 sequence of any one of SEQ ID NOs: 181-195, 271-285, 385-411, and 605-633. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 90% identical to a CDRH3 sequence of any one of SEQ ID NOs: 181-195, 271-285, 385-411, and 605-633. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 95% identical to a CDRH3 sequence of any one of SEQ ID NOs: 181-195, 271-285, 385-411, and 605-633.

[00111] In some instances, an antibody or antibody fragment described herein comprises a CDRH1 sequence of any one of SEQ ID NOs: 1-50, 779-919, 1344-1523, and 2381-2452. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 80% identical to a

CDRH1 sequence of any one of SEQ ID NOs: 1-50, 779-919, 1344-1523, and 2381-2452. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 85% identical to a CDRH1 sequence of any one of SEQ ID NOs: 1-50, 779-919, 1344-1523, and 2381-2452. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 90% identical to a CDRH1 sequence of any one of SEQ ID NOs: 1-50, 779-919, 1344-1523, and 2381-2452. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 95% identical to a CDRH1 sequence of any one of SEQ ID NOs: 1-50, 779-919, 1344-1523, and 2381-2452. In some instances, an antibody or antibody fragment described herein comprises a CDRH2 sequence of any one of SEQ ID NOs: 51-100, 920-1061, 1524-1703, and 2453-2524. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 80% identical to a CDRH2 sequence of any one of SEQ ID NOs: 51-100, 920-1061, 1524-1703, and 2453-2524. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 85% identical to a CDRH2 sequence of any one of SEQ ID NOs: 51-100, 920-1061, 1524-1703, and 2453-2524. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 90% identical to a CDRH2 sequence of any one of SEQ ID NOs: 51-100, 920-1061, 1524-1703, and 2453-2524. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 95% identical to a CDRH2 sequence of any one of SEQ ID NOs: 51-100, 920-1061, 1524-1703, and 2453-2524. In some instances, an antibody or antibody fragment described herein comprises a CDRH3 sequence of any one of SEQ ID NOs: 101-150, 1062-1202, 1704-1883, and 2525-2596. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 80% identical to a CDRH3 sequence of any one of SEQ ID NOs: 101-150, 1062-1202, 1704-1883, and 2525-2596. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 85% identical to a CDRH3 sequence of any one of SEQ ID NOs: 101-150, 1062-1202, 1704-1883, and 2525-2596. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 90% identical to a CDRH3 sequence of any one of SEQ ID NOs: 101-150, 1062-1202, 1704-1883, and 2525-2596. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 95% identical to a CDRH3 sequence of any one of SEQ ID NOs: 101-150, 1062-1202, 1704-1883, and 2525-2596.

[00112] In some instances, an antibody or antibody fragment described herein comprises a CDRL1 sequence of any one of SEQ ID NOs: 196-210, 286-300, 412-438, and 634-662. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 80% identical to a CDRL1 sequence of any one of SEQ ID NOs: 196-210, 286-300, 412-438, and 634-662. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 85% identical to a CDRL1 sequence of any one of SEQ ID NOs: 196-210, 286-300, 412-438, and 634-662. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 90% identical to a CDRL1 sequence of any one of SEQ ID NOs: 196-210, 286-300, 412-438, and 634-662. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 95% identical to a

CDRL1 sequence of any one of SEQ ID NOs: 196-210, 286-300, 412-438, and 634-662. In some instances, an antibody or antibody fragment described herein comprises a CDRL2 sequence of any one of SEQ ID NOs: 211-225, 301-315, 439-465, and 663-691. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 80% identical to a CDRL2 sequence of any one of SEQ ID NOs: 211-225, 301-315, 439-465, and 663-691. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 85% identical to a CDRL2 sequence of any one of SEQ ID NOs: 211-225, 301-315, 439-465, and 663-691. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 90% identical to a CDRL2 sequence of any one of SEQ ID NOs: 211-225, 301-315, 439-465, and 663-691. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 95% identical to a CDRL2 sequence of any one of SEQ ID NOs: 211-225, 301-315, 439-465, and 663-691. In some instances, an antibody or antibody fragment described herein comprises a CDRL3 sequence of any one of SEQ ID NOs: 226-240, 316-330, 466-492, and 692-720. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 80% identical to a CDRL3 sequence of any one of SEQ ID NOs: 226-240, 316-330, 466-492, and 692-720. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 85% identical to a CDRL3 sequence of any one of SEQ ID NOs: 226-240, 316-330, 466-492, and 692-720. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 90% identical to a CDRL3 sequence of any one of SEQ ID NOs: 226-240, 316-330, 466-492, and 692-720. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 95% identical to a CDRL3 sequence of any one of SEQ ID NOs: 226-240, 316-330, 466-492, and 692-720.

[00113] In some embodiments, the antibody or antibody fragment comprising a variable domain, heavy chain region (VH) and a variable domain, light chain region (VL), wherein VH comprises complementarity determining regions CDRH1, CDRH2, and CDRH3, wherein VL comprises complementarity determining regions CDRL1, CDRL2, and CDRL3, and wherein (a) an amino acid sequence of CDRH1 is as set forth in any one of SEQ ID NOs: 151-165, 241-255, 331-357, and 547-575; (b) an amino acid sequence of CDRH2 is as set forth in any one of SEQ ID NOs: 166-180, 256-270, 358-384, and 576-604; (c) an amino acid sequence of CDRH3 is as set forth in any one of SEQ ID NOs: 181-195, 271-285, 385-411, and 605-633; (d) an amino acid sequence of CDRL1 is as set forth in any one of SEQ ID NOs: 196-210, 286-300, 412-438, and 634-662; (e) an amino acid sequence of CDRL2 is as set forth in any one of SEQ ID NOs: 211-225, 301-315, 439-465, and 663-691; and (f) an amino acid sequence of CDRL3 is as set forth in any one of SEQ ID NOs: 226-240, 316-330, 466-492, and 692-720. In some embodiments, the antibody or antibody fragment comprising a variable domain, heavy chain region (VH) and a variable domain, light chain region (VL), wherein VH comprises complementarity determining regions CDRH1, CDRH2, and CDRH3, wherein VL comprises complementarity determining regions CDRL1, CDRL2, and CDRL3, and wherein (a) an amino acid sequence of CDRH1 is at least or about 80%, 85%, 90%, or 95% identical to any one of SEQ ID NOs: 151-165, 241-255, 331-357, and 547-575; (b) an amino acid sequence of CDRH2 is at least or about

80%, 85%, 90%, or 95% identical to any one of SEQ ID NOs: 166-180, 256-270, 358-384, and 576-604; (c) an amino acid sequence of CDRH3 is at least or about 80%, 85%, 90%, or 95% identical to any one of SEQ ID NOs: 181-195, 271-285, 385-411, and 605-633; (d) an amino acid sequence of CDRL1 is at least or about 80%, 85%, 90%, or 95% identical to any one of SEQ ID NOs: 196-210, 286-300, 412-438, and 634-662; (e) an amino acid sequence of CDRL2 is at least or about 80%, 85%, 90%, or 95% identical to any one of SEQ ID NOs: 211-225, 301-315, 439-465, and 663-691; and (f) an amino acid sequence of CDRL3 is at least or about 80%, 85%, 90%, or 95% identical to any one of SEQ ID NOs: 226-240, 316-330, 466-492, and 692-720.

[00114] Described herein, in some embodiments, are antibodies or antibody fragments comprising a variable domain, heavy chain region (VH) and a variable domain, light chain region (VL), wherein the VH comprises an amino acid sequence at least about 90% identical to a sequence as set forth in any one of SEQ ID NOs: 493-519 and 721-749, and wherein the VL comprises an amino acid sequence at least about 90% identical to a sequence as set forth in any one of SEQ ID NOs: 520-546 and 750-778. In some instances, the antibodies or antibody fragments comprise VH comprising at least or about 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to any one of SEQ ID NOs: 493-519 and 721-749, and VL comprising at least or about 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to any one of SEQ ID NOs: 520-546 and 750-778.

[00115] Described herein, in some embodiments, are antibodies or antibody fragments comprising a variable domain, heavy chain region (VH), wherein the VH comprises an amino acid sequence at least about 90% identical to a sequence as set forth in any one of SEQ ID NOs: 1884-2063, 2302-2380, and 2597-2668. In some instances, the antibodies or antibody fragments comprise a heavy chain variable domain comprising at least or about 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to any one of SEQ ID NOs: 1884-2063, 2302-2380, and 2597-2668.

[00116] The term “sequence identity” means that two polynucleotide sequences are identical (i.e., on a nucleotide-by-nucleotide basis) over the window of comparison. The term “percentage of sequence identity” is calculated by comparing two optimally aligned sequences over the window of comparison, determining the number of positions at which the identical nucleic acid base (e.g., A, T, C, G, U, or I) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison (i.e., the window size), and multiplying the result by 100 to yield the percentage of sequence identity.

[00117] The term “homology” or “similarity” between two proteins is determined by comparing the amino acid sequence and its conserved amino acid substitutes of one protein sequence to the second protein sequence. Similarity may be determined by procedures which are well-known in the art, for example, a BLAST program (Basic Local Alignment Search Tool at the National Center for Biological Information).

[00118] Provided herein are libraries comprising nucleic acids encoding for SARS-CoV-2 antibodies. Antibodies described herein allow for improved stability for a range of SARS-CoV-2 or ACE2 binding

domain encoding sequences. In some instances, the binding domain encoding sequences are determined by interactions between SARS-CoV-2 and ACE2.

[00119] Sequences of binding domains based on surface interactions between SARS-CoV-2 and ACE2 are analyzed using various methods. For example, multispecies computational analysis is performed. In some instances, a structure analysis is performed. In some instances, a sequence analysis is performed. Sequence analysis can be performed using a database known in the art. Non-limiting examples of databases include, but are not limited to, NCBI BLAST (blast.ncbi.nlm.nih.gov/Blast.cgi), UCSC Genome Browser (genome.ucsc.edu/), UniProt (www.uniprot.org/), and IUPHAR/BPS Guide to PHARMACOLOGY (guidetopharmacology.org/).

[00120] Described herein are SARS-CoV-2 or ACE2 binding domains designed based on sequence analysis among various organisms. For example, sequence analysis is performed to identify homologous sequences in different organisms. Exemplary organisms include, but are not limited to, mouse, rat, equine, sheep, cow, primate (*e.g.*, chimpanzee, baboon, gorilla, orangutan, monkey), dog, cat, pig, donkey, rabbit, fish, fly, and human. In some instances, homologous sequences are identified in the same organism, across individuals.

[00121] Following identification of SARS-CoV-2 or ACE2 binding domains, libraries comprising nucleic acids encoding for the SARS-CoV-2 or ACE2 binding domains may be generated. In some instances, libraries of SARS-CoV-2 or ACE2 binding domains comprise sequences of SARS-CoV-2 or ACE2 binding domains designed based on conformational ligand interactions, peptide ligand interactions, small molecule ligand interactions, extracellular domains of SARS-CoV-2 or ACE2, or antibodies that target SARS-CoV-2 or ACE2. Libraries of SARS-CoV-2 or ACE2 binding domains may be translated to generate protein libraries. In some instances, libraries of SARS-CoV-2 or ACE2 binding domains are translated to generate peptide libraries, immunoglobulin libraries, derivatives thereof, or combinations thereof. In some instances, libraries of SARS-CoV-2 or ACE2 binding domains are translated to generate protein libraries that are further modified to generate peptidomimetic libraries. In some instances, libraries of SARS-CoV-2 or ACE2 binding domains are translated to generate protein libraries that are used to generate small molecules.

[00122] Methods described herein provide for synthesis of libraries of SARS-CoV-2 or ACE2 binding domains comprising nucleic acids each encoding for a predetermined variant of at least one predetermined reference nucleic acid sequence. In some cases, the predetermined reference sequence is a nucleic acid sequence encoding for a protein, and the variant library comprises sequences encoding for variation of at least a single codon such that a plurality of different variants of a single residue in the subsequent protein encoded by the synthesized nucleic acid are generated by standard translation processes. In some instances, the libraries of SARS-CoV-2 or ACE2 binding domains comprise varied nucleic acids collectively encoding variations at multiple positions. In some instances, the variant library comprises sequences encoding for variation of at least a single codon in a SARS-CoV-2 or ACE2 binding domain. In some instances, the variant library comprises sequences encoding for variation of multiple codons in a SARS-CoV-2 or ACE2

binding domain. An exemplary number of codons for variation include, but are not limited to, at least or about 1, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 225, 250, 275, 300, or more than 300 codons.

[00123] Methods described herein provide for synthesis of libraries comprising nucleic acids encoding for the SARS-CoV-2 or ACE2 binding domains, wherein the libraries comprise sequences encoding for variation of length of the SARS-CoV-2 or ACE2 binding domains. In some instances, the library comprises sequences encoding for variation of length of at least or about 1, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 225, 250, 275, 300, or more than 300 codons less as compared to a predetermined reference sequence. In some instances, the library comprises sequences encoding for variation of length of at least or about 1, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200, 225, 250, 275, 300, or more than 300 codons more as compared to a predetermined reference sequence.

[00124] Following identification of SARS-CoV-2 or ACE2 binding domains, antibodies may be designed and synthesized to comprise the SARS-CoV-2 or ACE2 binding domains. Antibodies comprising SARS-CoV-2 or ACE2 binding domains may be designed based on binding, specificity, stability, expression, folding, or downstream activity. In some instances, the antibodies comprising SARS-CoV-2 or ACE2 binding domains enable contact with the SARS-CoV-2 or ACE2. In some instances, the antibodies comprising SARS-CoV-2 or ACE2 binding domains enables high affinity binding with the SARS-CoV-2 or ACE2. Exemplary amino acid sequences of SARS-CoV-2 or ACE2 binding domains comprise any one of SEQ ID NOs: 1-2668.

[00125] In some instances, the SARS-CoV-2 antibody comprises a binding affinity (e.g., K_D) to SARS-CoV-2 of less than 1 nM, less than 1.2 nM, less than 2 nM, less than 5 nM, less than 10 nM, less than 11 nM, less than 13.5 nM, less than 15 nM, less than 20 nM, less than 25 nM, or less than 30 nM. In some instances, the SARS-CoV-2 antibody comprises a K_D of less than 1 nM. In some instances, the SARS-CoV-2 antibody comprises a K_D of less than 1.2 nM. In some instances, the SARS-CoV-2 antibody comprises a K_D of less than 2 nM. In some instances, the SARS-CoV-2 antibody comprises a K_D of less than 5 nM. In some instances, the SARS-CoV-2 antibody comprises a K_D of less than 10 nM. In some instances, the SARS-CoV-2 antibody comprises a K_D of less than 13.5 nM. In some instances, the SARS-CoV-2 antibody comprises a K_D of less than 15 nM. In some instances, the SARS-CoV-2 antibody comprises a K_D of less than 20 nM. In some instances, the SARS-CoV-2 antibody comprises a K_D of less than 25 nM. In some instances, the SARS-CoV-2 antibody comprises a K_D of less than 30 nM.

[00126] In some instances, the ACE2 antibody comprises a binding affinity (e.g., K_D) to ACE2 of less than 1 nM, less than 1.2 nM, less than 2 nM, less than 5 nM, less than 10 nM, less than 11 nM, less than 13.5 nM, less than 15 nM, less than 20 nM, less than 25 nM, or less than 30 nM. In some instances, the ACE2 antibody comprises a K_D of less than 1 nM. In some instances, the ACE2 antibody comprises a K_D of less than 1.2 nM. In some instances, the ACE2 antibody comprises a K_D of less than 2 nM. In some instances, the ACE2 antibody comprises a K_D of less than 5 nM. In some instances, the ACE2 antibody comprises a K_D

of less than 10 nM. In some instances, the ACE2 antibody comprises a K_D of less than 13.5 nM. In some instances, the ACE2 antibody comprises a K_D of less than 15 nM. In some instances, the ACE2 antibody comprises a K_D of less than 20 nM. In some instances, the ACE2 antibody comprises a K_D of less than 25 nM. In some instances, the ACE2 antibody comprises a K_D of less than 30 nM.

[00127] In some instances, the SARS-CoV-2 or ACE2 immunoglobulin is an agonist. In some instances, the SARS-CoV-2 or ACE2 immunoglobulin is an antagonist. In some instances, the SARS-CoV-2 or ACE2 immunoglobulin is an allosteric modulator. In some instances, the allosteric modulator is a negative allosteric modulator. In some instances, the allosteric modulator is a positive allosteric modulator. In some instances, the SARS-CoV-2 or ACE2 immunoglobulin results in agonistic, antagonistic, or allosteric effects at a concentration of at least or about 1 nM, 2 nM, 4 nM, 6 nM, 8 nM, 10 nM, 20 nM, 30 nM, 40 nM, 50 nM, 60 nM, 70 nM, 80 nM, 90 nM, 100 nM, 120 nM, 140 nM, 160 nM, 180 nM, 200 nM, 300 nM, 400 nM, 500 nM, 600 nM, 700 nM, 800 nM, 900 nM, 1000 nM, or more than 1000 nM. In some instances, the SARS-CoV-2 or ACE2 immunoglobulin is a negative allosteric modulator. In some instances, the SARS-CoV-2 or ACE2 immunoglobulin is a negative allosteric modulator at a concentration of at least or about 0.001, 0.005, 0.01, 0.05, 0.1, 0.5, 1 nM, 2 nM, 4 nM, 6 nM, 8 nM, 10 nM, 20 nM, 30 nM, 40 nM, 50 nM, 60 nM, 70 nM, 80 nM, 90 nM, 100 nM, or more than 100 nM. In some instances, the SARS-CoV-2 or ACE2 immunoglobulin is a negative allosteric modulator at a concentration in a range of about 0.001 to about 100, 0.01 to about 90, about 0.1 to about 80, 1 to about 50, about 10 to about 40 nM, or about 1 to about 10 nM. In some instances, the SARS-CoV-2 or ACE2 immunoglobulin comprises an EC_{50} or IC_{50} of at least or about 0.001, 0.0025, 0.005, 0.01, 0.025, 0.05, 0.06, 0.07, 0.08, 0.9, 0.1, 0.5, 1, 2, 3, 4, 5, 6, or more than 6 nM. In some instances, the SARS-CoV-2 or ACE2 immunoglobulin comprises an EC_{50} or IC_{50} of at least or about 1 nM, 2 nM, 4 nM, 6 nM, 8 nM, 10 nM, 20 nM, 30 nM, 40 nM, 50 nM, 60 nM, 70 nM, 80 nM, 90 nM, 100 nM, or more than 100 nM.

[00128] In some instances, the affinity of the SARS-CoV-2 or ACE2 antibody generated by methods as described herein is at least or about 1.5x, 2.0x, 5x, 10x, 20x, 30x, 40x, 50x, 60x, 70x, 80x, 90x, 100x, 200x, or more than 200x improved binding affinity as compared to a comparator antibody. In some instances, the SARS-CoV-2 or ACE2 antibody generated by methods as described herein is at least or about 1.5x, 2.0x, 5x, 10x, 20x, 30x, 40x, 50x, 60x, 70x, 80x, 90x, 100x, 200x, or more than 200x improved function as compared to a comparator antibody. In some instances, the comparator antibody is an antibody with similar structure, sequence, or antigen target.

[00129] Provided herein are SARS-CoV-2 or ACE2 binding libraries comprising nucleic acids encoding for antibodies comprising SARS-CoV-2 or ACE2 binding domains comprise variation in domain type, domain length, or residue variation. In some instances, the domain is a region in the antibody comprising the SARS-CoV-2 or ACE2 binding domains. For example, the region is the VH, CDRH3, or VL domain. In some instances, the domain is the SARS-CoV-2 or ACE2 binding domain.

[00130] Methods described herein provide for synthesis of a SARS-CoV-2 or ACE2 binding library of nucleic acids each encoding for a predetermined variant of at least one predetermined reference nucleic acid

sequence. In some cases, the predetermined reference sequence is a nucleic acid sequence encoding for a protein, and the variant library comprises sequences encoding for variation of at least a single codon such that a plurality of different variants of a single residue in the subsequent protein encoded by the synthesized nucleic acid are generated by standard translation processes. In some instances, the SARS-CoV-2 or ACE2 binding library comprises varied nucleic acids collectively encoding variations at multiple positions. In some instances, the variant library comprises sequences encoding for variation of at least a single codon of a VH or VL domain. In some instances, the variant library comprises sequences encoding for variation of at least a single codon in a SARS-CoV-2 or ACE2 binding domain. For example, at least one single codon of a SARS-CoV-2 or ACE2 binding domain is varied. In some instances, the variant library comprises sequences encoding for variation of multiple codons of a VH or VL domain. In some instances, the variant library comprises sequences encoding for variation of multiple codons in a SARS-CoV-2 or ACE2 binding domain. An exemplary number of codons for variation include, but are not limited to, at least or about 1, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 225, 250, 275, 300, or more than 300 codons.

[00131] Methods described herein provide for synthesis of a SARS-CoV-2 or ACE2 binding library of nucleic acids each encoding for a predetermined variant of at least one predetermined reference nucleic acid sequence, wherein the SARS-CoV-2 or ACE2 binding library comprises sequences encoding for variation of length of a domain. In some instances, the domain is VH or VL domain. In some instances, the domain is the SARS-CoV-2 or ACE2 binding domain. In some instances, the library comprises sequences encoding for variation of length of at least or about 1, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 225, 250, 275, 300, or more than 300 codons less as compared to a predetermined reference sequence. In some instances, the library comprises sequences encoding for variation of length of at least or about 1, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200, 225, 250, 275, 300, or more than 300 codons more as compared to a predetermined reference sequence.

[00132] Provided herein are SARS-CoV-2 or ACE2 binding libraries comprising nucleic acids encoding for antibodies comprising SARS-CoV-2 or ACE2 binding domains, wherein the SARS-CoV-2 or ACE2 binding libraries are synthesized with various numbers of fragments. In some instances, the fragments comprise the VH or VL domain. In some instances, the SARS-CoV-2 or ACE2 binding libraries are synthesized with at least or about 2 fragments, 3 fragments, 4 fragments, 5 fragments, or more than 5 fragments. The length of each of the nucleic acid fragments or average length of the nucleic acids synthesized may be at least or about 50, 75, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 525, 550, 575, 600, or more than 600 base pairs. In some instances, the length is about 50 to 600, 75 to 575, 100 to 550, 125 to 525, 150 to 500, 175 to 475, 200 to 450, 225 to 425, 250 to 400, 275 to 375, or 300 to 350 base pairs.

[00133] SARS-CoV-2 or ACE2 binding libraries comprising nucleic acids encoding for antibodies comprising SARS-CoV-2 or ACE2 binding domains as described herein comprise various lengths of amino acids when translated. In some instances, the length of each of the amino acid fragments or average length

of the amino acid synthesized may be at least or about 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, or more than 150 amino acids. In some instances, the length of the amino acid is about 15 to 150, 20 to 145, 25 to 140, 30 to 135, 35 to 130, 40 to 125, 45 to 120, 50 to 115, 55 to 110, 60 to 110, 65 to 105, 70 to 100, or 75 to 95 amino acids. In some instances, the length of the amino acid is about 22 to about 75 amino acids.

[00134] SARS-CoV-2 or ACE2 binding libraries comprising de novo synthesized variant sequences encoding for antibodies comprising SARS-CoV-2 or ACE2 binding domains comprise a number of variant sequences. In some instances, a number of variant sequences is de novo synthesized for a CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, CDRL3, VL, VH, or a combination thereof. In some instances, a number of variant sequences is de novo synthesized for framework element 1 (FW1), framework element 2 (FW2), framework element 3 (FW3), or framework element 4 (FW4). In some instances, a number of variant sequences are de novo synthesized for a SARS-CoV-2 or ACE2 binding domain. The number of variant sequences may be at least or about 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, or more than 500 sequences. In some instances, the number of variant sequences is about 10 to 300, 25 to 275, 50 to 250, 75 to 225, 100 to 200, or 125 to 150 sequences.

[00135] SARS-CoV-2 or ACE2 binding libraries comprising de novo synthesized variant sequences encoding for antibodies comprising SARS-CoV-2 or ACE2 binding domains comprise improved diversity. In some instances, variants include affinity maturation variants. Alternatively or in combination, variants include variants in other regions of the antibody including, but not limited to, CDRH1, CDRH2, CDRL1, CDRL2, and CDRL3. In some instances, the number of variants of the SARS-CoV-2 or ACE2 binding libraries is least or about 10^4 , 10^5 , 10^6 , 10^7 , 10^8 , 10^9 , 10^{10} , 10^{11} , 10^{12} , 10^{13} , 10^{14} or more than 10^{14} non-identical sequences.

[00136] Following synthesis of SARS-CoV-2 or ACE2 binding libraries comprising nucleic acids encoding antibodies comprising SARS-CoV-2 or ACE2 binding domains, libraries may be used for screening and analysis. For example, libraries are assayed for library displayability and panning. In some instances, displayability is assayed using a selectable tag. Exemplary tags include, but are not limited to, a radioactive label, a fluorescent label, an enzyme, a chemiluminescent tag, a colorimetric tag, an affinity tag or other labels or tags that are known in the art. In some instances, the tag is histidine, polyhistidine, myc, hemagglutinin (HA), or FLAG. For example, SARS-CoV-2 or ACE2 binding libraries comprise nucleic acids encoding antibodies comprising SARS-CoV-2 or ACE2 binding domains with multiple tags such as GFP, FLAG, and Lucy as well as a DNA barcode. In some instances, libraries are assayed by sequencing using various methods including, but not limited to, single-molecule real-time (SMRT) sequencing, Polony sequencing, sequencing by ligation, reversible terminator sequencing, proton detection sequencing, ion semiconductor sequencing, nanopore sequencing, electronic sequencing, pyrosequencing, Maxam-Gilbert sequencing, chain termination (e.g., Sanger) sequencing, +S sequencing, or sequencing by synthesis.

[00137] As used herein, the term antibody will be understood to include proteins having the characteristic two-armed, Y-shape of a typical antibody molecule as well as one or more fragments of an antibody that retain the ability to specifically bind to an antigen. Exemplary antibodies include, but are not limited to, a monoclonal antibody, a polyclonal antibody, a bi-specific antibody, a multispecific antibody, a grafted antibody, a human antibody, a humanized antibody, a synthetic antibody, a chimeric antibody, a camelized antibody, a single-chain Fvs (scFv) (including fragments in which the VL and VH are joined using recombinant methods by a synthetic or natural linker that enables them to be made as a single protein chain in which the VL and VH regions pair to form monovalent molecules, including single chain Fab and scFab), a single chain antibody, a Fab fragment (including monovalent fragments comprising the VL, VH, CL, and CH1 domains), a F(ab')₂ fragment (including bivalent fragments comprising two Fab fragments linked by a disulfide bridge at the hinge region), a Fd fragment (including fragments comprising the VH and CH1 fragment), a Fv fragment (including fragments comprising the VL and VH domains of a single arm of an antibody), a single-domain antibody (dAb or sdAb) (including fragments comprising a VH domain), an isolated complementarity determining region (CDR), a diabody (including fragments comprising bivalent dimers such as two VL and VH domains bound to each other and recognizing two different antigens), a fragment comprised of only a single monomeric variable domain, disulfide-linked Fvs (sdFv), an intrabody, an anti-idiotypic (anti-Id) antibody, or ab antigen-binding fragments thereof. In some instances, the libraries disclosed herein comprise nucleic acids encoding for an antibody, wherein the antibody is a Fv antibody, including Fv antibodies comprised of the minimum antibody fragment which contains a complete antigen-recognition and antigen-binding site. In some embodiments, the Fv antibody consists of a dimer of one heavy chain and one light chain variable domain in tight, non-covalent association, and the three hypervariable regions of each variable domain interact to define an antigen-binding site on the surface of the VH-VL dimer. In some embodiments, the six hypervariable regions confer antigen-binding specificity to the antibody. In some embodiments, a single variable domain (or half of an Fv comprising only three hypervariable regions specific for an antigen, including single domain antibodies isolated from camelid animals comprising one heavy chain variable domain such as VHH antibodies or nanobodies) has the ability to recognize and bind antigen. In some instances, the libraries disclosed herein comprise nucleic acids encoding for an antibody, wherein the antibody is a single-chain Fv or scFv, including antibody fragments comprising a VH, a VL, or both a VH and VL domain, wherein both domains are present in a single polypeptide chain. In some embodiments, the Fv polypeptide further comprises a polypeptide linker between the VH and VL domains allowing the scFv to form the desired structure for antigen binding. In some instances, a scFv is linked to the Fc fragment or a VHH is linked to the Fc fragment (including minibodies). In some instances, the antibody comprises immunoglobulin molecules and immunologically active fragments of immunoglobulin molecules, e.g., molecules that contain an antigen binding site. Immunoglobulin molecules are of any type (e.g., IgG, IgE, IgM, IgD, IgA and IgY), class (e.g., IgG 1, IgG 2, IgG 3, IgG 4, IgA 1 and IgA 2) or subclass.

[00138] In some embodiments, the antibody is a multivalent antibody. In some embodiments, the antibody is a monovalent, bivalent, or multivalent antibody. In some instances, the antibody is monospecific, bispecific, or multispecific. In some embodiments, the antibody is monovalent monospecific, monovalent bispecific, monovalent multispecific, bivalent monospecific, bivalent bispecific, bivalent multispecific, multivalent monospecific, multivalent bispecific, multivalent multispecific. In some instances, the antibody is homodimeric, heterodimeric, or heterotrimeric.

[00139] In some embodiments, libraries comprise immunoglobulins that are adapted to the species of an intended therapeutic target. Generally, these methods include “mammalization” and comprises methods for transferring donor antigen-binding information to a less immunogenic mammal antibody acceptor to generate useful therapeutic treatments. In some instances, the mammal is mouse, rat, equine, sheep, cow, primate (*e.g.*, chimpanzee, baboon, gorilla, orangutan, monkey), dog, cat, pig, donkey, rabbit, and human. In some instances, provided herein are libraries and methods for felinization and caninization of antibodies.

[00140] “Humanized” forms of non-human antibodies can be chimeric antibodies that contain minimal sequence derived from the non-human antibody. A humanized antibody is generally a human antibody (recipient antibody) in which residues from one or more CDRs are replaced by residues from one or more CDRs of a non-human antibody (donor antibody). The donor antibody can be any suitable non-human antibody, such as a mouse, rat, rabbit, chicken, or non-human primate antibody having a desired specificity, affinity, or biological effect. In some instances, selected framework region residues of the recipient antibody are replaced by the corresponding framework region residues from the donor antibody. Humanized antibodies may also comprise residues that are not found in either the recipient antibody or the donor antibody. In some instances, these modifications are made to further refine antibody performance.

[00141] “Caninization” can comprise a method for transferring non-canine antigen-binding information from a donor antibody to a less immunogenic canine antibody acceptor to generate treatments useful as therapeutics in dogs. In some instances, caninized forms of non-canine antibodies provided herein are chimeric antibodies that contain minimal sequence derived from non-canine antibodies. In some instances, caninized antibodies are canine antibody sequences (“acceptor” or “recipient” antibody) in which hypervariable region residues of the recipient are replaced by hypervariable region residues from a non-canine species (“donor” antibody) such as mouse, rat, rabbit, cat, dogs, goat, chicken, bovine, horse, llama, camel, dromedaries, sharks, non-human primates, human, humanized, recombinant sequence, or an engineered sequence having the desired properties. In some instances, framework region (FR) residues of the canine antibody are replaced by corresponding non-canine FR residues. In some instances, caninized antibodies include residues that are not found in the recipient antibody or in the donor antibody. In some instances, these modifications are made to further refine antibody performance. The caninized antibody may also comprise at least a portion of an immunoglobulin constant region (Fc) of a canine antibody.

[00142] “Felinization” can comprise a method for transferring non-feline antigen-binding information from a donor antibody to a less immunogenic feline antibody acceptor to generate treatments useful as therapeutics in cats. In some instances, felinized forms of non-feline antibodies provided herein are

chimeric antibodies that contain minimal sequence derived from non-feline antibodies. In some instances, felinized antibodies are feline antibody sequences (“acceptor” or “recipient” antibody) in which hypervariable region residues of the recipient are replaced by hypervariable region residues from a non-feline species (“donor” antibody) such as mouse, rat, rabbit, cat, dogs, goat, chicken, bovine, horse, llama, camel, dromedaries, sharks, non-human primates, human, humanized, recombinant sequence, or an engineered sequence having the desired properties. In some instances, framework region (FR) residues of the feline antibody are replaced by corresponding non-feline FR residues. In some instances, felinized antibodies include residues that are not found in the recipient antibody or in the donor antibody. In some instances, these modifications are made to further refine antibody performance. The felinized antibody may also comprise at least a portion of an immunoglobulin constant region (Fc) of a felinized antibody.

[00143] Methods as described herein may be used for optimization of libraries encoding a non-immunoglobulin. In some instances, the libraries comprise antibody mimetics. Exemplary antibody mimetics include, but are not limited to, anticalins, affilins, affibody molecules, affimers, affitins, alphabodies, avimers, atrimers, DARPinS, fynomers, Kunitz domain-based proteins, monobodies, anticalins, knottins, armadillo repeat protein-based proteins, and bicyclic peptides.

[00144] Libraries described herein comprising nucleic acids encoding for an antibody comprise variations in at least one region of the antibody. Exemplary regions of the antibody for variation include, but are not limited to, a complementarity-determining region (CDR), a variable domain, or a constant domain. In some instances, the CDR is CDR1, CDR2, or CDR3. In some instances, the CDR is a heavy domain including, but not limited to, CDRH1, CDRH2, and CDRH3. In some instances, the CDR is a light domain including, but not limited to, CDRL1, CDRL2, and CDRL3. In some instances, the variable domain is variable domain, light chain (VL) or variable domain, heavy chain (VH). In some instances, the VL domain comprises kappa or lambda chains. In some instances, the constant domain is constant domain, light chain (CL) or constant domain, heavy chain (CH).

[00145] Methods described herein provide for synthesis of libraries comprising nucleic acids encoding an antibody, wherein each nucleic acid encodes for a predetermined variant of at least one predetermined reference nucleic acid sequence. In some cases, the predetermined reference sequence is a nucleic acid sequence encoding for a protein, and the variant library comprises sequences encoding for variation of at least a single codon such that a plurality of different variants of a single residue in the subsequent protein encoded by the synthesized nucleic acid are generated by standard translation processes. In some instances, the antibody library comprises varied nucleic acids collectively encoding variations at multiple positions. In some instances, the variant library comprises sequences encoding for variation of at least a single codon of a CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, CDRL3, VL, or VH domain. In some instances, the variant library comprises sequences encoding for variation of multiple codons of a CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, CDRL3, VL, or VH domain. In some instances, the variant library comprises sequences encoding for variation of multiple codons of framework element 1 (FW1), framework element 2 (FW2), framework element 3 (FW3), or framework element 4 (FW4). An exemplary number of codons for

variation include, but are not limited to, at least or about 1, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 225, 250, 275, 300, or more than 300 codons.

[00146] In some instances, the at least one region of the antibody for variation is from heavy chain V-gene family, heavy chain D-gene family, heavy chain J-gene family, light chain V-gene family, or light chain J-gene family. In some instances, the light chain V-gene family comprises immunoglobulin kappa (IGK) gene or immunoglobulin lambda (IGL). Exemplary regions of the antibody for variation include, but are not limited to, IGHV1-18, IGHV1-69, IGHV1-8, IGHV3-21, IGHV3-23, IGHV3-30/33m, IGHV3-28, IGHV1-69, IGHV3-74, IGHV4-39, IGHV4-59/61, IGKV1-39, IGKV1-9, IGKV2-28, IGKV3-11, IGKV3-15, IGKV3-20, IGKV4-1, IGLV1-51, IGLV2-14, IGLV1-40, and IGLV3-1. In some instances, the gene is IGHV1-69, IGHV3-30, IGHV3-23, IGHV3, IGHV1-46, IGHV3-7, IGHV1, or IGHV1-8. In some instances, the gene is IGHV1-69 and IGHV3-30. In some instances, the region of the antibody for variation is IGHJ3, IGHJ6, IGHJ, IGHJ4, IGHJ5, IGHJ2, or IGH1. In some instances, the region of the antibody for variation is IGHJ3, IGHJ6, IGHJ, or IGHJ4. In some instances, the at least one region of the antibody for variation is IGHV1-69, IGHV3-23, IGKV3-20, IGKV1-39, or combinations thereof. In some instances, the at least one region of the antibody for variation is IGHV1-69 and IGKV3-20. In some instances, the at least one region of the antibody for variation is IGHV1-69 and IGKV1-39. In some instances, the at least one region of the antibody for variation is IGHV3-23 and IGKV3-20. In some instances, the at least one region of the antibody for variation is IGHV3-23 and IGKV1-39.

[00147] Provided herein are libraries comprising nucleic acids encoding for antibodies, wherein the libraries are synthesized with various numbers of fragments. In some instances, the fragments comprise the CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, CDRL3, VL, or VH domain. In some instances, the fragments comprise framework element 1 (FW1), framework element 2 (FW2), framework element 3 (FW3), or framework element 4 (FW4). In some instances, the antibody libraries are synthesized with at least or about 2 fragments, 3 fragments, 4 fragments, 5 fragments, or more than 5 fragments. The length of each of the nucleic acid fragments or average length of the nucleic acids synthesized may be at least or about 50, 75, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 525, 550, 575, 600, or more than 600 base pairs. In some instances, the length is about 50 to 600, 75 to 575, 100 to 550, 125 to 525, 150 to 500, 175 to 475, 200 to 450, 225 to 425, 250 to 400, 275 to 375, or 300 to 350 base pairs.

[00148] Libraries comprising nucleic acids encoding for antibodies as described herein comprise various lengths of amino acids when translated. In some instances, the length of each of the amino acid fragments or average length of the amino acid synthesized may be at least or about 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, or more than 150 amino acids. In some instances, the length of the amino acid is about 15 to 150, 20 to 145, 25 to 140, 30 to 135, 35 to 130, 40 to 125, 45 to 120, 50 to 115, 55 to 110, 60 to 110, 65 to 105, 70 to 100, or 75 to 95 amino acids. In some instances, the length of the amino acid is about 22 amino acids to about 75 amino acids. In some instances, the antibodies comprise at least or about 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 2000, 3000, 4000, 5000, or more than 5000 amino acids.

[00149] A number of variant sequences for the at least one region of the antibody for variation are de novo synthesized using methods as described herein. In some instances, a number of variant sequences is de novo synthesized for CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, CDRL3, VL, VH, or combinations thereof. In some instances, a number of variant sequences is de novo synthesized for framework element 1 (FW1), framework element 2 (FW2), framework element 3 (FW3), or framework element 4 (FW4). The number of variant sequences may be at least or about 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, or more than 500 sequences. In some instances, the number of variant sequences is at least or about 500, 600, 700, 800, 900, 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, or more than 8000 sequences. In some instances, the number of variant sequences is about 10 to 500, 25 to 475, 50 to 450, 75 to 425, 100 to 400, 125 to 375, 150 to 350, 175 to 325, 200 to 300, 225 to 375, 250 to 350, or 275 to 325 sequences.

[00150] Variant sequences for the at least one region of the antibody, in some instances, vary in length or sequence. In some instances, the at least one region that is de novo synthesized is for CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, CDRL3, VL, VH, or combinations thereof. In some instances, the at least one region that is de novo synthesized is for framework element 1 (FW1), framework element 2 (FW2), framework element 3 (FW3), or framework element 4 (FW4). In some instances, the variant sequence comprises at least or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50, or more than 50 variant nucleotides or amino acids as compared to wild-type. In some instances, the variant sequence comprises at least or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, or 50 additional nucleotides or amino acids as compared to wild-type. In some instances, the variant sequence comprises at least or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, or 50 less nucleotides or amino acids as compared to wild-type. In some instances, the libraries comprise at least or about 10^1 , 10^2 , 10^3 , 10^4 , 10^5 , 10^6 , 10^7 , 10^8 , 10^9 , 10^{10} , or more than 10^{10} variants.

[00151] Following synthesis of antibody libraries, antibody libraries may be used for screening and analysis. For example, antibody libraries are assayed for library displayability and panning. In some instances, displayability is assayed using a selectable tag. Exemplary tags include, but are not limited to, a radioactive label, a fluorescent label, an enzyme, a chemiluminescent tag, a colorimetric tag, an affinity tag or other labels or tags that are known in the art. In some instances, the tag is histidine, polyhistidine, myc, hemagglutinin (HA), or FLAG. In some instances, antibody libraries are assayed by sequencing using various methods including, but not limited to, single-molecule real-time (SMRT) sequencing, Polony sequencing, sequencing by ligation, reversible terminator sequencing, proton detection sequencing, ion semiconductor sequencing, nanopore sequencing, electronic sequencing, pyrosequencing, Maxam-Gilbert sequencing, chain termination (e.g., Sanger) sequencing, +S sequencing, or sequencing by synthesis. In some instances, antibody libraries are displayed on the surface of a cell or phage. In some instances, antibody libraries are enriched for sequences with a desired activity using phage display.

[00152] In some instances, the antibody libraries are assayed for functional activity, structural stability (e.g., thermal stable or pH stable), expression, specificity, or a combination thereof. In some instances, the

antibody libraries are assayed for antibody capable of folding. In some instances, a region of the antibody is assayed for functional activity, structural stability, expression, specificity, folding, or a combination thereof. For example, a VH region or VL region is assayed for functional activity, structural stability, expression, specificity, folding, or a combination thereof.

[00153] In some instances, the affinity of antibodies or IgGs generated by methods as described herein is at least or about 1.5x, 2.0x, 5x, 10x, 20x, 30x, 40x, 50x, 60x, 70x, 80x, 90x, 100x, 200x, or more than 200x improved binding affinity as compared to a comparator antibody. In some instances, the affinity of antibodies or IgGs generated by methods as described herein is at least or about 1.5x, 2.0x, 5x, 10x, 20x, 30x, 40x, 50x, 60x, 70x, 80x, 90x, 100x, 200x, or more than 200x improved function as compared to a comparator antibody. In some instances, the comparator antibody is an antibody with similar structure, sequence, or antigen target.

[00154] *Expression Systems*

[00155] Provided herein are libraries comprising nucleic acids encoding for antibody comprising binding domains, wherein the libraries have improved specificity, stability, expression, folding, or downstream activity. In some instances, libraries described herein are used for screening and analysis.

[00156] Provided herein are libraries comprising nucleic acids encoding for antibody comprising binding domains, wherein the nucleic acid libraries are used for screening and analysis. In some instances, screening and analysis comprises *in vitro*, *in vivo*, or *ex vivo* assays. Cells for screening include primary cells taken from living subjects or cell lines. Cells may be from prokaryotes (e.g., bacteria and fungi) or eukaryotes (e.g., animals and plants). Exemplary animal cells include, without limitation, those from a mouse, rabbit, primate, and insect. In some instances, cells for screening include a cell line including, but not limited to, Chinese Hamster Ovary (CHO) cell line, human embryonic kidney (HEK) cell line, or baby hamster kidney (BHK) cell line. In some instances, nucleic acid libraries described herein may also be delivered to a multicellular organism. Exemplary multicellular organisms include, without limitation, a plant, a mouse, rabbit, primate, and insect.

[00157] Nucleic acid libraries described herein may be screened for various pharmacological or pharmacokinetic properties. In some instances, the libraries are screened using *in vitro* assays, *in vivo* assays, or *ex vivo* assays. For example, *in vitro* pharmacological or pharmacokinetic properties that are screened include, but are not limited to, binding affinity, binding specificity, and binding avidity. Exemplary *in vivo* pharmacological or pharmacokinetic properties of libraries described herein that are screened include, but are not limited to, therapeutic efficacy, activity, preclinical toxicity properties, clinical efficacy properties, clinical toxicity properties, immunogenicity, potency, and clinical safety properties.

[00158] Provided herein are nucleic acid libraries, wherein the nucleic acid libraries may be expressed in a vector. Expression vectors for inserting nucleic acid libraries disclosed herein may comprise eukaryotic or prokaryotic expression vectors. Exemplary expression vectors include, without limitation, mammalian expression vectors: pSF-CMV-NEO-NH2-PPT-3XFLAG, pSF-CMV-NEO-COOH-3XFLAG, pSF-CMV-PURO-NH2-GST-TEV, pSF-OXB20-COOH-TEV-FLAG(R)-6His, pCEP4 pDEST27, pSF-CMV-Ub-

KrYFP, pSF-CMV-FMDV-daGFP, pEF1a-mCherry-N1 Vector, pEF1a-tdTomato Vector, pSF-CMV-FMDV-Hygro, pSF-CMV-PGK-Puro, pMCP-tag(m), and pSF-CMV-PURO-NH2-CMYC; bacterial expression vectors: pSF-OXB20-BetaGal, pSF-OXB20-Fluc, pSF-OXB20, and pSF-Tac; plant expression vectors: pRI 101-AN DNA and pCambia2301; and yeast expression vectors: pTYB21 and pKLAC2, and insect vectors: pAc5.1/V5-His A and pDEST8. In some instances, the vector is pcDNA3 or pcDNA3.1.

[00159] Described herein are nucleic acid libraries that are expressed in a vector to generate a construct comprising an antibody. In some instances, a size of the construct varies. In some instances, the construct comprises at least or about 500, 600, 700, 800, 900, 1000, 1100, 1300, 1400, 1500, 1600, 1700, 1800, 2000, 2400, 2600, 2800, 3000, 3200, 3400, 3600, 3800, 4000, 4200, 4400, 4600, 4800, 5000, 6000, 7000, 8000, 9000, 10000, or more than 10000 bases. In some instances, a the construct comprises a range of about 300 to 1,000, 300 to 2,000, 300 to 3,000, 300 to 4,000, 300 to 5,000, 300 to 6,000, 300 to 7,000, 300 to 8,000, 300 to 9,000, 300 to 10,000, 1,000 to 2,000, 1,000 to 3,000, 1,000 to 4,000, 1,000 to 5,000, 1,000 to 6,000, 1,000 to 7,000, 1,000 to 8,000, 1,000 to 9,000, 1,000 to 10,000, 2,000 to 3,000, 2,000 to 4,000, 2,000 to 5,000, 2,000 to 6,000, 2,000 to 7,000, 2,000 to 8,000, 2,000 to 9,000, 2,000 to 10,000, 3,000 to 4,000, 3,000 to 5,000, 3,000 to 6,000, 3,000 to 7,000, 3,000 to 8,000, 3,000 to 9,000, 3,000 to 10,000, 4,000 to 5,000, 4,000 to 6,000, 4,000 to 7,000, 4,000 to 8,000, 4,000 to 9,000, 4,000 to 10,000, 5,000 to 6,000, 5,000 to 7,000, 5,000 to 8,000, 5,000 to 9,000, 5,000 to 10,000, 6,000 to 7,000, 6,000 to 8,000, 6,000 to 9,000, 6,000 to 10,000, 7,000 to 8,000, 7,000 to 9,000, 7,000 to 10,000, 8,000 to 9,000, 8,000 to 10,000, or 9,000 to 10,000 bases.

[00160] Provided herein are libraries comprising nucleic acids encoding for antibodies, wherein the nucleic acid libraries are expressed in a cell. In some instances, the libraries are synthesized to express a reporter gene. Exemplary reporter genes include, but are not limited to, acetohydroxyacid synthase (AHAS), alkaline phosphatase (AP), beta galactosidase (LacZ), beta glucuronidase (GUS), chloramphenicol acetyltransferase (CAT), green fluorescent protein (GFP), red fluorescent protein (RFP), yellow fluorescent protein (YFP), cyan fluorescent protein (CFP), cerulean fluorescent protein, citrine fluorescent protein, orange fluorescent protein, cherry fluorescent protein, turquoise fluorescent protein, blue fluorescent protein, horseradish peroxidase (HRP), luciferase (Luc), nopaline synthase (NOS), octopine synthase (OCS), luciferase, and derivatives thereof. Methods to determine modulation of a reporter gene are well known in the art, and include, but are not limited to, fluorometric methods (*e.g.* fluorescence spectroscopy, Fluorescence Activated Cell Sorting (FACS), fluorescence microscopy), and antibiotic resistance determination.

[00161] Diseases and Disorders

[00162] Provided herein are SARS-CoV-2 or ACE2 binding libraries comprising nucleic acids encoding for antibodies comprising SARS-CoV-2 or ACE2 binding domains may have therapeutic effects. In some instances, the SARS-CoV-2 or ACE2 binding libraries result in protein when translated that is used to treat a disease or disorder. In some instances, the protein is an immunoglobulin. In some instances, the protein is a

peptidomimetic. In some instances, the disease or disorder is a viral infection caused by SARS-CoV-2. In some instances, the disease or disorder is a respiratory disease or disorder caused by SARS-CoV-2.

[00163] SARS-CoV-2 or ACE2 variant antibody libraries as described herein may be used to treat SARS-CoV-2. In some embodiments, the SARS-CoV-2 or ACE2 variant antibody libraries are used to treat or prevent symptoms of SARS-CoV-2. These symptoms include, but are not limited to, fever, chills, cough, fatigue, headaches, loss of taste, loss of smell, nausea, vomiting, muscle weakness, sleep difficulties, anxiety, and depression. In some embodiments, the SARS-CoV-2 or ACE2 variant antibody libraries are used to treat a subject who has symptoms for an extended period of time. In some embodiments, the subject has symptoms for an extended period of time after testing negative for SARS-CoV-2. In some embodiments, the subject has symptoms for an extended period of time including at least 1 week, 2 weeks, 3 weeks, 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 1 year, or more than 1 year.

[00164] In some instances, the subject is a mammal. In some instances, the subject is a mouse, rabbit, dog, or human. Subjects treated by methods described herein may be infants, adults, or children. Pharmaceutical compositions comprising antibodies or antibody fragments as described herein may be administered intravenously or subcutaneously. In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a CDRH1 sequence of any one of SEQ ID NOs: 1-50, 779-919, 1344-1523, and 2381-2452. In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a CDRH2 sequence of any one of SEQ ID NOs: 51-100, 920-1061, 1524-1703, and 2453-2524. In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a CDRH3 sequence of any one of SEQ ID NOs: 101-150, 1062-1202, 1704-1883, and 2525-2596. In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a variable domain, heavy chain region (VH) and a variable domain, light chain region (VL), wherein VH comprises complementarity determining regions CDRH1, CDRH2, and CDRH3, wherein VL comprises complementarity determining regions CDRL1, CDRL2, and CDRL3, and wherein (a) an amino acid sequence of CDRH1 is as set forth in any one of SEQ ID NOs: 151-165, 241-255, 331-357, and 547-575; (b) an amino acid sequence of CDRH2 is as set forth in any one of SEQ ID NOs: 166-180, 256-270, 358-384, and 576-604; (c) an amino acid sequence of CDRH3 is as set forth in any one of SEQ ID NOs: 181-195, 271-285, 385-411, and 605-633; (d) an amino acid sequence of CDRL1 is as set forth in any one of SEQ ID NOs: 196-210, 286-300, 412-438, and 634-662; (e) an amino acid sequence of CDRL2 is as set forth in any one of SEQ ID NOs: 211-225, 301-315, 439-465, and 663-691; and (f) an amino acid sequence of CDRL3 is as set forth in any one of SEQ ID NOs: 226-240, 316-330, 466-492, and 692-720. In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a VH comprising at least or about 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to any one of SEQ ID NOs: 493-519 and 721-749, and VL comprising at least or about 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity

to any one of SEQ ID NOs: 520-546 and 750-778. In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a heavy chain variable domain comprising at least or about 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to any one of SEQ ID NOs: 1918-2058, 2599-2778, and 3095-3173.

[00165] SARS-CoV-2 or ACE2 antibodies as described herein may confer immunity after exposure to SARS-CoV-2 or ACE2 antibodies. In some embodiments, the SARS-CoV-2 or ACE2 antibodies described herein are used for passive immunization of a subject. In some instances, the subject is actively immunized after exposure to SARS-CoV-2 or ACE2 antibodies followed by exposure to SARS-CoV-2. In some embodiments, SARS-CoV-2 or ACE2 antibodies are derived from a subject who has recovered from SARS-CoV-2.

[00166] In some embodiments, the immunity occurs at least about 30 minutes, 1 hour, 5 hours, 10 hours, 16 hours, 20 hours, 24 hours, 2 days, 3 days, 4 days, 5 days, 6 days, 1 week, 2 weeks, or more than 2 weeks after exposure to SARS-CoV-2 or ACE2 antibodies. In some instances, the immunity lasts for at least about 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 1 week, 2 weeks, 3 weeks, 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 1 year, 2 years, 3 years, 4 years, 5 years, or more than 5 years after exposure to SARS-CoV-2 or ACE2 antibodies.

[00167] In some embodiments, the subject receives the SARS-CoV-2 or ACE2 antibodies prior to exposure to SARS-CoV-2. In some embodiments, the subject receives the SARS-CoV-2 or ACE2 antibodies at least about 30 minutes, 1 hour, 4 hours, 8 hours, 12 hours, 16 hours, 20 hours, 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 1 week, 2 weeks, 3 weeks, 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 1 year, 2 years, 3 years, 4 years, 5 years, or more than 5 years prior to exposure to SARS-CoV-2. In some embodiments, the subject receives the SARS-CoV-2 or ACE2 antibodies after exposure to SARS-CoV-2. In some embodiments, the subject receives the SARS-CoV-2 or ACE2 antibodies at least about 30 minutes, 1 hour, 4 hours, 8 hours, 12 hours, 16 hours, 20 hours, 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 1 week, 2 weeks, 3 weeks, 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 1 year, 2 years, 3 years, 4 years, 5 years, or more than 5 years after exposure to SARS-CoV-2.

[00168] SARS-CoV-2 or ACE2 antibodies described herein may be administered through various routes. The administration may, depending on the composition being administered, for example, be oral, pulmonary, intravenous, intraperitoneal, intramuscular, intracavity, subcutaneous, or transdermal.

[00169] Described herein are compositions or pharmaceutical compositions comprising SARS-CoV-2 or ACE2 antibodies or antibody fragment thereof that comprise various dosages of the antibodies or antibody fragment. In some instances, the dosage is ranging from about 1 to 25 mg/kg, from about 1 to 50 mg/kg, from about 1 to 80 mg/kg, from about 1 to about 100 mg/kg, from about 5 to about 100 mg/kg, from about 5 to about 80 mg/kg, from about 5 to about 60 mg/kg, from about 5 to about 50 mg/kg or from about 5 to about 500 mg/kg which can be administered in single or multiple doses. In some instances, the dosage is administered in an amount of about 0.01 mg/kg, about 0.05 mg/kg, about 0.10 mg/kg, about 0.25 mg/kg,

about 0.5 mg/kg, about 1 mg/kg, about 5 mg/kg, about 10 mg/kg, about 15 mg/kg, about 20 mg/kg, about 25 mg/kg, about 30 mg/kg, about 35 mg/kg, about 40 mg/kg, about 45 mg/kg, about 50 mg/kg, about 55 mg/kg, about 60 mg/kg, about 65 mg/kg, about 70 mg/kg, about 75 mg/kg, about 80 mg/kg, about 85 mg/kg, about 90 mg/kg, about 95 mg/kg, about 100 mg/kg, about 105 mg/kg, about 110 mg/kg, about 115 mg/kg, about 120, about 125, about 130, about 135, about 140, about 145, about 150, about 155, about 160, about 165, about 170, about 175, about 180, about 185, about 190, about 195, about 200, about 205, about 210, about 215, about 220, about 225, about 230, about 240, about 250, about 260, about 270, about 275, about 280, about 290, about 300, about 310, about 320, about 330, about 340, about 350, about 360 mg/kg, about 370 mg/kg, about 380 mg/kg, about 390 mg/kg, about 400 mg/kg, 410 mg/kg, about 420 mg/kg, about 430 mg/kg, about 440 mg/kg, about 450 mg/kg, about 460 mg/kg, about 470 mg/kg, about 480 mg/kg, about 490 mg/kg, or about 500 mg/kg.

[00170] SARS-CoV-2 or ACE2 antibodies or antibody fragment thereof described herein, in some embodiments, improve disease severity. In some embodiments, the SARS-CoV-2 or ACE2 antibodies or antibody fragment thereof improve disease severity at a dose level of about 0.01 mg/kg, about 0.05 mg/kg, about 0.10 mg/kg, about 0.25 mg/kg, about 0.5 mg/kg, about 1 mg/kg, about 5 mg/kg, about 10 mg/kg, about 15 mg/kg, or about 20 mg/kg. In some embodiments, the SARS-CoV-2 or ACE2 antibodies or antibody fragment thereof improve disease severity at a dose level of about 1 mg/kg, about 5 mg/kg, or about 10 mg/kg. In some embodiments, disease severity is determined by percent weight loss. In some embodiments, the SARS-CoV-2 or ACE2 antibodies or antibody fragment thereof protects against weight loss at a dose level of about 0.01 mg/kg, about 0.05 mg/kg, about 0.10 mg/kg, about 0.25 mg/kg, about 0.5 mg/kg, about 1 mg/kg, about 5 mg/kg, about 10 mg/kg, about 15 mg/kg, or about 20 mg/kg. In some embodiments, the SARS-CoV-2 or ACE2 antibodies or antibody fragment thereof protects against weight loss at a dose level of about 1 mg/kg, about 5 mg/kg, or about 10 mg/kg. In some embodiments, SARS-CoV-2 or ACE2 antibodies or antibody fragment thereof

[00171] Variant Libraries

[00172] *Codon variation*

[00173] Variant nucleic acid libraries described herein may comprise a plurality of nucleic acids, wherein each nucleic acid encodes for a variant codon sequence compared to a reference nucleic acid sequence. In some instances, each nucleic acid of a first nucleic acid population contains a variant at a single variant site. In some instances, the first nucleic acid population contains a plurality of variants at a single variant site such that the first nucleic acid population contains more than one variant at the same variant site. The first nucleic acid population may comprise nucleic acids collectively encoding multiple codon variants at the same variant site. The first nucleic acid population may comprise nucleic acids collectively encoding up to 19 or more codons at the same position. The first nucleic acid population may comprise nucleic acids collectively encoding up to 60 variant triplets at the same position, or the first nucleic acid population may comprise nucleic acids collectively encoding up to 61 different triplets of codons at the

same position. Each variant may encode for a codon that results in a different amino acid during translation.

Table 1 provides a listing of each codon possible (and the representative amino acid) for a variant site.

Table 1. List of codons and amino acids

Amino Acids	One letter code	Three letter code	Codons					
Alanine	A	Ala	GCA	GCC	GCG	GCT		
Cysteine	C	Cys	TGC	TGT				
Aspartic acid	D	Asp	GAC	GAT				
Glutamic acid	E	Glu	GAA	GAG				
Phenylalanine	F	Phe	TTC	TTT				
Glycine	G	Gly	GGA	GGC	GGG	GGT		
Histidine	H	His	CAC	CAT				
Isoleucine	I	Iso	ATA	ATC	ATT			
Lysine	K	Lys	AAA	AAG				
Leucine	L	Leu	TTA	TTG	CTA	CTC	CTG	CTT
Methionine	M	Met	ATG					
Asparagine	N	Asn	AAC	AAT				
Proline	P	Pro	CCA	CCC	CCG	CCT		
Glutamine	Q	Gln	CAA	CAG				
Arginine	R	Arg	AGA	AGG	CGA	CGC	CGG	CGT
Serine	S	Ser	AGC	AGT	TCA	TCC	TCG	TCT
Threonine	T	Thr	ACA	ACC	ACG	ACT		
Valine	V	Val	GTA	GTC	GTG	GTT		
Tryptophan	W	Trp	TGG					
Tyrosine	Y	Tyr	TAC	TAT				

[00174] A nucleic acid population may comprise varied nucleic acids collectively encoding up to 20 codon variations at multiple positions. In such cases, each nucleic acid in the population comprises variation for codons at more than one position in the same nucleic acid. In some instances, each nucleic acid in the population comprises variation for codons at 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more codons in a single nucleic acid. In some instances, each variant long nucleic acid comprises variation for codons at 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more codons in a single long nucleic acid. In some instances, the variant nucleic acid population comprises variation for codons at 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more codons in a single nucleic acid. In some instances, the variant

nucleic acid population comprises variation for codons in at least about 10, 20, 30, 40, 50, 60, 70, 80, 90, 100 or more codons in a single long nucleic acid.

[00175] Highly Parallel Nucleic Acid Synthesis

[00176] Provided herein is a platform approach utilizing miniaturization, parallelization, and vertical integration of the end-to-end process from polynucleotide synthesis to gene assembly within nanowells on silicon to create a revolutionary synthesis platform. Devices described herein provide, with the same footprint as a 96-well plate, a silicon synthesis platform is capable of increasing throughput by a factor of up to 1,000 or more compared to traditional synthesis methods, with production of up to approximately 1,000,000 or more polynucleotides, or 10,000 or more genes in a single highly-parallelized run.

[00177] With the advent of next-generation sequencing, high resolution genomic data has become an important factor for studies that delve into the biological roles of various genes in both normal biology and disease pathogenesis. At the core of this research is the central dogma of molecular biology and the concept of “residue-by-residue transfer of sequential information.” Genomic information encoded in the DNA is transcribed into a message that is then translated into the protein that is the active product within a given biological pathway.

[00178] Another exciting area of study is on the discovery, development and manufacturing of therapeutic molecules focused on a highly-specific cellular target. High diversity DNA sequence libraries are at the core of development pipelines for targeted therapeutics. Gene variants are used to express proteins in a design, build, and test protein engineering cycle that ideally culminates in an optimized gene for high expression of a protein with high affinity for its therapeutic target. As an example, consider the binding pocket of a receptor. The ability to test all sequence permutations of all residues within the binding pocket simultaneously will allow for a thorough exploration, increasing chances of success. Saturation mutagenesis, in which a researcher attempts to generate all possible mutations or variants at a specific site within the receptor, represents one approach to this development challenge. Though costly and time and labor-intensive, it enables each variant to be introduced into each position. In contrast, combinatorial mutagenesis, where a few selected positions or short stretch of DNA may be modified extensively, generates an incomplete repertoire of variants with biased representation.

[00179] To accelerate the drug development pipeline, a library with the desired variants available at the intended frequency in the right position available for testing—in other words, a precision library, enables reduced costs as well as turnaround time for screening. Provided herein are methods for synthesizing nucleic acid synthetic variant libraries which provide for precise introduction of each intended variant at the desired frequency. To the end user, this translates to the ability to not only thoroughly sample sequence space but also be able to query these hypotheses in an efficient manner, reducing cost and screening time. Genome-wide editing can elucidate important pathways, libraries where each variant and sequence permutation can be tested for optimal functionality, and thousands of genes can be used to reconstruct entire pathways and genomes to re-engineer biological systems for drug discovery.

[00180] In a first example, a drug itself can be optimized using methods described herein. For example, to improve a specified function of an antibody, a variant polynucleotide library encoding for a portion of the antibody is designed and synthesized. A variant nucleic acid library for the antibody can then be generated by processes described herein (e.g., PCR mutagenesis followed by insertion into a vector). The antibody is then expressed in a production cell line and screened for enhanced activity. Example screens include examining modulation in binding affinity to an antigen, stability, or effector function (e.g., ADCC, complement, or apoptosis). Exemplary regions to optimize the antibody include, without limitation, the Fc region, Fab region, variable region of the Fab region, constant region of the Fab region, variable domain of the heavy chain or light chain (V_H or V_L), and specific complementarity-determining regions (CDRs) of V_H or V_L .

[00181] Nucleic acid libraries synthesized by methods described herein may be expressed in various cells associated with a disease state. Cells associated with a disease state include cell lines, tissue samples, primary cells from a subject, cultured cells expanded from a subject, or cells in a model system. Exemplary model systems include, without limitation, plant and animal models of a disease state.

[00182] To identify a variant molecule associated with prevention, reduction or treatment of a disease state, a variant nucleic acid library described herein is expressed in a cell associated with a disease state, or one in which a cell a disease state can be induced. In some instances, an agent is used to induce a disease state in cells. Exemplary tools for disease state induction include, without limitation, a Cre/Lox recombination system, LPS inflammation induction, and streptozotocin to induce hypoglycemia. The cells associated with a disease state may be cells from a model system or cultured cells, as well as cells from a subject having a particular disease condition. Exemplary disease conditions include a bacterial, fungal, viral, autoimmune, or proliferative disorder (e.g., cancer). In some instances, the variant nucleic acid library is expressed in the model system, cell line, or primary cells derived from a subject, and screened for changes in at least one cellular activity. Exemplary cellular activities include, without limitation, proliferation, cycle progression, cell death, adhesion, migration, reproduction, cell signaling, energy production, oxygen utilization, metabolic activity, and aging, response to free radical damage, or any combination thereof.

[00183] Substrates

[00184] Devices used as a surface for polynucleotide synthesis may be in the form of substrates which include, without limitation, homogenous array surfaces, patterned array surfaces, channels, beads, gels, and the like. Provided herein are substrates comprising a plurality of clusters, wherein each cluster comprises a plurality of loci that support the attachment and synthesis of polynucleotides. In some instances, substrates comprise a homogenous array surface. For example, the homogenous array surface is a homogenous plate. The term “locus” as used herein refers to a discrete region on a structure which provides support for polynucleotides encoding for a single predetermined sequence to extend from the surface. In some instances, a locus is on a two dimensional surface, e.g., a substantially planar surface. In some instances, a locus is on a three-dimensional surface, e.g., a well, microwell, channel, or post. In some instances, a surface of a locus comprises a material that is actively functionalized to attach to at least one nucleotide for

polynucleotide synthesis, or preferably, a population of identical nucleotides for synthesis of a population of polynucleotides. In some instances, polynucleotide refers to a population of polynucleotides encoding for the same nucleic acid sequence. In some cases, a surface of a substrate is inclusive of one or a plurality of surfaces of a substrate. The average error rates for polynucleotides synthesized within a library described here using the systems and methods provided are often less than 1 in 1000, less than about 1 in 2000, less than about 1 in 3000 or less often without error correction.

[00185] Provided herein are surfaces that support the parallel synthesis of a plurality of polynucleotides having different predetermined sequences at addressable locations on a common support. In some instances, a substrate provides support for the synthesis of more than 50, 100, 200, 400, 600, 800, 1000, 1200, 1400, 1600, 1800, 2,000; 5,000; 10,000; 20,000; 50,000; 100,000; 200,000; 300,000; 400,000; 500,000; 600,000; 700,000; 800,000; 900,000; 1,000,000; 1,200,000; 1,400,000; 1,600,000; 1,800,000; 2,000,000; 2,500,000; 3,000,000; 3,500,000; 4,000,000; 4,500,000; 5,000,000; 10,000,000 or more non-identical polynucleotides. In some cases, the surfaces provide support for the synthesis of more than 50, 100, 200, 400, 600, 800, 1000, 1200, 1400, 1600, 1800, 2,000; 5,000; 10,000; 20,000; 50,000; 100,000; 200,000; 300,000; 400,000; 500,000; 600,000; 700,000; 800,000; 900,000; 1,000,000; 1,200,000; 1,400,000; 1,600,000; 1,800,000; 2,000,000; 2,500,000; 3,000,000; 3,500,000; 4,000,000; 4,500,000; 5,000,000; 10,000,000 or more polynucleotides encoding for distinct sequences. In some instances, at least a portion of the polynucleotides have an identical sequence or are configured to be synthesized with an identical sequence. In some instances, the substrate provides a surface environment for the growth of polynucleotides having at least 80, 90, 100, 120, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500 bases or more.

[00186] Provided herein are methods for polynucleotide synthesis on distinct loci of a substrate, wherein each locus supports the synthesis of a population of polynucleotides. In some cases, each locus supports the synthesis of a population of polynucleotides having a different sequence than a population of polynucleotides grown on another locus. In some instances, each polynucleotide sequence is synthesized with 1, 2, 3, 4, 5, 6, 7, 8, 9 or more redundancy across different loci within the same cluster of loci on a surface for polynucleotide synthesis. In some instances, the loci of a substrate are located within a plurality of clusters. In some instances, a substrate comprises at least 10, 500, 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000, 10000, 11000, 12000, 13000, 14000, 15000, 20000, 30000, 40000, 50000 or more clusters. In some instances, a substrate comprises more than 2,000; 5,000; 10,000; 100,000; 200,000; 300,000; 400,000; 500,000; 600,000; 700,000; 800,000; 900,000; 1,000,000; 1,100,000; 1,200,000; 1,300,000; 1,400,000; 1,500,000; 1,600,000; 1,700,000; 1,800,000; 1,900,000; 2,000,000; 300,000; 400,000; 500,000; 600,000; 700,000; 800,000; 900,000; 1,000,000; 1,200,000; 1,400,000; 1,600,000; 1,800,000; 2,000,000; 2,500,000; 3,000,000; 3,500,000; 4,000,000; 4,500,000; 5,000,000; or 10,000,000 or more distinct loci. In some instances, a substrate comprises about 10,000 distinct loci. The amount of loci within a single cluster is varied in different instances. In some cases, each cluster includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 130, 150, 200, 300, 400, 500 or more loci. In some instances, each cluster includes about 50-500 loci. In some instances, each cluster includes about 100-200 loci. In

some instances, each cluster includes about 100-150 loci. In some instances, each cluster includes about 109, 121, 130 or 137 loci. In some instances, each cluster includes about 19, 20, 61, 64 or more loci.

Alternatively or in combination, polynucleotide synthesis occurs on a homogenous array surface.

[00187] In some instances, the number of distinct polynucleotides synthesized on a substrate is dependent on the number of distinct loci available in the substrate. In some instances, the density of loci within a cluster or surface of a substrate is at least or about 1, 10, 25, 50, 65, 75, 100, 130, 150, 175, 200, 300, 400, 500, 1,000 or more loci per mm^2 . In some cases, a substrate comprises 10-500, 25-400, 50-500, 100-500, 150-500, 10-250, 50-250, 10-200, or 50-200 mm^2 . In some instances, the distance between the centers of two adjacent loci within a cluster or surface is from about 10-500, from about 10-200, or from about 10-100 μm . In some instances, the distance between two centers of adjacent loci is greater than about 10, 20, 30, 40, 50, 60, 70, 80, 90 or 100 μm . In some instances, the distance between the centers of two adjacent loci is less than about 200, 150, 100, 80, 70, 60, 50, 40, 30, 20 or 10 μm . In some instances, each locus has a width of about 0.5, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90 or 100 μm . In some cases, each locus has a width of about 0.5-100, 0.5-50, 10-75, or 0.5-50 μm .

[00188] In some instances, the density of clusters within a substrate is at least or about 1 cluster per 100 mm^2 , 1 cluster per 10 mm^2 , 1 cluster per 5 mm^2 , 1 cluster per 4 mm^2 , 1 cluster per 3 mm^2 , 1 cluster per 2 mm^2 , 1 cluster per 1 mm^2 , 2 clusters per 1 mm^2 , 3 clusters per 1 mm^2 , 4 clusters per 1 mm^2 , 5 clusters per 1 mm^2 , 10 clusters per 1 mm^2 , 50 clusters per 1 mm^2 or more. In some instances, a substrate comprises from about 1 cluster per 10 mm^2 to about 10 clusters per 1 mm^2 . In some instances, the distance between the centers of two adjacent clusters is at least or about 50, 100, 200, 500, 1000, 2000, or 5000 μm . In some cases, the distance between the centers of two adjacent clusters is between about 50-100, 50-200, 50-300, 50-500, and 100-2000 μm . In some cases, the distance between the centers of two adjacent clusters is between about 0.05-50, 0.05-10, 0.05-5, 0.05-4, 0.05-3, 0.05-2, 0.1-10, 0.2-10, 0.3-10, 0.4-10, 0.5-10, 0.5-5, or 0.5-2 mm. In some cases, each cluster has a cross section of about 0.5 to about 2, about 0.5 to about 1, or about 1 to about 2 mm. In some cases, each cluster has a cross section of about 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9 or 2 mm. In some cases, each cluster has an interior cross section of about 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.15, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9 or 2 mm.

[00189] In some instances, a substrate is about the size of a standard 96 well plate, for example between about 100 and about 200 mm by between about 50 and about 150 mm. In some instances, a substrate has a diameter less than or equal to about 1000, 500, 450, 400, 300, 250, 200, 150, 100 or 50 mm. In some instances, the diameter of a substrate is between about 25-1000, 25-800, 25-600, 25-500, 25-400, 25-300, or 25-200 mm. In some instances, a substrate has a planar surface area of at least about 100; 200; 500; 1,000; 2,000; 5,000; 10,000; 12,000; 15,000; 20,000; 30,000; 40,000; 50,000 mm^2 or more. In some instances, the thickness of a substrate is between about 50- 2000, 50- 1000, 100-1000, 200-1000, or 250-1000 mm.

[00190] *Surface materials*

[00191] Substrates, devices, and reactors provided herein are fabricated from any variety of materials suitable for the methods, compositions, and systems described herein. In certain instances, substrate

materials are fabricated to exhibit a low level of nucleotide binding. In some instances, substrate materials are modified to generate distinct surfaces that exhibit a high level of nucleotide binding. In some instances, substrate materials are transparent to visible and/or UV light. In some instances, substrate materials are sufficiently conductive, *e.g.*, are able to form uniform electric fields across all or a portion of a substrate. In some instances, conductive materials are connected to an electric ground. In some instances, the substrate is heat conductive or insulated. In some instances, the materials are chemical resistant and heat resistant to support chemical or biochemical reactions, for example polynucleotide synthesis reaction processes. In some instances, a substrate comprises flexible materials. For flexible materials, materials can include, without limitation: nylon, both modified and unmodified, nitrocellulose, polypropylene, and the like. In some instances, a substrate comprises rigid materials. For rigid materials, materials can include, without limitation: glass; fused silica; silicon, plastics (for example polytetrafluoroethylene, polypropylene, polystyrene, polycarbonate, and blends thereof, and the like); metals (for example, gold, platinum, and the like). The substrate, solid support or reactors can be fabricated from a material selected from the group consisting of silicon, polystyrene, agarose, dextran, cellulosic polymers, polyacrylamides, polydimethylsiloxane (PDMS), and glass. The substrates/solid supports or the microstructures, reactors therein may be manufactured with a combination of materials listed herein or any other suitable material known in the art.

[00192] Surface Architecture

[00193] Provided herein are substrates for the methods, compositions, and systems described herein, wherein the substrates have a surface architecture suitable for the methods, compositions, and systems described herein. In some instances, a substrate comprises raised and/or lowered features. One benefit of having such features is an increase in surface area to support polynucleotide synthesis. In some instances, a substrate having raised and/or lowered features is referred to as a three-dimensional substrate. In some cases, a three-dimensional substrate comprises one or more channels. In some cases, one or more loci comprise a channel. In some cases, the channels are accessible to reagent deposition via a deposition device such as a material deposition device. In some cases, reagents and/or fluids collect in a larger well in fluid communication one or more channels. For example, a substrate comprises a plurality of channels corresponding to a plurality of loci with a cluster, and the plurality of channels are in fluid communication with one well of the cluster. In some methods, a library of polynucleotides is synthesized in a plurality of loci of a cluster.

[00194] Provided herein are substrates for the methods, compositions, and systems described herein, wherein the substrates are configured for polynucleotide synthesis. In some instances, the structure is configured to allow for controlled flow and mass transfer paths for polynucleotide synthesis on a surface. In some instances, the configuration of a substrate allows for the controlled and even distribution of mass transfer paths, chemical exposure times, and/or wash efficacy during polynucleotide synthesis. In some instances, the configuration of a substrate allows for increased sweep efficiency, for example by providing sufficient volume for a growing polynucleotide such that the excluded volume by the growing

polynucleotide does not take up more than 50, 45, 40, 35, 30, 25, 20, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, 1%, or less of the initially available volume that is available or suitable for growing the polynucleotide.

In some instances, a three-dimensional structure allows for managed flow of fluid to allow for the rapid exchange of chemical exposure.

[00195] Provided herein are substrates for the methods, compositions, and systems described herein, wherein the substrates comprise structures suitable for the methods, compositions, and systems described herein. In some instances, segregation is achieved by physical structure. In some instances, segregation is achieved by differential functionalization of the surface generating active and passive regions for polynucleotide synthesis. In some instances, differential functionalization is achieved by alternating the hydrophobicity across the substrate surface, thereby creating water contact angle effects that cause beading or wetting of the deposited reagents. Employing larger structures can decrease splashing and cross-contamination of distinct polynucleotide synthesis locations with reagents of the neighboring spots. In some cases, a device, such as a material deposition device, is used to deposit reagents to distinct polynucleotide synthesis locations. Substrates having three-dimensional features are configured in a manner that allows for the synthesis of a large number of polynucleotides (*e.g.*, more than about 10,000) with a low error rate (*e.g.*, less than about 1:500, 1:1000, 1:1500, 1:2,000, 1:3,000, 1:5,000, or 1:10,000). In some cases, a substrate comprises features with a density of about or greater than about 1, 5, 10, 20, 30, 40, 50, 60, 70, 80, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 300, 400 or 500 features per mm².

[00196] A well of a substrate may have the same or different width, height, and/or volume as another well of the substrate. A channel of a substrate may have the same or different width, height, and/or volume as another channel of the substrate. In some instances, the diameter of a cluster or the diameter of a well comprising a cluster, or both, is between about 0.05-50, 0.05-10, 0.05-5, 0.05-4, 0.05-3, 0.05-2, 0.05-1, 0.05-0.5, 0.05-0.1, 0.1-10, 0.2-10, 0.3-10, 0.4-10, 0.5-10, 0.5-5, or 0.5-2 mm. In some instances, the diameter of a cluster or well or both is less than or about 5, 4, 3, 2, 1, 0.5, 0.1, 0.09, 0.08, 0.07, 0.06, or 0.05 mm. In some instances, the diameter of a cluster or well or both is between about 1.0 and 1.3 mm. In some instances, the diameter of a cluster or well, or both is about 1.150 mm. In some instances, the diameter of a cluster or well, or both is about 0.08 mm. The diameter of a cluster refers to clusters within a two-dimensional or three-dimensional substrate.

[00197] In some instances, the height of a well is from about 20-1000, 50-1000, 100-1000, 200-1000, 300-1000, 400-1000, or 500-1000 μm . In some cases, the height of a well is less than about 1000, 900, 800, 700, or 600 μm .

[00198] In some instances, a substrate comprises a plurality of channels corresponding to a plurality of loci within a cluster, wherein the height or depth of a channel is 5-500, 5-400, 5-300, 5-200, 5-100, 5-50, or 10-50 μm . In some cases, the height of a channel is less than 100, 80, 60, 40, or 20 μm .

[00199] In some instances, the diameter of a channel, locus (*e.g.*, in a substantially planar substrate) or both channel and locus (*e.g.*, in a three-dimensional substrate wherein a locus corresponds to a channel) is from about 1-1000, 1-500, 1-200, 1-100, 5-100, or 10-100 μm , for example, about 90, 80, 70, 60, 50, 40, 30,

20 or 10 μm . In some instances, the diameter of a channel, locus, or both channel and locus is less than about 100, 90, 80, 70, 60, 50, 40, 30, 20 or 10 μm . In some instances, the distance between the center of two adjacent channels, loci, or channels and loci is from about 1-500, 1-200, 1-100, 5-200, 5-100, 5-50, or 5-30, for example, about 20 μm .

[00200] Surface Modifications

[00201] Provided herein are methods for polynucleotide synthesis on a surface, wherein the surface comprises various surface modifications. In some instances, the surface modifications are employed for the chemical and/or physical alteration of a surface by an additive or subtractive process to change one or more chemical and/or physical properties of a substrate surface or a selected site or region of a substrate surface. For example, surface modifications include, without limitation, (1) changing the wetting properties of a surface, (2) functionalizing a surface, i.e., providing, modifying or substituting surface functional groups, (3) defunctionalizing a surface, i.e., removing surface functional groups, (4) otherwise altering the chemical composition of a surface, *e.g.*, through etching, (5) increasing or decreasing surface roughness, (6) providing a coating on a surface, *e.g.*, a coating that exhibits wetting properties that are different from the wetting properties of the surface, and/or (7) depositing particulates on a surface.

[00202] In some cases, the addition of a chemical layer on top of a surface (referred to as adhesion promoter) facilitates structured patterning of loci on a surface of a substrate. Exemplary surfaces for application of adhesion promotion include, without limitation, glass, silicon, silicon dioxide and silicon nitride. In some cases, the adhesion promoter is a chemical with a high surface energy. In some instances, a second chemical layer is deposited on a surface of a substrate. In some cases, the second chemical layer has a low surface energy. In some cases, surface energy of a chemical layer coated on a surface supports localization of droplets on the surface. Depending on the patterning arrangement selected, the proximity of loci and/or area of fluid contact at the loci are alterable.

[00203] In some instances, a substrate surface, or resolved loci, onto which nucleic acids or other moieties are deposited, *e.g.*, for polynucleotide synthesis, are smooth or substantially planar (*e.g.*, two-dimensional) or have irregularities, such as raised or lowered features (*e.g.*, three-dimensional features). In some instances, a substrate surface is modified with one or more different layers of compounds. Such modification layers of interest include, without limitation, inorganic and organic layers such as metals, metal oxides, polymers, small organic molecules and the like.

[00204] In some instances, resolved loci of a substrate are functionalized with one or more moieties that increase and/or decrease surface energy. In some cases, a moiety is chemically inert. In some cases, a moiety is configured to support a desired chemical reaction, for example, one or more processes in a polynucleotide synthesis reaction. The surface energy, or hydrophobicity, of a surface is a factor for determining the affinity of a nucleotide to attach onto the surface. In some instances, a method for substrate functionalization comprises: (a) providing a substrate having a surface that comprises silicon dioxide; and (b) silanizing the surface using, a suitable silanizing agent described herein or otherwise known in the art,

for example, an organofunctional alkoxysilane molecule. Methods and functionalizing agents are described in U.S. Patent No. 5474796, which is herein incorporated by reference in its entirety.

[00205] In some instances, a substrate surface is functionalized by contact with a derivatizing composition that contains a mixture of silanes, under reaction conditions effective to couple the silanes to the substrate surface, typically via reactive hydrophilic moieties present on the substrate surface. Silanization generally covers a surface through self-assembly with organofunctional alkoxysilane molecules. A variety of siloxane functionalizing reagents can further be used as currently known in the art, *e.g.*, for lowering or increasing surface energy. The organofunctional alkoxysilanes are classified according to their organic functions.

[00206] Polynucleotide Synthesis

[00207] Methods of the current disclosure for polynucleotide synthesis may include processes involving phosphoramidite chemistry. In some instances, polynucleotide synthesis comprises coupling a base with phosphoramidite. Polynucleotide synthesis may comprise coupling a base by deposition of phosphoramidite under coupling conditions, wherein the same base is optionally deposited with phosphoramidite more than once, *i.e.*, double coupling. Polynucleotide synthesis may comprise capping of unreacted sites. In some instances, capping is optional. Polynucleotide synthesis may also comprise oxidation or an oxidation step or oxidation steps. Polynucleotide synthesis may comprise deblocking, detritylation, and sulfurization. In some instances, polynucleotide synthesis comprises either oxidation or sulfurization. In some instances, between one or each step during a polynucleotide synthesis reaction, the device is washed, for example, using tetrazole or acetonitrile. Time frames for any one step in a phosphoramidite synthesis method may be less than about 2 min, 1 min, 50 sec, 40 sec, 30 sec, 20 sec and 10 sec.

[00208] Polynucleotide synthesis using a phosphoramidite method may comprise a subsequent addition of a phosphoramidite building block (*e.g.*, nucleoside phosphoramidite) to a growing polynucleotide chain for the formation of a phosphite triester linkage. Phosphoramidite polynucleotide synthesis proceeds in the 3' to 5' direction. Phosphoramidite polynucleotide synthesis allows for the controlled addition of one nucleotide to a growing nucleic acid chain per synthesis cycle. In some instances, each synthesis cycle comprises a coupling step. Phosphoramidite coupling involves the formation of a phosphite triester linkage between an activated nucleoside phosphoramidite and a nucleoside bound to the substrate, for example, via a linker. In some instances, the nucleoside phosphoramidite is provided to the device activated. In some instances, the nucleoside phosphoramidite is provided to the device with an activator. In some instances, nucleoside phosphoramidites are provided to the device in a 1.5, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100-fold excess or more over the substrate-bound nucleosides. In some instances, the addition of nucleoside phosphoramidite is performed in an anhydrous environment, for example, in anhydrous acetonitrile. Following addition of a nucleoside phosphoramidite, the device is optionally washed. In some instances, the coupling step is repeated one or more additional times, optionally with a wash step between nucleoside phosphoramidite additions to the substrate. In some instances, a polynucleotide synthesis method used herein comprises 1, 2, 3 or more sequential coupling

steps. Prior to coupling, in many cases, the nucleoside bound to the device is de-protected by removal of a protecting group, where the protecting group functions to prevent polymerization. A common protecting group is 4,4'-dimethoxytrityl (DMT).

[00209] Following coupling, phosphoramidite polynucleotide synthesis methods optionally comprise a capping step. In a capping step, the growing polynucleotide is treated with a capping agent. A capping step is useful to block unreacted substrate-bound 5'-OH groups after coupling from further chain elongation, preventing the formation of polynucleotides with internal base deletions. Further, phosphoramidites activated with 1H-tetrazole may react, to a small extent, with the O6 position of guanosine. Without being bound by theory, upon oxidation with I₂/water, this side product, possibly via O6-N7 migration, may undergo depurination. The apurinic sites may end up being cleaved in the course of the final deprotection of the polynucleotide thus reducing the yield of the full-length product. The O6 modifications may be removed by treatment with the capping reagent prior to oxidation with I₂/water. In some instances, inclusion of a capping step during polynucleotide synthesis decreases the error rate as compared to synthesis without capping. As an example, the capping step comprises treating the substrate-bound polynucleotide with a mixture of acetic anhydride and 1-methylimidazole. Following a capping step, the device is optionally washed.

[00210] In some instances, following addition of a nucleoside phosphoramidite, and optionally after capping and one or more wash steps, the device bound growing nucleic acid is oxidized. The oxidation step comprises the phosphite triester is oxidized into a tetracoordinated phosphate triester, a protected precursor of the naturally occurring phosphate diester internucleoside linkage. In some instances, oxidation of the growing polynucleotide is achieved by treatment with iodine and water, optionally in the presence of a weak base (*e.g.*, pyridine, lutidine, collidine). Oxidation may be carried out under anhydrous conditions using, *e.g.* tert-Butyl hydroperoxide or (1S)-(+)-(10-camphorsulfonyl)-oxaziridine (CSO). In some methods, a capping step is performed following oxidation. A second capping step allows for device drying, as residual water from oxidation that may persist can inhibit subsequent coupling. Following oxidation, the device and growing polynucleotide is optionally washed. In some instances, the step of oxidation is substituted with a sulfurization step to obtain polynucleotide phosphorothioates, wherein any capping steps can be performed after the sulfurization. Many reagents are capable of the efficient sulfur transfer, including but not limited to 3-(Dimethylaminomethylidene)amino)-3H-1,2,4-dithiazole-3-thione, DDTT, 3H-1,2-benzodithiol-3-one 1,1-dioxide, also known as Beaucage reagent, and N,N,N',N'-Tetraethylthiuram disulfide (TETD).

[00211] In order for a subsequent cycle of nucleoside incorporation to occur through coupling, the protected 5' end of the device bound growing polynucleotide is removed so that the primary hydroxyl group is reactive with a next nucleoside phosphoramidite. In some instances, the protecting group is DMT and deblocking occurs with trichloroacetic acid in dichloromethane. Conducting detritylation for an extended time or with stronger than recommended solutions of acids may lead to increased depurination of solid support-bound polynucleotide and thus reduces the yield of the desired full-length product. Methods and compositions of the disclosure described herein provide for controlled deblocking conditions limiting

undesired depurination reactions. In some instances, the device bound polynucleotide is washed after deblocking. In some instances, efficient washing after deblocking contributes to synthesized polynucleotides having a low error rate.

[00212] Methods for the synthesis of polynucleotides typically involve an iterating sequence of the following steps: application of a protected monomer to an actively functionalized surface (*e.g.*, locus) to link with either the activated surface, a linker or with a previously deprotected monomer; deprotection of the applied monomer so that it is reactive with a subsequently applied protected monomer; and application of another protected monomer for linking. One or more intermediate steps include oxidation or sulfurization. In some instances, one or more wash steps precede or follow one or all of the steps.

[00213] Methods for phosphoramidite-based polynucleotide synthesis comprise a series of chemical steps. In some instances, one or more steps of a synthesis method involve reagent cycling, where one or more steps of the method comprise application to the device of a reagent useful for the step. For example, reagents are cycled by a series of liquid deposition and vacuum drying steps. For substrates comprising three-dimensional features such as wells, microwells, channels and the like, reagents are optionally passed through one or more regions of the device via the wells and/or channels.

[00214] Methods and systems described herein relate to polynucleotide synthesis devices for the synthesis of polynucleotides. The synthesis may be in parallel. For example, at least or about at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 1000, 10000, 50000, 75000, 100000 or more polynucleotides can be synthesized in parallel. The total number polynucleotides that may be synthesized in parallel may be from 2-100000, 3-50000, 4-10000, 5-1000, 6-900, 7-850, 8-800, 9-750, 10-700, 11-650, 12-600, 13-550, 14-500, 15-450, 16-400, 17-350, 18-300, 19-250, 20-200, 21-150, 22-100, 23-50, 24-45, 25-40, 30-35. Those of skill in the art appreciate that the total number of polynucleotides synthesized in parallel may fall within any range bound by any of these values, for example 25-100. The total number of polynucleotides synthesized in parallel may fall within any range defined by any of the values serving as endpoints of the range. Total molar mass of polynucleotides synthesized within the device or the molar mass of each of the polynucleotides may be at least or at least about 10, 20, 30, 40, 50, 100, 250, 500, 750, 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000, 10000, 25000, 50000, 75000, 100000 picomoles, or more. The length of each of the polynucleotides or average length of the polynucleotides within the device may be at least or about at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 100, 150, 200, 300, 400, 500 nucleotides, or more. The length of each of the polynucleotides or average length of the polynucleotides within the device may be at most or about at most 500, 400, 300, 200, 150, 100, 50, 45, 35, 30, 25, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10 nucleotides, or less. The length of each of the polynucleotides or average length of the polynucleotides within the device may fall from 10-500, 9-400, 11-300, 12-200, 13-150, 14-100, 15-50, 16-45, 17-40, 18-35, 19-25. Those of skill in the art appreciate that the length of each of the polynucleotides or average length of the polynucleotides within the device may fall within any range bound by any of these values, for example 100-300. The length of each of the polynucleotides or average length of

the polynucleotides within the device may fall within any range defined by any of the values serving as endpoints of the range.

[00215] Methods for polynucleotide synthesis on a surface provided herein allow for synthesis at a fast rate. As an example, at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 70, 80, 90, 100, 125, 150, 175, 200 nucleotides per hour, or more are synthesized. Nucleotides include adenine, guanine, thymine, cytosine, uridine building blocks, or analogs/modified versions thereof. In some instances, libraries of polynucleotides are synthesized in parallel on substrate. For example, a device comprising about or at least about 100; 1,000; 10,000; 30,000; 75,000; 100,000; 1,000,000; 2,000,000; 3,000,000; 4,000,000; or 5,000,000 resolved loci is able to support the synthesis of at least the same number of distinct polynucleotides, wherein polynucleotide encoding a distinct sequence is synthesized on a resolved locus. In some instances, a library of polynucleotides is synthesized on a device with low error rates described herein in less than about three months, two months, one month, three weeks, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2 days, 24 hours or less. In some instances, larger nucleic acids assembled from a polynucleotide library synthesized with low error rate using the substrates and methods described herein are prepared in less than about three months, two months, one month, three weeks, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2 days, 24 hours or less.

[00216] In some instances, methods described herein provide for generation of a library of nucleic acids comprising variant nucleic acids differing at a plurality of codon sites. In some instances, a nucleic acid may have 1 site, 2 sites, 3 sites, 4 sites, 5 sites, 6 sites, 7 sites, 8 sites, 9 sites, 10 sites, 11 sites, 12 sites, 13 sites, 14 sites, 15 sites, 16 sites, 17 sites 18 sites, 19 sites, 20 sites, 30 sites, 40 sites, 50 sites, or more of variant codon sites.

[00217] In some instances, the one or more sites of variant codon sites may be adjacent. In some instances, the one or more sites of variant codon sites may not be adjacent and separated by 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more codons.

[00218] In some instances, a nucleic acid may comprise multiple sites of variant codon sites, wherein all the variant codon sites are adjacent to one another, forming a stretch of variant codon sites. In some instances, a nucleic acid may comprise multiple sites of variant codon sites, wherein none the variant codon sites are adjacent to one another. In some instances, a nucleic acid may comprise multiple sites of variant codon sites, wherein some the variant codon sites are adjacent to one another, forming a stretch of variant codon sites, and some of the variant codon sites are not adjacent to one another.

[00219] Referring to the Figures, **FIG. 2** illustrates an exemplary process workflow for synthesis of nucleic acids (e.g., genes) from shorter nucleic acids. The workflow is divided generally into phases: (1) de novo synthesis of a single stranded nucleic acid library, (2) joining nucleic acids to form larger fragments, (3) error correction, (4) quality control, and (5) shipment. Prior to de novo synthesis, an intended nucleic acid sequence or group of nucleic acid sequences is preselected. For example, a group of genes is preselected for generation.

[00220] Once large nucleic acids for generation are selected, a predetermined library of nucleic acids is designed for de novo synthesis. Various suitable methods are known for generating high density polynucleotide arrays. In the workflow example, a device surface layer is provided. In the example, chemistry of the surface is altered in order to improve the polynucleotide synthesis process. Areas of low surface energy are generated to repel liquid while areas of high surface energy are generated to attract liquids. The surface itself may be in the form of a planar surface or contain variations in shape, such as protrusions or microwells which increase surface area. In the workflow example, high surface energy molecules selected serve a dual function of supporting DNA chemistry, as disclosed in International Patent Application Publication WO/2015/021080, which is herein incorporated by reference in its entirety.

[00221] In situ preparation of polynucleotide arrays is generated on a solid support and utilizes single nucleotide extension process to extend multiple oligomers in parallel. A deposition device, such as a material deposition device **201**, is designed to release reagents in a step wise fashion such that multiple polynucleotides extend, in parallel, one residue at a time to generate oligomers with a predetermined nucleic acid sequence **202**. In some instances, polynucleotides are cleaved from the surface at this stage. Cleavage includes gas cleavage, *e.g.*, with ammonia or methylamine.

[00222] The generated polynucleotide libraries are placed in a reaction chamber. In this exemplary workflow, the reaction chamber (also referred to as “nanoreactor”) is a silicon coated well, containing PCR reagents and lowered onto the polynucleotide library **203**. Prior to or after the sealing **204** of the polynucleotides, a reagent is added to release the polynucleotides from the substrate. In the exemplary workflow, the polynucleotides are released subsequent to sealing of the nanoreactor **205**. Once released, fragments of single stranded polynucleotides hybridize in order to span an entire long range sequence of DNA. Partial hybridization **205** is possible because each synthesized polynucleotide is designed to have a small portion overlapping with at least one other polynucleotide in the pool.

[00223] After hybridization, a PCA reaction is commenced. During the polymerase cycles, the polynucleotides anneal to complementary fragments and gaps are filled in by a polymerase. Each cycle increases the length of various fragments randomly depending on which polynucleotides find each other. Complementarity amongst the fragments allows for forming a complete large span of double stranded DNA **206**.

[00224] After PCA is complete, the nanoreactor is separated from the device **207** and positioned for interaction with a device having primers for PCR **208**. After sealing, the nanoreactor is subject to PCR **209** and the larger nucleic acids are amplified. After PCR **210**, the nanochamber is opened **211**, error correction reagents are added **212**, the chamber is sealed **213** and an error correction reaction occurs to remove mismatched base pairs and/or strands with poor complementarity from the double stranded PCR amplification products **214**. The nanoreactor is opened and separated **215**. Error corrected product is next subject to additional processing steps, such as PCR and molecular bar coding, and then packaged **222** for shipment **223**.

[00225] In some instances, quality control measures are taken. After error correction, quality control steps include for example interaction with a wafer having sequencing primers for amplification of the error corrected product **216**, sealing the wafer to a chamber containing error corrected amplification product **217**, and performing an additional round of amplification **218**. The nanoreactor is opened **219** and the products are pooled **220** and sequenced **221**. After an acceptable quality control determination is made, the packaged product **222** is approved for shipment **223**.

[00226] In some instances, a nucleic acid generate by a workflow such as that in **FIG. 2** is subject to mutagenesis using overlapping primers disclosed herein. In some instances, a library of primers are generated by in situ preparation on a solid support and utilize single nucleotide extension process to extend multiple oligomers in parallel. A deposition device, such as a material deposition device, is designed to release reagents in a step wise fashion such that multiple polynucleotides extend, in parallel, one residue at a time to generate oligomers with a predetermined nucleic acid sequence **202**.

[00227] Computer systems

[00228] Any of the systems described herein, may be operably linked to a computer and may be automated through a computer either locally or remotely. In various instances, the methods and systems of the disclosure may further comprise software programs on computer systems and use thereof. Accordingly, computerized control for the synchronization of the dispense/vacuum/refill functions such as orchestrating and synchronizing the material deposition device movement, dispense action and vacuum actuation are within the bounds of the disclosure. The computer systems may be programmed to interface between the user specified base sequence and the position of a material deposition device to deliver the correct reagents to specified regions of the substrate.

[00229] The computer system **300** illustrated in **FIG. 3** may be understood as a logical apparatus that can read instructions from media **311** and/or a network port **305**, which can optionally be connected to server **309** having fixed media **312**. The system, such as shown in **FIG. 3** can include a CPU **301**, disk drives **303**, optional input devices such as keyboard **315** and/or mouse **316** and optional monitor **307**. Data communication can be achieved through the indicated communication medium to a server at a local or a remote location. The communication medium can include any means of transmitting and/or receiving data. For example, the communication medium can be a network connection, a wireless connection or an internet connection. Such a connection can provide for communication over the World Wide Web. It is envisioned that data relating to the present disclosure can be transmitted over such networks or connections for reception and/or review by a party **322** as illustrated in **FIG. 3**.

[00230] **FIG. 4** is a block diagram illustrating a first example architecture of a computer system **400** that can be used in connection with example instances of the present disclosure. As depicted in **FIG. 4**, the example computer system can include a processor **402** for processing instructions. Non-limiting examples of processors include: Intel Xeon™ processor, AMD Opteron™ processor, Samsung 32-bit RISC ARM 1176JZ(F)-S v1.0™ processor, ARM Cortex-A8 Samsung S5PC100™ processor, ARM Cortex-A8 Apple A4™ processor, Marvell PXA 930™ processor, or a functionally-equivalent processor. Multiple threads

of execution can be used for parallel processing. In some instances, multiple processors or processors with multiple cores can also be used, whether in a single computer system, in a cluster, or distributed across systems over a network comprising a plurality of computers, cell phones, and/or personal data assistant devices.

[00231] As illustrated in FIG. 4, a high speed cache 404 can be connected to, or incorporated in, the processor 402 to provide a high speed memory for instructions or data that have been recently, or are frequently, used by processor 402. The processor 402 is connected to a north bridge 406 by a processor bus 408. The north bridge 406 is connected to random access memory (RAM) 410 by a memory bus 412 and manages access to the RAM 410 by the processor 402. The north bridge 406 is also connected to a south bridge 414 by a chipset bus 416. The south bridge 414 is, in turn, connected to a peripheral bus 418. The peripheral bus can be, for example, PCI, PCI-X, PCI Express, or other peripheral bus. The north bridge and south bridge are often referred to as a processor chipset and manage data transfer between the processor, RAM, and peripheral components on the peripheral bus 418. In some alternative architectures, the functionality of the north bridge can be incorporated into the processor instead of using a separate north bridge chip. In some instances, system 400 can include an accelerator card 422 attached to the peripheral bus 418. The accelerator can include field programmable gate arrays (FPGAs) or other hardware for accelerating certain processing. For example, an accelerator can be used for adaptive data restructuring or to evaluate algebraic expressions used in extended set processing.

[00232] Software and data are stored in external storage 424 and can be loaded into RAM 410 and/or cache 404 for use by the processor. The system 400 includes an operating system for managing system resources; non-limiting examples of operating systems include: Linux, Windows™, MACOS™, BlackBerry OST™, iOS™, and other functionally-equivalent operating systems, as well as application software running on top of the operating system for managing data storage and optimization in accordance with example instances of the present disclosure. In this example, system 400 also includes network interface cards (NICs) 420 and 421 connected to the peripheral bus for providing network interfaces to external storage, such as Network Attached Storage (NAS) and other computer systems that can be used for distributed parallel processing.

[00233] FIG. 5 is a diagram showing a network 500 with a plurality of computer systems 502a, and 502b, a plurality of cell phones and personal data assistants 502c, and Network Attached Storage (NAS) 504a, and 504b. In example instances, systems 502a, 502b, and 502c can manage data storage and optimize data access for data stored in Network Attached Storage (NAS) 504a and 504b. A mathematical model can be used for the data and be evaluated using distributed parallel processing across computer systems 502a, and 502b, and cell phone and personal data assistant systems 502c. Computer systems 502a, and 502b, and cell phone and personal data assistant systems 502c can also provide parallel processing for adaptive data restructuring of the data stored in Network Attached Storage (NAS) 504a and 504b. FIG. 5 illustrates an example only, and a wide variety of other computer architectures and systems can be used in conjunction with the various instances of the present disclosure. For example, a blade server can be used to provide parallel processing. Processor blades can be connected through a back plane to provide parallel processing.

Storage can also be connected to the back plane or as Network Attached Storage (NAS) through a separate network interface. In some example instances, processors can maintain separate memory spaces and transmit data through network interfaces, back plane or other connectors for parallel processing by other processors. In other instances, some or all of the processors can use a shared virtual address memory space.

[00234] FIG. 6 is a block diagram of a multiprocessor computer system using a shared virtual address memory space in accordance with an example instance. The system includes a plurality of processors 602a-f that can access a shared memory subsystem 604. The system incorporates a plurality of programmable hardware memory algorithm processors (MAPs) 606a-f in the memory subsystem 604. Each MAP 606a-f can comprise a memory 608a-f and one or more field programmable gate arrays (FPGAs) 610a-f. The MAP provides a configurable functional unit and particular algorithms or portions of algorithms can be provided to the FPGAs 610a-f for processing in close coordination with a respective processor. For example, the MAPs can be used to evaluate algebraic expressions regarding the data model and to perform adaptive data restructuring in example instances. In this example, each MAP is globally accessible by all of the processors for these purposes. In one configuration, each MAP can use Direct Memory Access (DMA) to access an associated memory 608a-f, allowing it to execute tasks independently of, and asynchronously from the respective microprocessor 602a-f. In this configuration, a MAP can feed results directly to another MAP for pipelining and parallel execution of algorithms.

[00235] The above computer architectures and systems are examples only, and a wide variety of other computer, cell phone, and personal data assistant architectures and systems can be used in connection with example instances, including systems using any combination of general processors, co-processors, FPGAs and other programmable logic devices, system on chips (SOCs), application specific integrated circuits (ASICs), and other processing and logic elements. In some instances, all or part of the computer system can be implemented in software or hardware. Any variety of data storage media can be used in connection with example instances, including random access memory, hard drives, flash memory, tape drives, disk arrays, Network Attached Storage (NAS) and other local or distributed data storage devices and systems.

[00236] In example instances, the computer system can be implemented using software modules executing on any of the above or other computer architectures and systems. In other instances, the functions of the system can be implemented partially or completely in firmware, programmable logic devices such as field programmable gate arrays (FPGAs) as referenced in FIG. 4, system on chips (SOCs), application specific integrated circuits (ASICs), or other processing and logic elements. For example, the Set Processor and Optimizer can be implemented with hardware acceleration through the use of a hardware accelerator card, such as accelerator card 422 illustrated in FIG. 4.

[00237] The following examples are set forth to illustrate more clearly the principle and practice of embodiments disclosed herein to those skilled in the art and are not to be construed as limiting the scope of any claimed embodiments. Unless otherwise stated, all parts and percentages are on a weight basis.

EXAMPLES

[00238] The following examples are given for the purpose of illustrating various embodiments of the disclosure and are not meant to limit the present disclosure in any fashion. The present examples, along with the methods described herein are presently representative of preferred embodiments, are exemplary, and are not intended as limitations on the scope of the disclosure. Changes therein and other uses which are encompassed within the spirit of the disclosure as defined by the scope of the claims will occur to those skilled in the art.

[00239] Example 1: Functionalization of a device surface

[00240] A device was functionalized to support the attachment and synthesis of a library of polynucleotides. The device surface was first wet cleaned using a piranha solution comprising 90% H₂SO₄ and 10% H₂O₂ for 20 minutes. The device was rinsed in several beakers with DI water, held under a DI water gooseneck faucet for 5 min, and dried with N₂. The device was subsequently soaked in NH₄OH (1:100; 3 mL:300 mL) for 5 min, rinsed with DI water using a handgun, soaked in three successive beakers with DI water for 1 min each, and then rinsed again with DI water using the handgun. The device was then plasma cleaned by exposing the device surface to O₂. A SAMCO PC-300 instrument was used to plasma etch O₂ at 250 watts for 1 min in downstream mode.

[00241] The cleaned device surface was actively functionalized with a solution comprising N-(3-triethoxysilylpropyl)-4-hydroxybutyramide using a YES-1224P vapor deposition oven system with the following parameters: 0.5 to 1 torr, 60 min, 70 °C, 135 °C vaporizer. The device surface was resist coated using a Brewer Science 200X spin coater. SPR™ 3612 photoresist was spin coated on the device at 2500 rpm for 40 sec. The device was pre-baked for 30 min at 90 °C on a Brewer hot plate. The device was subjected to photolithography using a Karl Suss MA6 mask aligner instrument. The device was exposed for 2.2 sec and developed for 1 min in MSF 26A. Remaining developer was rinsed with the handgun and the device soaked in water for 5 min. The device was baked for 30 min at 100 °C in the oven, followed by visual inspection for lithography defects using a Nikon L200. A descum process was used to remove residual resist using the SAMCO PC-300 instrument to O₂ plasma etch at 250 watts for 1 min.

[00242] The device surface was passively functionalized with a 100 µL solution of perfluorooctyltrichlorosilane mixed with 10 µL light mineral oil. The device was placed in a chamber, pumped for 10 min, and then the valve was closed to the pump and left to stand for 10 min. The chamber was vented to air. The device was resist stripped by performing two soaks for 5 min in 500 mL NMP at 70 °C with ultrasonication at maximum power (9 on Crest system). The device was then soaked for 5 min in 500 mL isopropanol at room temperature with ultrasonication at maximum power. The device was dipped in 300 mL of 200 proof ethanol and blown dry with N₂. The functionalized surface was activated to serve as a support for polynucleotide synthesis.

[00243] Example 2: Synthesis of a 50-mer sequence on an oligonucleotide synthesis device

[00244] A two dimensional oligonucleotide synthesis device was assembled into a flowcell, which was connected to a flowcell (Applied Biosystems (ABI394 DNA Synthesizer)). The two-dimensional oligonucleotide synthesis device was uniformly functionalized with N-(3-TRIETHOXSILYLPROPYL)-4-

HYDROXYBUTYRAMIDE (Gelest) was used to synthesize an exemplary polynucleotide of 50 bp ("50-mer polynucleotide") using polynucleotide synthesis methods described herein.

[00245] The sequence of the 50-mer was as described.

5'AGACAATCAACCATTTGGGGTGGACAGCCTTGACCTCTAGACTTCGGCAT##TTTTTTTTTT3', where # denotes Thymidine-succinyl hexamide CED phosphoramidite (CLP-2244 from ChemGenes), which is a cleavable linker enabling the release of oligos from the surface during deprotection.

[00246] The synthesis was done using standard DNA synthesis chemistry (coupling, capping, oxidation, and deblocking) according to the protocol in **Table 2** and an ABI synthesizer.

Table 2: Synthesis protocols

Table 2		
General DNA Synthesis Process Name	Process Step	Time (sec)
WASH (Acetonitrile Wash Flow)	Acetonitrile System Flush	4
	Acetonitrile to Flowcell	23
	N2 System Flush	4
	Acetonitrile System Flush	4
DNA BASE ADDITION (Phosphoramidite + Activator Flow)	Activator Manifold Flush	2
	Activator to Flowcell	6
	Activator + Phosphoramidite to Flowcell	6
	Activator to Flowcell	0.5
	Activator + Phosphoramidite to Flowcell	5
	Activator to Flowcell	0.5
	Activator + Phosphoramidite to Flowcell	5
	Activator to Flowcell	0.5
	Activator + Phosphoramidite to Flowcell	5
	Incubate for 25sec	25
WASH (Acetonitrile Wash Flow)	Acetonitrile System Flush	4
	Acetonitrile to Flowcell	15
	N2 System Flush	4
	Acetonitrile System Flush	4
DNA BASE ADDITION (Phosphoramidite + Activator Flow)	Activator Manifold Flush	2
	Activator to Flowcell	5
	Activator + Phosphoramidite to Flowcell	18
	Incubate for 25sec	25
WASH (Acetonitrile Wash Flow)	Acetonitrile System Flush	4
	Acetonitrile to Flowcell	15
	N2 System Flush	4
	Acetonitrile System Flush	4
CAPPING (CapA+B, 1:1, Flow)	CapA+B to Flowcell	15
WASH (Acetonitrile Wash Flow)	Acetonitrile System Flush	4
	Acetonitrile to Flowcell	15
	Acetonitrile System Flush	4
OXIDATION (Oxidizer Flow)	Oxidizer to Flowcell	18

General DNA Synthesis Process Name	Table 2	
	Process Step	Time (sec)
WASH (Acetonitrile Wash Flow)	Acetonitrile System Flush	4
	N2 System Flush	4
	Acetonitrile System Flush	4
	Acetonitrile to Flowcell	15
	Acetonitrile System Flush	4
	Acetonitrile to Flowcell	15
	N2 System Flush	4
	Acetonitrile System Flush	4
	Acetonitrile to Flowcell	23
	N2 System Flush	4
	Acetonitrile System Flush	4
DEBLOCKING (Deblock Flow)	Deblock to Flowcell	36
WASH (Acetonitrile Wash Flow)	Acetonitrile System Flush	4
	N2 System Flush	4
	Acetonitrile System Flush	4
	Acetonitrile to Flowcell	18
	N2 System Flush	4.13
	Acetonitrile System Flush	4.13
	Acetonitrile to Flowcell	15

[00247] The phosphoramidite/activator combination was delivered similar to the delivery of bulk reagents through the flowcell. No drying steps were performed as the environment stays "wet" with reagent the entire time.

[00248] The flow restrictor was removed from the ABI 394 synthesizer to enable faster flow. Without flow restrictor, flow rates for amidites (0.1M in ACN), Activator, (0.25M Benzoylthiotetrazole ("BTT"; 30-3070-xx from GlenResearch) in ACN), and Ox (0.02M I2 in 20% pyridine, 10% water, and 70% THF) were roughly ~100uL/sec, for acetonitrile ("ACN") and capping reagents (1:1 mix of CapA and CapB, wherein CapA is acetic anhydride in THF/Pyridine and CapB is 16% 1-methylimidazole in THF), roughly ~200uL/sec, and for Deblock (3% dichloroacetic acid in toluene), roughly ~300uL/sec (compared to ~50uL/sec for all reagents with flow restrictor). The time to completely push out Oxidizer was observed, the timing for chemical flow times was adjusted accordingly and an extra ACN wash was introduced between different chemicals. After polynucleotide synthesis, the chip was deprotected in gaseous ammonia overnight at 75 psi. Five drops of water were applied to the surface to recover polynucleotides. The recovered polynucleotides were then analyzed on a BioAnalyzer small RNA chip.

[00249] Example 3: Synthesis of a 100-mer sequence on an oligonucleotide synthesis device

[00250] The same process as described in Example 2 for the synthesis of the 50-mer sequence was used for the synthesis of a 100-mer polynucleotide ("100-mer polynucleotide"; 5'

CGGGATCCTTATCGTCATCGTCGTACAGATCCCGACCCATTTGCTGTCCACCAGTCATGCTAGC
CATAACCATGATGATGATGATGATGAGAACCCCGCAT##TTTTTTTTTTT3', where # denotes

Thymidine-succinyl hexamide CED phosphoramidite (CLP-2244 from ChemGenes) on two different silicon

chips, the first one uniformly functionalized with N-(3-TRIETHOXYSILYLPROPYL)-4-HYDROXYBUTYRAMIDE and the second one functionalized with 5/95 mix of 11-acetoxyundecyltriethoxysilane and n-decyltriethoxysilane, and the polynucleotides extracted from the surface were analyzed on a BioAnalyzer instrument.

[00251] All ten samples from the two chips were further PCR amplified using a forward (5'ATGCGGGGTTCTCATCATC3') and a reverse (5'CGGGATCCTTATCGTCATCG3') primer in a 50uL PCR mix (25uL NEB Q5 mastermix, 2.5uL 10uM Forward primer, 2.5uL 10uM Reverse primer, 1uL polynucleotide extracted from the surface, and water up to 50uL) using the following thermalcycling program:

98 °C, 30 sec

98 °C, 10 sec; 63 °C, 10 sec; 72 °C, 10 sec; repeat 12 cycles

72 °C, 2min

[00252] The PCR products were also run on a BioAnalyzer, demonstrating sharp peaks at the 100-mer position. Next, the PCR amplified samples were cloned, and Sanger sequenced. **Table 3** summarizes the results from the Sanger sequencing for samples taken from spots 1-5 from chip 1 and for samples taken from spots 6-10 from chip 2.

Table 3: Sequencing results

Spot	Error rate	Cycle efficiency
1	1/763 bp	99.87%
2	1/824 bp	99.88%
3	1/780 bp	99.87%
4	1/429 bp	99.77%
5	1/1525 bp	99.93%
6	1/1615 bp	99.94%
7	1/531 bp	99.81%
8	1/1769 bp	99.94%
9	1/854 bp	99.88%
10	1/1451 bp	99.93%

[00253] Thus, the high quality and uniformity of the synthesized polynucleotides were repeated on two chips with different surface chemistries. Overall, 89% of the 100-mers that were sequenced were perfect sequences with no errors, corresponding to 233 out of 262.

[00254] **Table 4** summarizes error characteristics for the sequences obtained from the polynucleotides samples from spots 1-10.

Table 4: Error characteristics

Sample ID/Spot no.	OSA_00 46/1	OSA_00 47/2	OSA_00 48/3	OSA_00 49/4	OSA_00 50/5	OSA_00 51/6	OSA_00 52/7	OSA_00 53/8	OSA_00 54/9	OSA_00 55/10
Total	32	32	32	32	32	32	32	32	32	32

Sequences										
Sequencing Quality	25 of 28	27 of 27	26 of 30	21 of 23	25 of 26	29 of 30	27 of 31	29 of 31	28 of 29	25 of 28
Oligo Quality	23 of 25	25 of 27	22 of 26	18 of 21	24 of 25	25 of 29	22 of 27	28 of 29	26 of 28	20 of 25
ROI Match Count	2500	2698	2561	2122	2499	2666	2625	2899	2798	2348
ROI Mutation	2	2	1	3	1	0	2	1	2	1
ROI Multi Base Deletion	0	0	0	0	0	0	0	0	0	0
ROI Small Insertion	1	0	0	0	0	0	0	0	0	0
ROI Single Base Deletion	0	0	0	0	0	0	0	0	0	0
Large Deletion Count	0	0	1	0	0	1	1	0	0	0
Mutation: G>A	2	2	1	2	1	0	2	1	2	1
Mutation: T>C	0	0	0	1	0	0	0	0	0	0
ROI Error Count	3	2	2	3	1	1	3	1	2	1
ROI Error Rate	Err: ~1 in 834	Err: ~1 in 1350	Err: ~1 in 1282	Err: ~1 in 708	Err: ~1 in 2500	Err: ~1 in 2667	Err: ~1 in 876	Err: ~1 in 2900	Err: ~1 in 1400	Err: ~1 in 2349
ROI Minus Primer Error Rate	MP Err: ~1 in 763	MP Err: ~1 in 824	MP Err: ~1 in 780	MP Err: ~1 in 429	MP Err: ~1 in 1525	MP Err: ~1 in 1615	MP Err: ~1 in 531	MP Err: ~1 in 1769	MP Err: ~1 in 854	MP Err: ~1 in 1451

[00255] Example 4: Panning and screening for identification of antibodies for SARS-CoV-2 and ACE2

[00256] This example describes identification of antibodies for SARS-CoV-2 and ACE2.

[00257] Phage displayed scFv, VHH, and Fab libraries were panned for binding to biotinylated SARS-CoV-2 S1 and human ACE2. **FIG. 7** shows a schema of the panning strategy. Biotinylated antigen was bound to streptavidin coated magnetic beads at a density of 100 pmol antigen per mg of beads (Thermo Fisher #11206D). Phage libraries were blocked with 5% BSA in PBS. Following magnetic bead depletion for 1 hour at room temperature (RT), the beads were removed, and phage supernatant was transferred to 1 mg of antigen-bound beads in 1 ml PBS and incubated at RT with rotation for 1 hour. Non-binding clones were washed away by addition of 1 ml PBST, increasing the number of washes with each panning round. Trypsin was used to elute the phage bound to the antigen-bead complex. Phage were amplified in TG1 *E. coli* for the next round of selection. This selection strategy was repeated for four rounds, with successively lower amounts of antigen per round. Following all four selection rounds, 400 clones from each of round 2, 3, and 4 were selected for phage expression and phage ELISA screening. Data from the panning is seen in **Table 5**.

Table 5. Panning Data

Antibody	Titer	Round 1	Round 2	Round 3	Round 4	Round 5
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1	Input titer	1.5×10^{12}	1.2×10^{13}	4.4×10^{13}	1.8×10^{13}	-
	Output titer	1.2×10^6	1.5×10^6	2.0×10^6	1.4×10^8	-
2	Input titer	1.4×10^{12}	2.6×10^{13}	3.0×10^{13}	1.0×10^{13}	-
	Output titer	9.5×10^5	1.2×10^6	2.2×10^6	1.2×10^8	-
3	Input titer	1.7×10^{12}	2.0×10^{13}	2.8×10^{13}	3.2×10^{13}	-
	Output titer	1.5×10^5	1.7×10^6	1.5×10^6	1.1×10^8	-
4	Input titer	1.2×10^{12}	1.6×10^{13}	3.6×10^{13}	1.5×10^{13}	-
	Output titer	1.3×10^5	2.2×10^7	2.6×10^7	2.5×10^8	-

[00258] To test for binding to SARS-CoV-2 S1 and ACE2, phage were expressed from each picked colony by KO7 superinfection in 384 well microtiter plates. Phage containing supernatant was blocked by 1:1 addition of 4% non-fat milk (NFM). Assay plates were prepared by passive immobilization of 0.4 μ g antigen in 384-well Maxisorp plates (Thermo Fisher #464718) and then blocked with 4% NFM. Following 3x wash in PBST, blocked phage supernatant was incubated for 1 hour at RT. After 3x wash in PBST, 0.3 μ g/ml anti-M13-HRP (Sino Biological #11973-MM05T-H) was aliquoted for 1 hour incubation at room temperature. Binding of phage-displayed antibody was determined by absorbance at 450 nm with 3,3',5,5'-tetramethylbenzidine (Thermo Fisher #34029). Phage that bound to antigen with 3x over background of human Fc protein were identified as potential binders for sequencing analysis. DNA was amplified by rolling circle amplification from glycerol stocks of each clone and submitted for Sanger sequencing (Genewiz) to capture the VH and VL domains. **FIGS. 8A-8D** shows phage ELISA data from round 4 of SARS-CoV-2 S1 (subunit 1) protein panning for antibody 1 (**FIG. 8A-8B**) and antibody 2 (**FIG. 8C-8D**). **FIGS. 9A-9D** shows phage ELISA data from round 4 of ACE2 protein panning for antibody 3 (**FIG. 9A-9B**) and antibody 4 (**FIG. 9C-9D**).

[00259] SARS-CoV-2 variants were tested for specificity using a phage ELISA as described above. The antigens used included Acro COVID S1 (S1N-C82E8), COVID S1 RBD Fc fusion (Antigen 1), and COVID S1 RBM Fc fusion (Antigen 2). Data from the phage ELISA is seen in **Table 6A**. **Table 6A** shows screening ELISA mean, fold over background (column A), specificity ELISA, fold over background (column B), and specificity ELISA, percent binding relative to binding to Acro S1 (column C). As seen in **Table 6A**, nearly all receptor binding domain (RBD) specific clones show good binding to full length subunit 1 (S1) and produced S1 RBD Fc. None of the S1 RBD variants were found to bind to S1 RBM Fc.

Table 6A. SARS-CoV-2 Phage ELISA

	Column A	Column B				Column C		
Variant	ELISA (Avg)	Acro S1	S1-RBD-Fc	S1-Fc	S1-RBM-Fc	S1-RBD-Fc	S1-Fc	S1-RBM-Fc

1-21	47.6	19.5	14.8	1.4	1.4	75.7%	7.2%	7.0%
1-22	40.6	32.7	26.5	2.5	1.5	81.2%	7.6%	4.7%
1-30	29.5	16.8	1.7	5.6	1.4	9.8%	33.3%	8.5%
1-35	28.6	21.6	1.8	1.4	1.6	8.2%	6.5%	7.3%
1-17	27.4	25.1	20.1	1.6	1.3	79.8%	6.2%	5.2%
1-27	27.2	1.5	1.9	1.3	1.6	124.5%	84.8%	108.8%
1-37	27.0	11.6	2.0	5.4	1.4	17.7%	46.7%	12.3%
1-12	25.7	1.7	1.7	1.3	1.7	104.0%	79.6%	102.5%
1-2	24.2	1.8	1.9	1.7	1.7	103.3%	95.4%	93.5%
1-3	23.9	1.6	1.8	1.5	1.5	109.3%	91.2%	91.9%
1-23	23.1	5.1	3.6	1.6	1.6	70.9%	31.1%	32.0%
1-7	22.5	6.8	3.3	1.7	1.6	48.7%	24.8%	23.0%
1-31	20.7	30.4	1.3	15.7	1.2	4.3%	51.6%	3.8%
1-4	20.6	1.0	1.4	0.9	1.1	137.5%	90.8%	105.3%
1-38	20.2	1.1	1.5	0.9	1.2	127.9%	82.8%	100.9%
1-8	19.3	12.0	11.2	1.1	1.2	92.9%	8.8%	10.3%
1-9	18.5	10.7	9.8	0.9	1.0	91.1%	8.7%	9.3%
1-32	17.9	11.5	1.5	4.0	1.1	13.1%	35.3%	9.5%
1-33	17.6	7.1	1.5	3.0	1.0	21.1%	42.1%	14.6%
1-24	32.9	12.9	11.0	1.1	1.3	85.4%	8.9%	10.3%
1-39	24.4	18.6	11.6	2.5	1.3	62.5%	13.2%	6.7%
1-40	22.9	18.7	14.3	1.3	1.1	76.7%	7.1%	6.0%
1-5	20.6	1.5	1.6	1.2	1.4	107.8%	82.9%	92.0%
1-41	18.1	4.5	2.7	1.3	1.2	58.8%	28.9%	26.3%
1-28	17.7	1.0	1.1	1.1	1.2	112.9%	109.7%	124.1%
1-10	16.9	17.4	17.4	1.3	1.1	100.5%	7.3%	6.2%
2-1	45.3	39.3	36.8	20.2	1.5	93.7%	51.3%	3.9%
2-10	43.8	38.9	39.9	9.4	1.2	102.7%	24.1%	3.1%
2-5	30.8	38.3	35.9	24.3	1.1	93.7%	63.3%	3.0%
2-2	23.4	39.4	39.6	4.7	1.1	100.4%	12.0%	2.8%
3-10	17.4	1.2	1.2	1.2	1.1	97.2%	99.6%	93.3%
1-26	19.5	1.4	1.1	1.3	1.0	76.8%	98.0%	74.7%
1-42	34.5	22.7	20.8	1.4	1.0	91.4%	6.4%	4.2%
1-13	28.2	4.8	4.3	0.9	1.2	89.3%	18.4%	24.2%
1-43	21.9	6.7	5.8	3.9	1.0	87.3%	58.3%	14.5%

1-44	24.6	10.4	8.2	1.0	0.8	78.6%	9.6%	7.6%
1-14	21.7	16.8	13.5	1.1	0.9	80.6%	6.7%	5.4%
1-6	20.8	1.8	1.3	1.1	0.8	69.6%	60.5%	45.4%
1-45	24.0	12.1	10.3	1.2	1.0	85.3%	9.6%	8.3%
1-46	21.7	4.6	3.1	1.1	0.9	66.6%	24.5%	19.8%
1-20	26.0	5.7	3.9	1.0	0.8	67.3%	17.0%	14.5%
1-47	22.6	8.1	5.5	1.2	0.9	68.9%	14.6%	11.1%
1-29	23.8	1.1	0.9	1.0	0.9	81.4%	94.0%	78.3%
1-1	32.5	4.5	4.0	1.6	1.1	90.7%	35.3%	24.5%
1-19	22.3	24.2	23.9	1.5	1.2	98.7%	6.4%	4.9%
1-16	22.1	3.4	3.1	1.0	0.9	89.7%	29.5%	27.3%
1-34	28.7	7.5	3.1	1.8	1.0	41.3%	24.5%	13.3%
1-48	22.6	2.5	2.1	0.8	0.8	84.7%	31.5%	30.3%
1-49	27.6	1.0	1.0	0.8	0.8	99.3%	85.6%	78.8%
1-18	22.7	9.8	7.0	1.1	0.8	71.0%	11.0%	8.0%
1-11	33.2	4.8	4.8	0.9	1.0	99.5%	18.7%	20.6%
1-50	21.1	13.9	12.4	1.2	0.8	88.9%	8.8%	5.9%
1-25	27.9	3.6	2.7	1.0	0.8	75.4%	28.1%	22.3%
1-36	23.6	10.1	1.2	1.1	0.8	11.5%	10.6%	8.4%
1-15	24.8	2.5	1.4	1.0	0.8	55.4%	41.5%	32.1%
2-4	15.5	37.7	38.8	7.2	1.2	102.7%	19.0%	3.1%
2-6	22.1	11.1	12.8	1.8	1.1	115.8%	16.4%	9.5%
2-11	28.1	1.1	1.0	1.2	0.9	86.3%	103.4%	76.1%
2-12	18.2	39.8	40.3	14.7	1.1	101.3%	37.0%	2.9%
2-13	19.1	27.3	32.1	3.7	0.9	117.5%	13.4%	3.1%
2-14	17.2	31.7	32.9	4.2	0.9	103.9%	13.3%	2.8%
2-7	25.3	37.2	37.3	7.7	0.9	100.3%	20.6%	2.4%
2-8	32.4	35.9	36.5	5.4	1.1	101.8%	15.0%	3.1%
2-15	13.7	31.0	28.1	3.8	0.9	90.6%	12.4%	3.0%
2-9	14.1	24.1	24.3	3.0	0.8	100.7%	12.2%	3.5%

[00260] Tables 6B-6C show Carterra SPR kinetics for SARS-CoV-2 variant antibodies ranked by off-rate (Table 6B) and by K_D (Table 6C). Tables 6D-6E show Carterra SPR kinetics for ACE2 variant antibodies ranked by off-rate (Table 6D) and by K_D (Table 6E). FIG. 10 shows that ACE2 binds to S1-RBD-Fc and S1-Fc variants.

Table 6B. SARS-CoV-2 Carterra SPR Kinetics Ranked by Off-Rate

IgG	Acro S1	S1-RBD-Fc	S1-Fc	S1-RBM-Fc	ka (M-1 s-1)	K _D (s-1)
2-10	38.9	39.9	9.4	1.2	2.08E+05	1.15E-04
2-5	38.3	35.9	24.3	1.1	9.39E+04	2.59E-04
1-31	30.4	1.3	15.7	1.2	2.05E+04	7.62E-04
2-2	39.4	39.6	4.7	1.1	7.74E+04	9.06E-04
1-13	4.8	4.3	0.9	1.2	2.17E+05	1.38E-03
1-30	16.8	1.7	5.6	1.4	4.39E+04	1.64E-03
1-29	1.1	0.9	1.0	0.9	5.35E+02	1.97E-03
1-27	1.5	1.9	1.3	1.6	2.27E+05	2.85E-03
1-35	21.6	1.8	1.4	1.6	5.90E+04	5.43E-03
1-36	10.1	1.2	1.1	0.8	1.14E+05	7.85E-03
1-67	18.6	11.6	2.5	1.3	7.36E+04	8.86E-03
1-2	1.8	1.9	1.7	1.7	1.58E+03	2.72E-02
1-5	1.5	1.6	1.2	1.4	2.15E+03	5.40E-02
1-68	6.7	5.8	3.9	1.0	2.46E+06	8.75E-02
1-69	1.1	1.5	0.9	1.2	3.08E+05	1.23E-01
1-4	1.0	1.4	0.9	1.1	4.20E+04	1.24E-01
1-12	1.7	1.7	1.3	1.7	3.59E+05	1.34E-01
1-11	4.8	4.8	0.9	1.0	5.92E+05	1.43E-01
1-10	17.4	17.4	1.3	1.1	1.04E+06	1.47E-01
1-7	4.5	2.7	1.3	1.2	2.09E+05	1.55E-01
1-15	2.5	1.4	1.0	0.8	4.49E+05	1.56E-01
1-25	3.6	2.7	1.0	0.8	1.98E+06	1.56E-01
1-23	5.1	3.6	1.6	1.6	5.06E+05	1.59E-01
1-7	6.8	3.3	1.7	1.6	1.34E+06	1.70E-01
1-47	8.1	5.5	1.2	0.9	6.32E+03	2.40E-01
1-3	1.6	1.8	1.5	1.5	1.42E+06	3.04E-01
1-32	11.5	1.5	4.0	1.1	5.49E+06	3.17E-01
1-20	5.7	3.9	1.0	0.8	5.17E+02	6.95E-01
1-28	1.0	1.1	1.1	1.2	1.23E+08	9.05E+00
1-48	2.5	2.1	0.8	0.8	5.56E+07	9.11E+00
1-24	12.9	11.0	1.1	1.3	1.94E+08	1.46E+01
1-6	1.8	1.3	1.1	0.8	4.49E+08	2.08E+01
1-17	25.1	20.1	1.6	1.3	3.92E+08	2.63E+01
1-49	1.0	1.0	0.8	0.8	6.00E+08	3.22E+01

1-71	11.6	2.0	5.4	1.4	3.69E+08	4.03E+01
1-42	22.7	20.8	1.4	1.0	9.10E+08	1.03E+02

Table 6C. SARS-CoV-2 Carterra SPR Kinetics Ranked by K_D

IgG	Acro S1	S1-RBD-Fc	S1-Fc	S1-RBM-Fc	k_a (M ⁻¹ s ⁻¹)	k_d (s ⁻¹)	K_D (nM)	Rmax (RU)
2-10	38.9	39.9	9.4	1.2	2.08E+05	1.15E-04	0.6	20
2-5	38.3	35.9	24.3	1.1	9.39E+04	2.59E-04	2.8	39
1-13	4.8	4.3	0.9	1.2	2.17E+05	1.38E-03	6.4	23
2-2	39.4	39.6	4.7	1.1	7.74E+04	9.06E-04	11.7	131
1-27	1.5	1.9	1.3	1.6	2.27E+05	2.85E-03	12.5	39
1-68	6.7	5.8	3.9	1.0	2.46E+06	8.75E-02	35.6	73
1-30	16.8	1.7	5.6	1.4	4.39E+04	1.64E-03	37.2	98
1-31	30.4	1.3	15.7	1.2	2.05E+04	7.62E-04	37.2	256
1-6	1.8	1.3	1.1	0.8	4.49E+08	2.08E+01	46.3	87
1-49	1.0	1.0	0.8	0.8	6.00E+08	3.22E+01	53.6	72
1-32	11.5	1.5	4.0	1.1	5.49E+06	3.17E-01	57.8	112
1-17	25.1	20.1	1.6	1.3	3.92E+08	2.63E+01	67.1	46
1-36	10.1	1.2	1.1	0.8	1.14E+05	7.85E-03	68.9	150
1-28	1.0	1.1	1.1	1.2	1.23E+08	9.05E+00	73.5	58
1-24	12.9	11.0	1.1	1.3	1.94E+08	1.46E+01	75.5	48
1-25	3.6	2.7	1.0	0.8	1.98E+06	1.56E-01	78.9	46
1-35	21.6	1.8	1.4	1.6	5.90E+04	5.43E-03	91.9	341
1-71	11.6	2.0	5.4	1.4	3.69E+08	4.03E+01	109.3	113
1-42	22.7	20.8	1.4	1.0	9.10E+08	1.03E+02	113.4	68
1-67	18.6	11.6	2.5	1.3	7.36E+04	8.86E-03	120.4	22
1-7	6.8	3.3	1.7	1.6	1.34E+06	1.70E-01	127.1	31
1-10	17.4	17.4	1.3	1.1	1.04E+06	1.47E-01	141.7	27
1-48	2.5	2.1	0.8	0.8	5.56E+07	9.11E+00	163.8	64
1-3	1.6	1.8	1.5	1.5	1.42E+06	3.04E-01	214.6	87
1-11	4.8	4.8	0.9	1.0	5.92E+05	1.43E-01	240.9	53
1-23	5.1	3.6	1.6	1.6	5.06E+05	1.59E-01	314.6	128
1-15	2.5	1.4	1.0	0.8	4.49E+05	1.56E-01	346.9	79
1-12	1.7	1.7	1.3	1.7	3.59E+05	1.34E-01	372.5	112
1-69	1.1	1.5	0.9	1.2	3.08E+05	1.23E-01	398.4	66
1-7	4.5	2.7	1.3	1.2	2.09E+05	1.55E-01	742.5	160
1-4	1.0	1.4	0.9	1.1	4.20E+04	1.24E-01	2946.4	385
1-29	1.1	0.9	1.0	0.9	5.35E+02	1.97E-03	3684.3	1206
1-2	1.8	1.9	1.7	1.7	1.58E+03	2.72E-02	17228.5	1652
1-5	1.5	1.6	1.2	1.4	2.15E+03	5.40E-02	25170.1	4457
1-47	8.1	5.5	1.2	0.9	6.32E+03	2.40E-01	37971.0	5497
1-20	5.7	3.9	1.0	0.8	5.17E+02	6.95E-01	1344113.2	64406

Table 6D. ACE2 Carterra SPR Kinetics Ranked by Off-Rate

IgG	k_a (M ⁻¹ s ⁻¹)	k_d (s ⁻¹)
4-29	1.66E+05	4.20E-04
4-33	2.29E+05	5.52E-04
4-89	2.04E+06	6.11E-04
4-18	6.61E+05	6.14E-04

4-6	4.84E+05	6.79E-04
4-64	2.90E+06	7.00E-04
4-2	1.40E+06	9.60E-04
4-49	2.91E+06	9.80E-04
4-45	8.03E+05	9.88E-04
4-41	1.80E+05	1.00E-03
4-63	6.10E+05	1.05E-03
4-73	2.27E+05	1.47E-03
4-52	1.26E+05	1.49E-03
4-5	3.22E+03	1.53E-03
4-12	2.51E+05	1.80E-03
4-14	1.32E+05	1.92E-03
4-46	7.87E+04	1.95E-03
4-7	1.61E+05	1.96E-03
3-15	1.53E+05	2.06E-03
4-67	9.39E+04	2.14E-03
4-56	1.30E+05	2.37E-03
3-3	3.28E+05	2.38E-03
4-57	3.07E+05	2.39E-03
3-14	1.72E+03	2.50E-03
4-69	9.94E+04	2.56E-03
4-78	2.47E+05	2.63E-03
4-3	5.33E+04	2.68E-03
4-34	5.25E+05	2.73E-03
4-20	3.54E+04	2.76E-03
4-31	2.17E+05	2.77E-03
4-74	2.48E+05	2.85E-03
4-61	3.48E+05	2.86E-03
4-25	7.87E+04	3.03E-03
4-82	3.01E+05	3.33E-03
4-62	2.45E+05	3.65E-03
4-21	3.16E+04	4.18E-03
4-76	1.35E+05	4.28E-03
4-75	2.99E+05	4.78E-03
3-6	2.23E+05	4.88E-03
3-8	1.14E+05	5.09E-03
3-7	4.69E+05	5.20E-03
3-9	8.36E+04	5.69E-03
4-32	1.26E+05	5.74E-03
3-12	1.55E+04	6.49E-03
4-9	2.86E+05	6.81E-03
4-95	4.15E+05	7.72E-03
3-11	2.69E+05	9.45E-03
3-13	8.09E+04	1.02E-02
4-15	5.54E+05	1.10E-02
4-39	1.36E+05	1.37E-02
3-10	2.22E+03	2.00E-02
4-42	8.79E+06	1.16E-01

Table 6E. ACE2 Carterra SPR Kinetics Ranked by K_D

IgG	k_a (M ⁻¹ s ⁻¹)	k_d (s ⁻¹)	K_D (nM)	Rmax
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	s-1)			(RU)
4-64	2.90E+06	7.00E-04	0.2	115
4-89	2.04E+06	6.11E-04	0.3	66
4-49	2.91E+06	9.80E-04	0.3	71
4-2	1.40E+06	9.60E-04	0.7	70
4-18	6.61E+05	6.14E-04	0.9	121
4-45	8.03E+05	9.88E-04	1.2	148
4-6	4.84E+05	6.79E-04	1.4	147
4-63	6.10E+05	1.05E-03	1.7	89
4-33	2.29E+05	5.52E-04	2.4	98
4-29	1.66E+05	4.20E-04	2.5	72
4-34	5.25E+05	2.73E-03	5.2	85
4-41	1.80E+05	1.00E-03	5.6	154
4-73	2.27E+05	1.47E-03	6.5	231
4-12	2.51E+05	1.80E-03	7.2	84
3-3	3.28E+05	2.38E-03	7.3	340
4-57	3.07E+05	2.39E-03	7.8	388
4-61	3.48E+05	2.86E-03	8.2	294
4-78	2.47E+05	2.63E-03	10.7	118
4-82	3.01E+05	3.33E-03	11.1	158
3-7	4.69E+05	5.20E-03	11.1	105
4-74	2.48E+05	2.85E-03	11.5	166
4-52	1.26E+05	1.49E-03	11.8	110
4-7	1.61E+05	1.96E-03	12.2	257
4-31	2.17E+05	2.77E-03	12.8	280
4-42	8.79E+06	1.16E-01	13.2	64
3-15	1.53E+05	2.06E-03	13.5	151
4-14	1.32E+05	1.92E-03	14.5	290
4-62	2.45E+05	3.65E-03	14.9	111
4-75	2.99E+05	4.78E-03	16.0	87
4-56	1.30E+05	2.37E-03	18.2	264
4-95	4.15E+05	7.72E-03	18.6	97
4-15	5.54E+05	1.10E-02	19.8	106
3-6	2.23E+05	4.88E-03	21.9	162
4-67	9.39E+04	2.14E-03	22.8	130
4-9	2.86E+05	6.81E-03	23.8	109
4-46	7.87E+04	1.95E-03	24.7	81
4-69	9.94E+04	2.56E-03	25.8	59
4-76	1.35E+05	4.28E-03	31.8	144
3-11	2.69E+05	9.45E-03	35.1	113
4-25	7.87E+04	3.03E-03	38.5	78
3-8	1.14E+05	5.09E-03	44.6	161
4-32	1.26E+05	5.74E-03	45.6	66
4-3	5.33E+04	2.68E-03	50.3	117
3-9	8.36E+04	5.69E-03	68.0	176
4-20	3.54E+04	2.76E-03	77.9	76
4-39	1.36E+05	1.37E-02	100.7	193
3-13	8.09E+04	1.02E-02	126.2	77
4-21	3.16E+04	4.18E-03	132.2	39
3-12	1.55E+04	6.49E-03	420.2	106
4-5	3.22E+03	1.53E-03	473.6	196
3-14	1.72E+03	2.50E-03	1452.3	300

3-10	2.22E+03	2.00E-02	8999.0	1681
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[00261] Example 5. SARS-CoV-2 and ACE Variants

[00262] SARS-CoV-2 and ACE variant antibodies were tested for specificity and affinity.

[00263] Recombinant S1 Protein (Acros Biosystems Cat. No. S1N-S52H5) was passively immobilized on a 384 well ELISA plate and blocked with BSA. The S1 Panel antibodies were diluted from 50 nM to 0.0076 nM and incubated with the blocked plate. Antibody binding was detected using Goat-anti-Human-HRP secondary and developed with HRP substrate (list here). The absorbance signal was plotted as % of maximal binding and fitted to determine the EC₅₀ of each antibody using GraphPad Prism.

[00264] Exemplary data for affinity of SARS-CoV-2 variant 2-6 is seen in **FIGS 11A-11B** and ACE2 variants 3-7 (**FIG. 12A**), 4-49 (**FIG. 12B**), and 4-55 (**FIG. 12C**). The binding of SARS-CoV-2 panel of antibodies was measured as seen in **FIG. 13** and **Tables 7A-7F** below.

Table 7A. SARS-CoV-2 Variants EC₅₀

Antibody	EC ₅₀ (nM)
1-31	0.03139
2-6	0.03364
ACRO	0.04831
1-34	0.06522
2-2	0.07992
1-27	0.09283
2-8	0.1029
1-22	0.1248
1-32	0.1406
1-16	0.1435
1-12	0.1585
2-5	0.1615
CR3022	0.1657
1-53	0.1691
1-30	0.2084
1-28	0.2224
1-71	0.2673
1-20	0.3236
1-4	0.4216
1-35	0.4922
1-47	0.5893
1-5	0.774
2-4	0.8792
1-3	0.9724
1-21	1.003
2-19	1.257
1-51	1.465

1-19	1.706
1-42	1.742
2-2	1.789
2-1	1.894
1-33	3.006
2-13	5.139
2-11	6.921
2-15	8.509
2-7	10.09
1-26	11.93
1-24	12.86
1-49	13.04
1-10	18.31
1-1	21.87
1-8	25.09
1-7	26.94
1-72	29.13
1-17	33.17
1-36	34.86
1-73	43.58
2-10	46.43
1-9	46.88
2-17	51.86
1-52	57.88
2-18	74.71
1-29	83.41
2-12	95.94
1-25	107
2-9	118.3
1-23	123.9
1-48	296
2-14	854.7

Table 7B. SARS-CoV-2 Variants Frequency and ELISA Data

IgG	Freq.	ELISA (Avg)
1-21	1	47.6
1-22	3	40.6
1-30	1	29.5
1-35	3	28.6
1-17	79	27.4
1-27	1	27.2
1-12	2	25.7
1-2	14	24.2

1-3	2	23.9
1-23	1	23.1
1-7	4	22.5
1-31	1	20.7
1-4	1	20.6
1-8	2	19.3
1-9	2	18.5
1-32	1	17.9
1-33	1	17.6
1-24	1	32.9
1-5	1	20.6
1-28	2	17.7
1-10	1	16.9
1-26	1	19.5
1-13	1	28.2
1-14	1	21.7
1-6	1	20.8
1-20	3	26.0
1-29	1	23.8
1-1	1	32.5
1-19	1	22.3
1-16	1	22.1
1-34	1	28.7
1-18	1	22.7
1-11	1	33.2
1-25	1	27.9
1-36	1	23.6
1-15	1	24.8
1-51	1	7.1
1-52	1	3.5
1-53	1	21.7

Table 7C. SARS-CoV-2 S1 Variants

			DB/S1	DB/S-T	DC/S1	DC/S-T	Inhibitor	Fc/S1	Fc/S-T
IgG	Freq	ELISA (Avg)	K _D (nM)	K _D (nM)	K _D (nM)	K _D (nM)	IC50 (nM)	K _D (nM)	K _D (nM)f
1-21	1	47.6					6.7		
1-22	3	40.6					73.2		
1-30	1	29.5	37.2		4.7	475861.6	25.3		
1-35	3	28.6	91.9	569.8	47.5	16.7	209.2	139.4	0.5
1-17	79	27.4	67.1		6649.2				10.0
1-27	1	27.2	12.5		5519.6			9.6	9.6
1-12	2	25.7	372.5		10.6		33.0	6.1	14.0
1-2	14	24.2	17228.5	304.3					
1-3	2	23.9	214.6	423.0	252.8	5306.9	15.7		10.0
1-23	1	23.1	314.6						
1-7	4	22.5	127.1						
1-31	1	20.7	37.2		14.4		9.2	17.5	
1-4	1	20.6	2946.4	6.6	659.2	129.2		25.5	12.3
1-8	2	19.3					97.3		

1-9	2	18.5					282.4		
1-32	1	17.9	57.8		14.8			2979.8	
1-33	1	17.6			8.1	1739312.4			
1-24	1	32.9	75.5		2043.7				
1-40	2	22.9							
1-5	1	20.6	25170.1	1155.7					
1-28	2	17.7	73.5	13.4	520.3	96.6		3236.7	8.6
1-10	1	16.9	141.7				17.7		
1-26	1	19.5					8.0		
1-13	1	28.2	6.4						
1-14	1	21.7		8.1					
1-6	1	20.8	46.3	684.2					
1-20	3	26.0	1344113.2		34.4	145.0		10.3	17.3
1-29	1	23.8	3684.3	36.1					19.3
1-1	1	32.5							
1-19	1	22.3			85.4	0.0		14.3	18.6
1-16	1	22.1			2282.0	4487.3	1.7	178.8	2.2
1-34	1	28.7			8.2	623.6		13.4	1.4
1-18	1	22.7							
1-11	1	33.2	240.9	30.2					
1-25	1	27.9	78.9				3.0		6.1
1-36	1	23.6	68.9	3.9			9.3		33.2
1-15	1	24.8	346.9						
1-51	1	7.1							
1-52	1	3.5					739.8		
1-53	1	21.7					1426.0		
2-16	1	7.1					433.4		
2-17	1	3.5							
2-18	1	43.0							
2-19	1	21.7							
2-2	1	12.8							

Table 7D. SARS-CoV-2 S1 Variants Frequency and ELISA Data

IgG	Freq.	ELISA(Avg)
2-1	1	45.3
2-10	1	43.8
2-5	46	30.8
2-2	2	23.4
2-4	1	15.5
2-6	5	22.1
2-11	3	28.1
2-12	1	18.2
2-13	1	19.1
2-14	1	17.2
2-7	1	25.3
2-8	1	32.4
2-15	1	13.7
2-9	1	14.1

2-16	1	7.1
2-17	1	3.5
2-18	1	43.0
2-19	1	21.7
2-2	1	12.8

Table 7E. SARS-CoV-2 S1 Variants

			DB/S1	DB/S-T	DC/S1	DC/S-T	Inhibitor	Fc/S1	Fc/S-T
IgG	Freq	ELISA (Avg)	K _D (nM)	K _D (nM)	K _D (nM)	K _D (nM)	IC50 (nM)	K _D (nM)	K _D (nM)
2-10	1	43.8	0.6	125.6					
2-5	46	30.8	2.8			17.3	4.2	1.9	90.2
2-2	2	23.4	11.7	1.2		1.4	3.6	58.3	0.8
2-4	1	15.5		4337.7					
2-6	5	22.1		3.0	563.8	0.4		32.3	0.01
2-11	3	28.1		3.1				90.0	284.5
2-12	1	18.2		6.4		63.8	1.0		3.2
2-13	1	19.1					45.0		
2-14	1	17.2		2.5					34.8
2-7	1	25.3							252.5
2-8	1	32.4		115.1	33.4	47.4	12.2	52.8	
2-15	1	13.7		3.5			4.7		
2-9	1	14.1					23.2		23582.5

Table 7F. Antibody Panel ELISA Binding Titrations (EC50)

ANTIBODY	EC50 (nM)
2-8	0.08001
1-35	0.09604
1-3	0.133
2-5	0.1332
1-27	0.1479
1-31	0.2035
2-6	0.283
1-2	0.523
1-34	0.5584
2-2	0.612
1-67	0.9402
1-16	1.409

1-12	2.15
1-28	2.284
1-4	2.559
1-1	4.157
1-19	4.413
1-22	6.548
1-5	7.833
1-42	7.92
2-15	7.92
1-49	8.669
1-53	10.25
2-9	12.58
1-33	17.5
1-26	48.46
2-29	63.43
1-7	95.66
1-25	95.66
1-51	98.17
2-17	100
2-2	100

[00265] The data for ACE2 variant antibodies is seen in Tables 8A-8B.

Table 8A. ACE2 Variants Frequency and ELISA Data

IgG	Freq.	ELISA (Avg)
3-10	1	17.4
3-4	1	15.2
3-7	1	17.1
3-1	7	18.4
3-5	4	18.1
3-6	1	24.0
3-15	1	13.1
3-3	12	22.0
3-11	1	13.7
3-8	1	19.9
3-2	1	15.7
3-12	1	19.1
3-14	1	24.0
3-9	1	26.0
3-13	1	24.9
3-16	1	8.0
3-17	1	12.3
3-18	1	9.8

3-19	1	5.4
3-2	1	3.0
3-21	1	6.2
3-22	1	6.2
3-23	1	3.7
3-24	1	6.5
3-25	1	5.3
3-26	1	4.1
3-27	1	11.7
3-28	1	3.5
3-29	1	5.0

Table 8B. ACE2 Variants Frequency and ELISA Data

IgG	Freq.	ELISA (Avg)
4-51	1	52.0
4-52	1	49.3
4-53	1	41.1
4-54	1	40.7
4-49	21	35.1
4-55	1	29.0
4-39	1	28.0
4-56	1	22.9
4-33	1	20.2
4-57	1	19.6
4-25	1	17.0
4-58	1	15.1
4-69	2	21.8
4-18	4	20.4
4-63	2	24.7
4-73	2	20.2
4-43	2	22.9
4-72	2	20.6
4-5	2	26.6
4-67	4	20.0
4-41	2	33.9
4-6	2	22.9
4-16	2	38.7
4-32	2	21.2
4-75	2	37.5
4-37	2	24.1
4-15	2	35.4
4-42	2	35.9
4-17	2	28.1
4-35	2	26.4
4-20	2	31.0
4-31	18	24.8
4-14	4	30.3
4-7	2	35.4
4-76	2	23.1
4-89	2	39.4
4-64	4	23.7
4-3	2	41.6

4-45	2	37.8
4-6	2	27.8
4-11	2	25.1
4-44	2	23.3
4-82	2	27.1
4-40	2	25.3
4-62	2	27.7
4-74	2	25.4
4-78	2	21.1
4-46	2	25.3
4-2	2	25.7
4-21	2	22.6
4-9	2	24.2
4-61	2	25.1
4-12	2	21.8
4-29	2	22.0
4-34	2	25.4
4-47	2	20.9
4-95	2	23.2
4-36	2	20.1
4-98	1	9.1
4-99	1	4.8
4-1	1	6.5
4-101	1	17.4
4-102	1	14.4
4-103	1	9.0
4-104	1	5.3
4-105	1	7.8
4-106	1	5.4
4-107	1	7.5
4-108	1	10.0
4-109	1	17.5
4-11	1	23.3
4-111	1	14.0
4-112	1	11.1
4-113	1	8.9
4-114	1	9.9
4-115	1	26.4
4-116	1	12.6
4-117	1	12.4
4-118	1	34.9
4-119	1	28.6
4-12	1	17.9
4-121	1	36.2
4-122	1	10.6
4-123	1	14.2
4-124	1	29.3
4-125	1	22.2
4-126	1	14.6
4-127	1	16.1
4-128	1	5.3
4-129	1	6.8
4-13	1	23.1

4-131	1	37.9
4-132	1	10.9
4-134	1	14.7
4-135	1	7.3
4-136	1	16.3
4-137	1	4.8
4-138	1	21.3
4-139	1	34.3
4-14	1	43.7
4-141	1	15.0
4-142	1	14.4
4-143	1	8.4
4-144	1	11.8
4-145	1	9.5
4-146	1	7.8
4-147	1	6.4
4-148	1	20.6
4-149	1	14.3
4-15	1	22.3
4-151	1	15.1

[00266] VERO C1008 [Vero 76, clone E6, Vero E6] (ATCC® CRL-1586™) are derived from the kidney of an African green monkey and are commonly used mammalian continuous cell lines. These cells are known to express ACE2 and have been used for SARS-CoV-2 neutralization assays. To assess the binding efficiency of this panel of antibodies, each antibody was incubated with 10⁵ VERO E6 cells at 100 nM, a labeled secondary antibody was used to measure binding using flow cytometry. The binding of each antibody was compared to a baseline value, consisting of secondary antibody alone, to derive a Mean Fluorescence Intensity (MFI) over baseline (MFI/Baseline). Data for antibody variant 4-23 is seen in **FIG. 14**. Data for variant 3-1 is seen in **FIG. 15A**.

[00267] The entire panel shows varying degrees of specific binding to VERO E6 cells as in **Tables 9A-9B**. S1 Fc fusion protein and S1 RBD Fc fusion (expressed in-house) were added as positive controls for ACE2 binding.

Table 9A. ACE2 Variant Binding

Antibody	MFI	MFI/Baseline
4-15	40911	103.1
4-101	30450	76.7
4-3	23871	73.7
4-44	23486	72.5
4-89	22369	69.0
4-142	25078	63.2
4-12	24964	62.9
4-148	23582.5	59.4
4-75	18861	58.2
4-52	18184	56.1
4-50	17964	55.4
4-25	17603	54.3
4-138	21564	54.3
4-35	17460	53.9

4-39	17390	53.7
4-49	17249	53.2
4-119	21061.5	53.1
4-137	20784.5	52.4
4-64	16834	52.0
4-37	15775	48.7
4-21	15024	46.4
4-68	14963	46.2
4-97	14963	46.2
4-11	14782	45.6
4-85	14194	43.8

Table 9B. ACE2 Variant Binding

Antibody	MFI	MFI/Baseline
4-67	13852	42.8
4-144	16698	42.1
4-63	13247	40.9
4-114	15946.5	40.2
4-47	12720	39.3
4-17	12720	39.3
4-43	12413	38.3
4-9	12115	37.4
4-28	11968	36.9
4-32	11823	36.5
4-4	11538	35.6
4-29	11492	35.5
4-3	11352	35.0
4-73	10989	33.9
4-62	10856	33.5
4-54	10812	33.4
4-16	10812	33.4
4-69	10509	32.4
4-77	10382	32.0
4-14	9928	30.6
4-53	9117	26.5
4-121	4882	12.3
4-14	2876	7.2
S1 Fc Fusion	55333	160.9
S1 RBD Fc	26102	75.9

[00268] Purified antibodies were quantified by Unchained Lunatic and analyzed by Perkin Elmer LabChip System, CE-SDS (R, purity) for quality control. Data is seen in **FIGS. 15B-15Ds Tables 10A-10D**. **Table 10D** shows kinetic data for the variant antibodies collected using the Carterra LSA instrument (Fc, Fc-capture; DC, Direct-capture). The variant antibodies exhibit very high specificity and affinity to their antigen targets with affinities in the picomolar to nanomolar range.

Table 10A. ACE2 Variant Quality

Antibody	MFI	MFI/Baseline
3-10	170440	495.5
4-15	40911	103.1
4-6	29246	90.3

4-101	30450	76.7
4-3	23871	73.7
4-44	23486	72.5
4-61	22921	70.7
4-89	22369	69.0
4-65	21742	67.1
4-142	25078	63.2
4-12	24964	62.9
4-148	23582.5	59.4
4-75	18861	58.2
4-52	18184	56.1
4-50	17964	55.4
4-25	17603	54.3
4-138	21564	54.3
4-35	17460	53.9
4-39	17390	53.7
4-49	17249	53.2
4-119	21061.5	53.1
4-137	20784.5	52.4
4-64	16834	52.0
4-37	15775	48.7
4-21	15024	46.4

Table 10B. ACE2 Variant Quality

Antibody	MFI	MFI/Baseline
4-68	14963	46.2
4-97	14963	46.2
4-11	14782	45.6
3-13	15647	45.5
4-85	14194	43.8
4-67	13852	42.8
4-144	16698	42.1
4-63	13247	40.9
4-43	12413	38.3
4-114	15946.5	40.2
4-47	12720	39.3
4-17	12720	39.3
4-54	10812	33.4
3-4	11261	32.7
3-2	10132	29.5
3-7	9117	26.5
3-15	8440	24.5
3-3	7174	20.9

4-121	4882	12.3
3-5	4030	11.7
3-6	3746	10.9
4-14	2876	7.2
4-118	1091.5	2.7
S1 Fc Fusion	55333	160.9
S1 RBD Fc Fusion	26102	75.9

Table 10C.

Ab	IC50 (nM)
3-7	101.1
3-5	4.929
3-6	60.02
3-3	0.9157
4-52	0.3499
4-54	1.995
4-49	58.01
4-39	1.148
4-17	0.7208
4-101	0.5675
4-121	0.9101
4-140	3.07

Table 10D.

Antibody	K _D , ACE2 Fc	K _D , ACE2 DC
3-7	3.4	32.6
3-5	6.7	>1000
3-6	5.6	>1
3-3	7.3	NA
4-52	11.5	557.1
4-54	NA	644.8
4-49	0.3	228.6
4-39	17.5	NA
4-17	18.8	30.6
4-101	NA	5.8

4-118	NA	NA
4-121	NA	NA
4-140	NA	8.9

[00269] The SARS-CoV-2 and ACE2 variant antibodies were also assayed for affinity (data not shown). As a negative control, Trastuzumab was found not to bind to ACE2.

[00270] Competition ELISAs were performed on the variant antibodies. Typical data for SARS-CoV-2 S1 RBD and ACE2 competition ELISA is seen in **FIGS. 16A-16B**. Data for competition ELISA for a first set of SARS-CoV-2 S1 RBD and ACE2 variant antibodies is seen in **FIGS. 17A-17B** and **FIG. 18A**. SARS-CoV-2 variant antibodies with high potency in order of potency included variant 2-2, Acro mAb (1.5333), variant 2-5, variant 1-12, and variant 2-9. ACE variant antibodies with high potency in order of potency included variant 4-52, variant 4-17, variant 4-39, Acro mAb (1.533), variant 4-54, and variant 3.5. Data for competition ELISA for a second set of ACE2 variant antibodies is seen in **FIG. 18B**. Variant antibodies with high potency in order of potency included variant 4-101, variant 4-140, variant 4-121, variant 4-118, and Acro mAb (2.76 nM). **FIGS. 18C-18D** show the SARS-CoV-2 variant antibodies show potent neutralization.

[00271] Anti-ACE2 inhibitors were also identified using ELISA as seen in **FIG. 19**. Variant antibodies with high potency in order of potency included variant 4-52, variant 4-17, variant 4-14, variant 4-139, variant 4-39, variant 4-54, and Acro mAb (1.887 nM). Inhibition assays were also performed as seen in **FIG. 20**.

[00272] SARS-CoV-2 variant antibodies were assayed for Vero inhibition using FACS. Briefly, Vero cells stripped with Cell Stripper (~20 minutes with 90% viability after removal). Cells were plated at 0.1×10^6 cells per well. Stock solution of the variant antibodies were at 200nM titrated 1:3. SARS-CoV-2 S protein RBD, SPD-C5259 were made up at 6ug/mL. Variant antibody titrations were mixed 1:1 with 6ug/mL S protein (50uL IgG: 50 uL S protein). 100 uL of the mixture were added to cells and then incubated on ice for 1 hour. The cells were washed 1X followed by addition of 50 uL of goat anti-mouse secondary made up at 1:200. The cells were then incubated on ice for 1 hour in the dark, washed three times, and the plates were then read. Data for SARS-CoV-2 variant antibodies is seen in **FIGS. 21A-21D**, **FIGS. 22A-22E**, and **Tables 10E-10F**. As seen in the data, several variant antibodies blocked labeled S1 RBD from binding to ACE2 on the Vero cells including variants 2-8, 2-5, 2-2, 2-4, and 1-63.

Table 10E.

Antibody	IC50 (nM)
Acro Anti-S1	2.7
1-30	NC
1-35	NC
1-12	NC
1-31	NC
1-63	106.6

2-5	4.4
2-2	3.0
2-4	46.3
2-6	NC
2-8	19.5

Table 10F.

	S1 Monomer (nM)	S Trimer (nM)
1-31	0.22	0.80
1-30	0.67	4.02
1-35	0.15	0.76
1-12	2.08	0.61
1-63	1.40	14.39
2-8	1.52	7.08
2-5	0.17	0.59
2-2	0.13	0.64
2-4	1.58	10.18
2-6	0.07	0.43

[00273] A summary of epitope binning for SARS-CoV-2 variant antibodies is seen in **Table 10G** below.

Table 10G. SARS-CoV-2 Epitope Binning

ID	Acro mAb	2-2	Abcam CR3022	2-5	2-8	2-11	1-32	1-16	2-6	1-35
*Acro mAb	0	0	2	1	1	1	1	1	1	1
*2-2	0	0	0	0	0	0	2	0	2	1
Abcam CR3022	2	0	0	0	0	1	1	2	2	2
*2-5	1	0	0	0	0	1	1	1	1	1
*2-8	1	0	0	0	0	1	1	1	1	1
2-11	1	0	0	0	0	0	1	2	1	1
**1-32	2	1	3	1	2	1	0	0	1	1
1-16	1	1	2	2	1	1	1	0	0	0
2-6	2	2	3	2	2	2	1	0	0	0
1-35	1	1	2	2	1	1	1	0	0	0

* Anti-S1 inhibiting IgG in FACS (Vero E6)

** Anti-S1 inhibiting IgG in ELISA (soluble ACE2)

[00274] The variant antibodies were also measured in binding against other coronaviruses. Data shows that the variant antibodies do not bind significantly to S1 HCoV-229E (Sino), S1 HCoV-HKU1 (Sino), S1 HCoV-NL63 (Sino), or S1 HCoV-OC43 (Sino) (data not shown).

[00275] BluDiagnostics initial testing was performed. Results as seen in **FIG. 23** indicated that variant 2-6 binding was similar to CR3022, which is a positive control.

[00276] The data shows that the SARS-CoV-2 and ACE2 variant antibodies have high specificity and affinity to their antigen targets with affinities in the picomolar to nanomolar range.

[00277] **Example 6. SARS-CoV-2 S1 and ACE2 Variants**

[00278] SARS-CoV-2 S1 and ACE2 variants were generated and panned as described in Examples 4 and 5. [00279] FIG. 7 shows a schema of the panning strategy. Biotinylated antigen was bound to streptavidin coated magnetic beads at a density of 100 pmol antigen per mg of beads (Thermo Fisher #11206D). Phage libraries were blocked with 5% BSA in PBS. Following magnetic bead depletion for 1 hour at room temperature (RT), the beads were removed, and phage supernatant was transferred to 1 mg of antigen-bound beads in 1 ml PBS and incubated at RT with rotation for 1 hour. Non-binding clones were washed away by addition of 1 ml PBST, increasing the number of washes with each panning round. Trypsin was used to elute the phage bound to the antigen-bead complex. Phage were amplified in TG1 *E. coli* for the next round of selection. This selection strategy was repeated for four rounds, with successively lower amounts of antigen per round. Following all four selection rounds, 400 clones from each of round 2, 3, and 4 were selected for phage expression and phage ELISA screening. Data from the panning is seen in Table 11.

Table 11. Panning Data

Antibody	Library	R1	R2	R3	R4	R5
5	Target	S1	S1	S1	S1	S1
	<i>Input Titer</i>	2.0×10^{13}	1.2×10^{13}	7.0×10^{12}	1.0×10^{13}	
	<i>Output Titer</i>	3.5×10^6	8.0×10^6	4.0×10^7	3.2×10^8	
6	Target	S1	S1	S1	S1	S1
	<i>Input Titer</i>	2.0×10^{13}	1.2×10^{13}	1.0×10^{13}	1.0×10^{13}	
	<i>Output Titer</i>	2.5×10^7	3.6×10^6	6.0×10^7	1.2×10^8	

[00280] To test for binding to SARS-CoV-2 S1, phage were expressed from each picked colony by KO7 superinfection in 384 well microtiter plates. Phage containing supernatant was blocked by 1:1 addition of 4% non-fat milk (NFM). Assay plates were prepared by passive immobilization of 0.4 μ g antigen in 384-well Maxisorp plates (Thermo Fisher #464718) and then blocked with 4% NFM. Following 3x wash in PBST, blocked phage supernatant was incubated for 1 hour at RT. After 3x wash in PBST, 0.3 μ g/ml anti-M13-HRP (Sino Biological #11973-MM05T-H) was aliquoted for 1 hour incubation at room temperature. Binding of phage-displayed antibody was determined by absorbance at 450 nm with 3,3',5,5'-tetramethylbenzidine (Thermo Fisher #34029). Phage that bound to antigen with 3x over background of human Fc protein were identified as potential binders for sequencing analysis. DNA was amplified by rolling circle amplification from glycerol stocks of each clone and submitted for Sanger sequencing (Genewiz) to capture the VH and VL domains. FIGS. 24A-24B shows phage ELISA data from panning data for antibody 5 and antibody 6. For Antibody 5 variants, 116 unique clones and 68 unique CDRH3 were identified. For Antibody 6 variants, 136 unique clones and 112 CDRH3 were identified.

[00281] SARS-CoV-2 variants were tested for specificity using a phage ELISA as described above. The antigens used included Acro SARS-CoV-2 (COVID-19) S1 protein and CV S-protein construct 6 trimer TP31001F. the antigens were coated at 1 μ g/mL, 20 μ L per well in 384 NUNC plate. Purified antibodies

were prepared in in PBS-Tween at 100 nM, 10 nM, 1 nM, 0.1 nM. Secondary detection was performed using MonoRab™ Rabbit Anti-Camelid VHH Antibody [HRP], mAb (GenScript cat # A01860-200) used at 1:10,000. Data from the phage ELISA is seen in **FIGS. 25A-25H** for antibody 5 variants and **FIGS. 26A-26I** for antibody 6 variants. **FIGS. 27A-27B** show ELISA data for select antibody 6 variants. **FIGS. 28A-28F** shows phage ELISA for antibody 5 variants using 1 nM and 0.1 nM concentrations of antibodies. **FIGS. 29A-29J** shows phage ELISA for antibody 6 variants using 1 nM and 0.1 nM concentrations of antibodies. The SARS-CoV-2 variant antibodies were also assayed for affinity. Direct coupling refers to direct amine coupling of the antibody to the chip surface for the SPR assays. **Tables 12-13** show SPR data for antibody 5 variants and antibody 6 variants.

Table 12.

New Name	S1 K _D (nM)	S Trimer K _D (nM)	Competition Factor
5-1	15.1	0.4	10.01
5-2	54.2	1.5	2.29
5-3	64.6	5.6	0.87
5-4	-	-	0.83
5-5	61.9	4.0	6.55
5-6	29.1	0.3	2.58
5-7	-	-	3.43
5-8	62.2	3.8	7.11
5-9	40.6	0.7	3.27
5-10	588.0	5.4	0.90
5-11	-	0.0	4.79
5-12	96.6	4.8	2.55
5-13	37.5	3.8	1.97
5-14	-	-	0.84
5-15	96.2	2.3	6.22
5-16	50.2	1.9	1.39
5-17	3628.8	18.9	0.88
5-18	-	-	0.80
5-19	80.1	0.1	4.56
5-20	14.3	1.1	12.44
5-21	1069.3	10.0	1.14
5-22	108.7	7.2	2.06
5-23	84.8	4.2	0.95
5-24	34.6	2.2	4.90
5-25	43.3	20.1	0.82
5-26	21846.3	-	0.81
5-27	92.9	109.8	0.93
5-28	40.0	1.0	3.61
5-29	42.4	1.0	7.08
5-30	53.1	1.8	2.04
5-31	-	-	0.78

5-32	22.4	0.1	0.79
5-33	38.0	0.2	0.84
5-34	-	-	5.69
5-35	-	16.0	0.78
5-36	-	-	0.83
5-37	30.2	1.8	8.19
5-38	28.5	0.7	8.41
5-39	117.5	37.6	1.11
5-40	-	-	0.86
5-41	243.8	4.1	3.64
5-42	115.9	0.6	0.91
5-43	-	-	0.89
5-44	59.2	2.4	6.02
5-45	-	-	0.96
5-46	255.7	7.2	10.49
5-47	27.7	0.7	11.67
5-48	-	-	0.83
5-49	74.5	3.4	5.01
5-50	60.5	3.8	5.09
5-51	25.5	0.0	1.03
5-52	99.0	0.9	2.86
5-53	-	683.6	0.83
5-54	-	-	0.79
5-55	63.5	0.6	6.86
5-56	54.3	2.8	5.36
5-57	-	37.0	0.83
5-58	1679.6	3.5	0.93
5-59	113.3	6.4	4.55
5-60	29.4	0.8	7.85
5-61	-	-	0.82
5-62	-	-	0.84
5-63	10.5	0.4	1.62
5-64	346.5	221.2	0.84
5-65	352.7	421.0	0.94
5-66	-	98.9	1.00
5-67	22.1	1.0	10.95
5-68	111.0	4.8	4.58
6-1	35.8	1.2	5.38
6-2	29.9	1.2	3.14
6-3	12.4	0.0	9.51
6-4	45.8	0.5	2.71
6-5	24.9	0.8	4.33
6-6	6.4	67.7	0.97
6-7	-	-	8.73
6-8	69.4	4.6	4.06

6-9	18.5	0.9	4.17
6-10	29.7	0.6	6.92
6-11	-	-	4.26
6-12	50.2	1.4	2.56
6-13	25.3	0.6	3.20
6-14	134.7	465.9	0.83
6-15	-	9054.3	1.06
6-16	52.1	2.2	2.32
6-17	65.2	0.6	3.04
6-18	30.1	5.3	5.87
6-19	71.0	1.0	0.93
6-20	20.9	0.3	9.95
6-21	-	-	0.83
6-22	25.6	1.8	2.35
6-23	59.3	0.3	4.30
6-24	29.9	0.2	1.26
6-25	248.0	5.8	0.80
6-26	38.7	0.1	6.41
6-27	-	-	0.85
6-28	54.1	0.4	4.64
6-29	97.5	1.6	2.87
6-30	11.8	0.1	10.51
6-31	39.6	20.7	0.92
6-32	27.2	0.1	1.43
6-33	76.4	0.2	2.88
6-34	21.3	0.7	5.22
6-35	251.1	-	0.94
6-36	32.1	0.8	4.40
6-37	22.5	0.7	4.77
6-38	26.6	0.5	5.68
6-39	11.3	0.1	7.26
6-40	44.3	1.9	7.20
6-41	51.5	1.0	7.27
6-42	10.1	7.8	1.12
6-43	17.9	0.7	4.07
6-44	8.2	0.9	6.10
6-45	17.5	1.3	5.14
6-46	18.1	1.9	4.88
6-47	43.9	5.6	6.26
6-48	-	-	0.93
6-49	58.2	2.2	1.07
6-50	-	67.6	1.05
6-51	35.2	0.8	0.82
6-52	31.2	1.1	2.77
6-53	139.7	24.2	0.88

6-54	143.7	0.9	6.84
6-55	25.2	0.3	7.98
6-56	-	14.9	3.31
6-57	205.3	0.7	6.63
6-58	20.7	1.0	2.96
6-59	-	27.6	2.21
6-60	20.1	0.1	12.61
6-61	-	-	2.60
6-62	151.4	198.1	4.89
6-63	21.8	0.3	7.76
6-64	-	20.1	0.89
6-65	889.8	-	9.47
6-66	293.1	7.7	2.45
6-67	55.6	0.1	6.01
6-68	101.5	0.7	2.32
6-69	-	-	0.82
6-70	35.9	1.1	1.41
6-71	155.2	0.6	2.77
6-72	92.8	2.0	2.08
6-73	103.2	0.5	7.99
6-74	73.9	498.2	0.90
6-75	181.0	1.0	3.56
6-76	33.5	1.8	9.96
6-77	24.6	3.5	6.84
6-78	18.9	0.4	9.27
6-79	157.8	0.0	0.78
6-80	33.7	0.8	3.04
6-81	12.9	3.9	11.92
6-82	7.1	0.6	1.35
6-83	163.2	4.4	4.09
6-84	82.6	0.7	0.89
6-85	15.0	0.5	6.47
6-86	25.0	0.9	3.07
6-87	33.4	2.5	3.68
6-88	308.2	2.3	8.17
6-89	-	-	0.82
6-90	113.6	17.1	0.86
6-91	75.2	3.4	8.30
6-92	62.3	1.9	2.85
6-93	37.4	6.4	2.26
6-94	30.6	1.6	4.16
6-95	-	7.6	0.88
6-96	24.6	3.3	4.49
6-97	4070.9	57.9	1.26
6-98	-	-	0.87

6-99	51.6	3.4	1.74
6-100	7.0	0.6	10.79
6-101	-	-	0.90
6-102	45.7	0.9	0.90
6-103	23.6	1.0	1.41
6-104	-	-	0.97
6-105	41.6	1.9	5.64
6-106	-	1072.2	0.94
6-107	24.1	0.5	3.20
6-108	69.4	0.3	0.99
6-109	48.7	12.2	10.03
6-110	15.6	0.3	4.59
6-111	98.6	4.4	4.23
6-112	3229.9	43.8	0.90

Table 13.

VHH-Fc	S1 K _D (nM)	S Trimer K _D (nM)	MFI Fold Decrease
6-6	6.4	67.70	0.97
6-100	7	0.60	10.79
6-82	7.1	0.60	1.35
6-44	8.2	0.90	6.1
6-42	10.1	7.80	1.12
5-63	10.5	0.40	1.62
6-39	11.3	0.10	7.26
6-30	11.8	0.10	10.51
6-3	12.4	0.00	9.51
6-81	12.9	3.90	11.92
5-20	14.3	1.10	12.44
6-85	15	0.50	6.47
5-1	15.1	0.40	10.01
6-110	15.6	0.30	4.59
6-45	17.5	1.30	5.14
6-43	17.9	0.70	4.07
6-46	18.1	1.90	4.88
6-9	18.5	0.90	4.17
6-78	18.9	0.40	9.27
6-60	20.1	0.10	12.61
6-58	20.7	1.00	2.96
6-20	20.9	0.30	9.95
6-34	21.3	0.70	5.22
6-63	21.8	0.30	7.76
5-67	22.1	1.00	10.95
5-32	22.4	0.10	0.79
6-37	22.5	0.70	4.77
6-103	23.6	1.00	1.41
6-107	24.1	0.50	3.2
6-96	24.6	3.30	4.49
6-77	24.6	3.50	6.84
6-5	24.9	0.80	4.33
6-86	25	0.90	3.07

6-55	25.2	0.30	7.98
6-13	25.3	0.60	3.2
5-51	25.5	0.00	1.03
6-22	25.6	1.80	2.35
6-38	26.6	0.50	5.68
6-32	27.2	0.10	1.43
5-47	27.7	0.70	11.67
5-38	28.5	0.70	8.41
5-6	29.1	0.30	2.58
5-60	29.4	0.80	7.85
6-10	29.7	0.60	6.92
6-2	29.9	1.20	3.14
6-24	29.9	0.20	1.26
6-18	30.1	5.30	5.87
5-37	30.2	1.80	8.19
6-94	30.6	1.60	4.16
6-52	31.2	1.10	2.77
5-56	54.3	2.77	5.36
5-8	62.2	3.80	7.11
6-91	75.2	3.45	8.30
6-73	103.2	0.52	7.99
5-34	-	-	5.69
6-26	38.7	0.07	6.41
6-76	33.5	1.77	9.96

[00282] VHH-Fc antibodies targeting S1 were titrated 1:3 starting at 200 nM and mixed 1:1 with SARS-COV2-S1 RBD (mouse IgG2Fc tag). The RBD/VHH-Fc complex was added to Vero E6 cells expressing endogenous ACE2 receptor and incubated. Cells were subsequently washed and an anti-mouse secondary was used to measure binding of S1 RBD to ACE2, thus assessing the inhibition of S1. Over 60 clones demonstrated potent inhibition. Data is seen in FIGS. 30A-30C and Tables 14A-14B.

Table 14A.

Sample	IC ₅₀ [nM]
2-2	0.56
5-56	0.68
5-1	0.75
5-67	0.76
5-47	0.80
5-8	0.94
5-38	0.96
5-37	1.01
5-34	1.21
5-20	1.23
5-55	1.45
5-46	1.52
5-50	1.61
5-5	1.79
2-5	2.146
5-60	2.15
5-15	2.19
5-29	2.19

Acro Anti S1	3.80
5-49	5.61
5-44	11.73

Table 14B.

Sample	IC ₅₀ [nM]
6-85	0.2044
2-2	0.56
6-63	0.74
6-3	0.74
6-78	0.7427
6-20	0.76
6-91	0.89
6-44	0.97
6-55	0.97
6-73	1.01
6-26	1.07
6-76	1.11
6-45	1.16
6-60	1.31
6-40	1.36
6-81	1.383
6-10	1.44
6-7	1.53
6-39	1.53
6-109	1.60
6-38	1.94
2-5	2.146
6-30	2.94
6-57	3.13
Acro Anti S1	3.49
6-67	3.80
6-77	4.041
6-100	5.07
6-47	5.86
6-41	6.60
6-88	7.118
6-105	7.82
6-34	8.24
6-54	8.90
6-18	12.29
6-1	15.76
6-65	37.47

[00283] Antibody kinetics were measured for variants 2-5, 2-2, and 2-6 (FIG. 31A) and variants 1-12, 1-42, 1-20, and 1-19 (FIG. 31B). Data is seen in FIGS. 31A-31B. The data shows that the antibodies bind with nanomolar affinities. FIG. 31C shows percent neutralization for variants 1-12, 1-42 and 1-20. FIG. 31D shows percent neutralization for variants 1-12, 1-42 and 1-20 using live virus.

[00284] The ACE2 variant antibodies were measured for effects on ACE activity. Using a Sigma-Aldrich ACE activity assay kit (CS0002), ACE positive control were premixed with 1, 10, 100 nM anti-ACE2 mAb and read at 320 nm excitation, 405 nm emission, 5 min kinetics. The data is seen in **FIG. 32** and shows the ACE2 variant antibodies do not inhibit enzyme activity.

[00285] Example 7. Neutralization of Live Virus

[00286] VHH-Fc antibodies targeting S1 were titrated 1:3 starting at 200 nM and mixed 1:1 with SARS-COV2-S1 RBD (mouse IgG2Fc tag). The RBD/VHH-Fc complex was added to Vero E6 cells expressing endogenous ACE2 receptor and incubated. Cells were subsequently washed and an anti-mouse secondary was used to measure binding of S1 RBD to ACE2, thus assessing the inhibition of S1. Over 60 clones demonstrated potent inhibition. The data is seen in **FIGS. 33A-33B** and **Table 15A**.

Table 15A.

Antibody	EC50 (ug/mL)
6-63	0.06
6-3	0.06
2165mAb*	0.08
5-1	0.10
6-60	0.15
6-55	0.21
5-20	0.27
1-20	0.37
5-34	0.54
6-85	0.84
6-76	1.08
6-73	1.46
1-42	2.03
1-12	2.10
6-26	2.97
6-20	5.03
6-78	8.26
2-6	11.77
2-5	18.31
2-2	67.57
1-63	106.90

[00287] **FIG. 33B** shows that variant 6-2 showed higher neutralization versus IgG in live virus. Variants 6-63, 6-3, and 5-1 showed comparable neutralization versus 2165 mAb derived from a COVID-19 subject.

[00288] **FIGS. 33C-33E** and **Table 15B** show data from VHH single domain antibodies in VSV-pseudotype SARS-CoV-2 neutralization assays. Variants 5-1, 6-3, and 6-63 showed improved neutralization in pseudovirus testing including in live virus FRNT (**FIG. 33E**). Variants 6-3, 6-60, 6-63, and 6-76 showed potent neutralization in live virus PRNT as seen in **Table 15C** and **FIG. 33F**. Data as seen in **Table 15D** and **FIGS. 33G-33H** show that variants 6-3, 6-63, and 1-20 exhibited potent neutralization in live virus PRNT.

Table 15B.

Antibody	NC50 (ug/mL)
6-63	0.06
6-3	0.06
5-1	0.10
6-60	0.15
6-55	0.21
5-20	0.27
1-20	0.37
5-34	0.54
6-85	0.84
6-76	1.08
6-73	1.46
1-42	2.03
1-12	2.10
6-26	2.97
6-20	5.03
6-78	8.26
2-6	11.77
2-5	18.31
2-2	67.57
1-63	106.90

Table 15C.

Antibody	PRNT90 (ng/mL)
5-1	15.6
5-20	3.9
5-34	15.6
6-26	62.5
6-60	<0.98
6-63	3.9
6-3	<0.98
6-55	62.5
6-76	3.9
6-78	250
6-20	15.6
6-73	250

6-85	62.5
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Table 15D.

Antibody	EC80 (ug/mL)
6-63	0.057861
6-3	0.115234
1-20	0.171875
6-60	0.236816
5-20	0.376
6-76	0.425781
6-55	0.445313
5-34	0.570313
6-42	0.734375
5-1	0.810547
1-12	0.855469
6-85	1.0625
5-38	1.5
5-67	1.566406
1-42	1.78125
6-73	2.015625
6-20	2.3125
5-47	2.457031
1-19	2.78125
6-44	3.15625
6-26	3.609375
6-45	4.015625
5-37	12.4375
6-78	13.75
5-63	14.1875
5-8	15.8125
6-6	24.375
6-13	25.6875
6-24	31.375
1-63	50.5
6-32	60.625
2-6	72.34043
6-22	103.25
5-56	104.75
2-5	106.5
6-82	107.75
5-32	180.1418
6-91	240.5
2-2	354.6099

5-51	387.9433
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[00289] The variants were also tested in pseudovirus neutralization and live virus PRNT studies. Variants 5-20, 6-60, 6-63, and 6-3 showed potent neutralization in live virus PRNT as seen in FIG. 33I.

[00290] Example 8. *In Vivo* Evaluation of Variant Coronavirus Immunoglobulins

[00291] This Example assesses the variant coronavirus immunoglobulins in a Syrian hamster model (immunosuppressed) of COVID-19 disease.

[00292] 8-10 week-old female Syrian hamsters were immunosuppressed using cyclophosphamide (140 mg/kg day 3 days before challenge and then 100 mg/kg every 4 days by i.p. route). Eleven groups of six hamsters per group were injected with antibody on day -1 relative to challenge by the intraperitoneal route (i.p.). On Day 0 all hamster were challenged with 1,000 PFU SARS CoV-2 Washington isolate by the intranasal route and weighed daily. % Weight change relative to starting weight was calculated. Pharyngeal swabs were collected on Days -1, 1, 4, 7, 9. Day 9 lungs were collected and homogenized for viral load. Groups are shown in Table 15E.

Table 15E. Groups

Group	Diluent/volume injected i.p.
Convalescent plasma	NA/2.5 mL
Negative control MAb c7d11	PBS/2.5 mL
6-63	PBS/2.5 mL
6-3	PBS/2.5 mL
6-36	PBS/2.5 mL

NA= not applicable

[00293] Animals injected intraperitoneally (i.p.) with the Negative Control antibody lost weight starting losing significant amounts of weight between Days 5 and 6 and continued to decline until the end of the experiment on Day 9. The maximum mean weight loss of the group was -11.7%. In contrast, animals injected with positive control human convalescent plasma maintained weight within -3.2% of their weight on Day 0 indicating this plasma protected against disease manifested by weight loss (FIG. 34A).

[00294] Groups of six animals were injected i.p. with 10, 5, or 1 mg/kg of monoclonal antibody 6-63 diluted in PBS. All groups maintained their weight at or above starting weight indicating the antibody protected against disease resulting weight loss (FIG. 34B).

[00295] Groups of six animals were injected i.p. with 10, 5, or 1 mg/kg of monoclonal antibody 6-3 diluted in PBS. The 1 and 10 mg/kg groups maintained their weight at or above starting weight at all time points. The 5 mg/kg group weight dipped slightly below the convalescent control on Days 7-9 but clearly was different from the Negative Control antibody. Together, these data indicate the antibody decreased weight loss associated with disease (FIG. 34C).

[00296] Groups of six animals were injected i.p. with 10, 5, or 1 mg/kg of monoclonal antibody 6-36 diluted in PBS. The 10 and 5 mg/kg groups maintained their weight at levels similar to the positive control at all time points. The 1 mg/kg group weight dropped significantly similar to the Negative Control. These data indicate antibody 6-36 at 1 mg/kg is insufficient to provide benefit, but a 5-fold or greater dose is adequate to reduce disease as determined by weight loss (**FIG. 34D**).

[00297] **FIG. 34E** shows data from the variant antibodies grouped by dose. **FIG. 34F** shows graphs of percent weight change for antibodies 6-3, 6-63, and 1-20.

[00298] In wild type hamsters, virus is typically cleared by Day 7. However, in the cyclophosphamide model, viral levels are not suppressed unless there is intervention (e.g. protective antibodies administered) or the cyclophosphamide is discontinued to allow immune response and clearance. In this experiment the positive control human convalescent serum eliminated virus from the lungs from all except one hamster. In contrast, all but one of the hamsters injected with negative control antibody still had infectious virus in the lungs. Interestingly, hamsters prophylactically treated (24 hour previous to exposure) with any of the three antibodies at the highest dose (10 mg/kg) had infectious virus in the lungs of at least half the animals assessed 9 days later. Paradoxically, 6-63 and 6-3 at the lower doses (5 and 1 mg/kg) had animals with relatively less infectious virus in the lungs. 4 of 6 animals injected with 1-20 at 5 mg/kg dose animals had no detectable virus in the lungs. When the doses of that antibody was reduced to 1 mg/kg, all but one animal had infectious virus. Data is seen in **FIGS. 34G-34H**.

[00299] Lung pathology inflammation and edema scores from three animals were added per group and plotted (**Fig. 34I**). These were the same lungs used to score ISH. The convalescent sera positive control median score was 2 and the negative control was 4. The only groups with a median score lower than the negative control group were 1 and 5 mg/kg 6-63, 10 and 5 mg/kg 6-3, and 5 mg/kg 1-20. The highest median pathology scores were the 1 and 10 mg/kg 1-20 groups. The lowest median pathology score was the 5 mg/kg 6-63 group.

[00300] Example 9. SARS-CoV-2 Membrane Protein Panning

[00301] Variant SARS-CoV-2 antibodies targeting the membrane protein were generated and panned similar to Example 4.

[00302] An exemplary construct is seen in **FIG. 35**. The membrane protein variants were assayed for binding affinity to SARS-CoV-2 membrane protein (data not shown). The membrane protein variants bound in the picomolar and nanomolar range and did not bind to GFP fusion protein as seen in **FIGS. 36A-36D**.

[00303] ELISA assays were performed. Briefly, 1 ug/ml antigen immobilized on Nunc Maxisorp plate. 0.01 – 333 nM of the antibodies were added to the plate. The secondary antibody used was anti-human Fc-HRP secondary. The data is seen in **Tables 16A-16B** and **FIGS. 37A-37B**.

Table 16A.

	9-1		10-55		10-16		10-15		10-28		10-27		10-20		Trastuzumab	
[Ab] (nM)	M- GFP	BSA	M- GFP	BSA	M- GFP	BSA	M- GFP	BSA	M- GFP	BSA	M- GFP	BSA	M- GFP	BSA	M- GFP	BSA
333.33	1.19	0.39	1.05	0.28	1.10	0.38	0.82	0.52	0.94	0.32	0.87	0.23	0.62	0.37	0.14	0.08

111.11	1.13	0.38	0.95	0.40	1.02	0.46	0.53	0.33	0.97	0.35	0.81	0.23	0.71	0.40	0.08	0.06
37.04	1.10	0.46	0.91	0.39	1.02	0.52	0.31	0.20	0.84	0.48	0.75	0.28	0.71	0.36	0.06	0.05
12.35	0.90	0.45	0.75	0.32	0.87	0.49	0.15	0.10	0.83	0.47	0.83	0.34	0.62	0.32	0.05	0.04
4.12	0.80	0.40	0.58	0.20	0.93	0.40	0.09	0.06	0.55	0.35	0.63	0.30	0.69	0.22	0.05	0.04
1.37	0.61	0.27	0.30	0.10	0.59	0.24	0.06	0.06	0.41	0.22	0.52	0.22	0.44	0.14	0.05	0.04
0.46	0.33	0.14	0.16	0.07	0.29	0.13	0.05	0.05	0.21	0.12	0.30	0.12	0.24	0.08	0.04	0.04
0.15	0.16	0.08	0.07	0.05	0.15	0.08	0.05	0.04	0.10	0.07	0.15	0.07	0.12	0.05	0.04	0.04
0.05	0.11	0.07	0.06	0.04	0.08	0.05	0.04	0.04	0.06	0.05	0.08	0.05	0.07	0.04	0.04	0.04
0.02	0.10	0.04	0.05	0.04	0.05	0.04	0.04	0.04	0.05	0.04	0.05	0.04	0.05	0.04	0.04	0.04
0.01	0.05	0.04	0.09	0.04	0.05	0.04	0.04	0.04	0.04	0.04	0.05	0.04	0.05	0.04	0.04	0.04

Table 16B.

[Ab] (nM)	9-11	10-55	10-16	10-15	10-28	10-27	10-20	Trastuzumab
333.33	3.04	3.74	2.88	1.57	2.94	3.87	1.67	1.69
111.11	2.96	2.39	2.22	1.61	2.77	3.52	1.79	1.49
37.04	2.39	2.36	1.98	1.57	1.74	2.71	1.96	1.31
12.35	2.02	2.39	1.77	1.47	1.76	2.46	1.94	1.17
4.12	2.02	2.89	2.35	1.49	1.59	2.11	3.07	1.13
1.37	2.27	2.95	2.47	1.06	1.90	2.40	3.21	1.13
0.46	2.38	2.23	2.20	1.06	1.79	2.42	3.21	1.08
0.15	1.97	1.44	1.82	1.09	1.47	2.09	2.27	1.01
0.05	1.72	1.23	1.51	1.07	1.23	1.54	1.51	1.04
0.02	2.16	1.06	1.20	0.97	1.11	1.24	1.21	1.03
0.01	1.12	2.24	1.15	1.07	1.08	1.12	1.09	1.04

[00304] FACS titration was also performed. Data is seen in Table 16C and FIGS. 38A-38J.

[IgG] nM	9-11	10-55	10-16	10-15	10-28	10-27	10-20	ProSci Sars- Cov2- M1	ProSci Sars- Cov2- M1	Protei nTech Sars- Cov2- M1
100	2.08	2.80	3.07	2.72	13.46	1.49	3.23	5.60	3.51	6.07
33.333	2.58	4.10	4.61	2.27	9.80	1.47	4.10	3.72	2.82	4.85
11.111	2.96	3.43	3.22	2.05	5.87	2.09	3.58	2.83	2.20	4.79
3.704	3.63	2.46	2.31	1.77	3.05	1.81	3.00	2.05	1.89	3.13
1.235	3.37	1.48	1.95	1.55	2.54	2.68	2.62	1.94	2.92	1.89
0.412	2.38	1.31	1.52	1.36	1.99	1.70	2.13	1.83	2.00	1.64
0.137	2.00	1.37	1.27	1.36	1.58	1.26	1.45	1.91	1.81	1.48
0.046	1.61	1.38	1.31	1.76	1.60	1.37	1.49	1.61	1.63	1.59

[00305] Data for antibodies having improved affinity and binding is seen in Table 16D and FIGS. 39A-39B.

Table 16D.

Variant	MFI Expressing	MFI Parent	MFI Ratio
10-13	31498	3565.5	8.83
9-1	35223	4299	8.19

10-18	8516	1056	8.06
10-45	18004	2691	6.69
10-26	8204.5	1577	5.20
10-22	14691	3285	4.47
10-48	11680	2838.5	4.11
10-52	2165	527	4.11
10-40	14490	3833	3.78
9-8	8705.5	2318	3.76
ProteinTech Sars-Cov2-M1	7390	2007	3.68
10-38	8777	2554	3.44
10-61	19571	6131.5	3.19
9-9	4843	1541	3.14
10-08	18743	5964	3.14
10-24	4735.5	1554	3.05
9-4	26899	8829.5	3.05
10-10	38014	12508.5	3.04
10-58	12538	4421	2.84
10-35	3279	1179	2.78
10-07	2631	1005	2.62
10-46	14703	5650	2.60
10-23	24789	10112	2.45
10-37	6580.5	2727	2.41
10-34	4416	1837	2.40
10-27	18804	8030	2.34
10-59	12781	5560	2.30
10-33	4429.5	1935	2.29
10-14	5189	2346	2.21
10-21	28963	13223.5	2.19
10-49	6702	3071.5	2.18
10-39	12127.5	5731	2.12
10-04	5561	2638	2.11
10-28	18309	8872.5	2.06
10-53	5940.5	2920	2.03
10-12	11043	5451	2.03
9-5	79505	40263	1.97
10-25	2231	1136	1.96
9-7	60739	31110	1.95
10-03	35529	19063.5	1.86
10-32	25569	13832	1.85
10-20	29454	16158	1.82
10-36	31774	17549	1.81
10-57	29745	16648	1.79
10-54	89446	50215	1.78

10-41	8910	5090.5	1.75
10-42	70764	40576	1.74
10-50	423775	246262	1.72
10-31	1460	880.5	1.66
9-11	141975	87474	1.62
10-47	70545.5	43576.5	1.62
10-09	41228	25611.5	1.61
9-3	45285	28206	1.61
10-05	70182	44064	1.59
10-17	69948	44097.5	1.59
10-30	37623.5	23973	1.57
10-11	43592	27861	1.56
10-43	16903.5	10901	1.55
10-19	74841	48651	1.54
9-10	123764	81408	1.52
10-29	6272	4230.5	1.48
10-51	91221	61911	1.47
9-6	669267	454499.5	1.47
10-44	19771	13568	1.46
10-56	11075.5	7946	1.39
9-2	936	721	1.30
Stained Control R	208	164	1.27
10-02	413	331	1.25
10-55	1951.5	1585	1.23
Stained Control H	198	166	1.19
10-60	100191.5	87809	1.14
10-01	958	884	1.08
10-06	1375	1273	1.08
10-15	1912	1777	1.08
10-16	910	866	1.05

[00306] The membrane protein antibodies were assayed in flow titration assay for pool and single pool HEK. Data is seen in **FIGS. 40A-40C**. Of the membrane protein antibodies, 9-11, 10-13, 9-28, 10-18, 10-48, and 10-55 exhibited improved characteristics (**FIG. 40D**).

[00307] **Example 10. VSV- pseudotype neutralization analysis of antibodies for SARS-CoV-2 B.135 (South African strain)**

[00308] Antibodies described herein were tested in a VSV-pseudotype neutralization assay for SARS-CoV-2 B.135 (South African strain).

[00309] Briefly, aerial semi-log dilutions of all test antibodies (TA) and control were prepared and mixed with the VSV-pseudotype virus in a 1:1 ratio for 1 h at RT followed by incubation over Vero cells (ATCC® CCL-81TM) seeded at 60,000 cells per well at 37°C. The cells were lysed the following day and luciferase activity was measured to assess the potency of each TA to block viral entry into the Vero cells. All samples

will be run in triplicate. Data analysis is conducted using XLFit and Graphpad Prism. The testing concentrations and plate plan are seen in **Table 17**.

Table 17. Testing Concentrations and Plate Plan

	Samples	Stock (mg/mL)	Target conc/dilution	In plate concentration
1	6-63	6.39	100 ug/mL	50.00 ug/mL
2	6-3	10.05	100 ug/mL	50.00 ug/mL
3	1-12	2.24	100 ug/mL	50.00 ug/mL
4	mouse pAb	1	1: 25	1: 50

[00310] Data is seen in **Figs. 41A-41B**. **Fig. 41A** illustrates positive control pAb has an NT50 of 1: 14,993 dilution as expected. **Fig. 41B** illustrates antibodies 6-63 and 6-3 neutralize VSV-SARS B.135 strain with IC50s of ~3.07 ug/mL and 0.143 ug/mL, respectively. Antibody 1-12 failed to neutralize VSV-SARS B.135 strain.

[00311] Example 11. VSV-pseudotype neutralization analysis of antibodies for SARS-CoV-2 D614G variant

[00312] Antibodies described herein were tested in a VSV-pseudotype neutralization assay for SARS-CoV-2 SARS CoV-2 S D614G variant.

[00313] Briefly, serial semi-log dilutions of all test antibodies (TA) and control were prepared and mixed with the VSV-pseudotype virus in a 1:1 ratio for 1 h at RT followed by incubation over Vero cells (ATCC® CCL-81TM) seeded at 60,000 cells per well at 37°C. The cells were lysed the following day and luciferase activity was measured to assess the potency of each TA to block viral entry into the Vero cells. All samples will be run in triplicate. Data analysis is conducted using XLFit and Graphpad Prism.

[00314] Data is seen in **Figs. 42A-42D**. **Fig. 42A** shows the positive control.

[00315] Example 13. Antibody cocktails for treating SARS-CoV-2 in Syrian hamsters

[00316] This Example demonstrates pre- and post-exposure efficacy of antibody cocktails in Syrian hamsters.

[00317] Methods

[00318] In this study the hamsters were transiently immunosuppressed using cyclophosphamide. As a strategy to de-risk selecting viruses with neutralization escape mutations a cocktail of a nanobody (nAb) and a monoclonal antibody (MAb) known to bind different spike protein epitopes were combined and used. The combined dose was 20 mg/Kg in this proof-of-concept experiment. The cocktail consisted of 10mg/Kg of VHH nanobody 6-63 and 10mg/Kg of monoclonal antibody 1-20. An equal number of male and female animals were used in each group.

[00319] Seventy-eight hamsters were used for this experiment according to **Table 18**. On Day 0, animals were exposed via intranasal (IN) instillation to 1,000 pfu of SARS-CoV-2 virus in 50 µL volume. The volume was distributed between both nares. To transiently immunosuppress, all animals were treated with

cyclophosphamide starting on Day -3 (140 mg/kg dose) followed by additional doses (100 mg/kg) on Days 1, 5, and 9.

[00320] On the indicated day post exposure, MAb/nAb cocktail or c7D11 was administered via the intraperitoneal (IP) route. On Day 0 blood samples were collected from Group I for hematology to confirm immunosuppression. Group I was also the control for any adverse effects of cyclophosphamide treatment on the hamsters. Clinical scores and individual animal weights were recorded daily. Pharyngeal swabs and other key events were measured. Animals in Groups A-I were euthanized on day 14 and lungs were collected for virology and pathology. Group J animals were used for a serial pathology component of this study. Two animals from Group J (2 male and 2 female) were euthanized starting on Day 1 and then each day up to and including Day 6.

Table 18. Experimental design

Group	Number of Hamsters (Pain Category)	Virus Exposure ^a (Day 0)	Treatment	Treatment Day
A	6 (3 male, 3 female) (D)	SARS CoV-2	Cocktail ^b 20 mg/Kg	-1
B	6 (3 male, 3 female) (D)		Cocktail ^b 20 mg/Kg	+1
C	6 (3 male, 3 female) (D)		Cocktail ^b 20 mg/Kg	+2
D	6 (3 male, 3 female) (D)		Cocktail ^b 20 mg/Kg	+3
E	6 (3 male, 3 female) (D)		Cocktail ^b 20 mg/Kg	+4
F	6 (3 male, 3 female) (D)		Cocktail ^b 20 mg/Kg	+5
G	6 (3 male, 3 female) (E)		Cocktail ^b 20 mg/Kg	+6
H	6 (3 male, 3 female) (E)		Neg IgG control	+1
I	6 (3 male, 3 female)(C)	No virus	none	Cyclophosphamide control
J	24 (12 male, 12 female) (E)	SARS CoV-2	none	No treatment-pathology control ^d

78 Syrian hamsters

^a challenge with 1,000 pfu of virus in 50 microliter volume

^b cocktail= 6-63 combined with 1-20 1:1 w/v delivered 2.5 mL per animal by i.p. route

^c negative control 20mg/kg

^d Two animals (2 male and 2 female) from Group J were euthanized for pathology/virology on Days 1, 2, 3, 4, 5, 6

[00321] Results

[00322] *Cyclophosphamide treatment in uninfected animals does not result in weight loss.* Control animals (CYP Controls, Group I), that were treated with CYP but not challenged gained weight overtime.

[00323] *Negative control antibody c7D11 at 20 mg/kg, Group H, does not protect against disease associated weight loss.* Hamsters in Group H lost weight starting on Day 6 (**FIG. 43A**). Weight loss continued until Day 10 when it leveled off. Animals were still below 10% of their starting weight on the last day of the experiment (Day 14).

[00324] *The cocktail administered one day prior to exposure protected against weight loss.* Hamsters in Group A maintained their weight and stayed within 1% of starting weight (**FIG. 43A**). This confirmed that treatment with neutralizing antibodies before exposure was sufficient to protect against significant weight loss.

[00325] *Post-exposure treatment of CYP hamster model of COVID19 produces variable weight loss effects/patterns.* A onetime treatment of a cocktail containing 1-20 and 6-63 at final dose of 20mg/Kg was administered on Days 1 (B), 2 (C), 3 (D), 4 (E), 5 (F), and 6 (G). The percent weight change relative to Day 0 are shown in **FIG. 43A**. Arrows and dotted vertical lines indicate the day of treatment specific for the treatment regimen being compared. The same data is shown collectively in **FIG. 43B**. Note that there were two animals in Group B (Day 1) that dropped weight atypically during the experiment and one animal succumbed on Day 12. That animal had a necrotic/hemorrhaging testicle due to an apparent torsion event and was excluded from analysis. No assignable cause was identified for the second animal so that animal was not excluded from analysis. Statistical analysis was performed to compare both the CYP Control (Group I) and the negative control antibody (c7d11, Group H) to all other groups. The significance between groups at individual timepoints and differences in area under the curve (AOC) were determined. Treatment with the cocktail one day after exposure (Group B) results were confounded by the outlier animal. There was not a significant differences in AOC between Group B and Group H suggesting no protection; however, there was also no significant difference in the AOC between Group A and Group I indicating Group B weight loss was not significantly different from the CYP control group that was not exposed. Treatment with the cocktail two days after exposure (Group C) clearly protected. There was significant differences in AOC between Group C and Group H; and no significant difference in the AOC between Group C and Group I. Treatment after three days (Day 3 Group D) did not result in a significant difference in AOC between Group D and H. However, treatment on day 4 or 5 after exposure (Groups E and F, respectively) did significant reduce the AOC relative to Group H. Treatment on day 6 (Group G) was similar to treatment on day 3 where no significant difference in AOR between Group G and H. Although there was no significance in the AOC for the Day 6 treatment group, the last three timepoints weight loss was significantly less than the negative control group. Interestingly, groups administered antibody on Days 3, 4, 5, or 6 started to gain weight starting on Day 9 whereas the negative control antibody treated animals did not. This suggests that there was a benefit of all cocktail treatment even at as late as 6 days post-exposure.

[00326] *Infectious virus in lungs (Day 14/15).* In wild type hamsters, virus is typically cleared by Day 7. However, in the cyclophosphamide model virus is not suppressed unless there is intervention (e.g. protective antibodies administered) or the cyclophosphamide is discontinued to allow immune response and clearance. Here, our controls demonstrate that unexposed hamsters were negative for virus (Cyp Cont), whereas all

hamsters exposed to virus and treated with an off-target monoclonal antibody (Neg Cont) had more than 10,000 pfu of virus per gram of lung tissue. Most of the hamsters treated with the Cocktail one day prior or one day post virus exposure had detectable levels of virus in lung samples collected on Day 14 (Groups A and B). However, almost all of the hamsters treated with antibody ≥ 2 day after exposure had undetectable levels of antibody in their lungs. There was only a single animal exception in the Day 2, 3, 4 and 6 treated groups. All of the hamsters treated on Day 5 had lungs that were free of infectious virus. See FIG. 43C.

[00327] Sequential Sampling. Hamsters immunosuppressed and exposed to virus on Day 0 were sampled overtime to monitor the infection. Infectious virus was detected in the lungs of 3 of 4 hamsters on Day 1. Levels of infectious virus then increased more than 4 logs by Day 2. Levels of virus then leveled off and stayed between 7-9 log₁₀ through the last sampling timepoint (Day 6) analyzed to-date. Thus, animals administered the cocktail after Day 1 likely had very high levels of infectious virus present in their lungs before treatment with the antibody. See FIG. 43D.

[00328] Conclusion

[00329] The data demonstrates that when administered at or before Day 2 relative to virus exposure, the combination of antibody and nanobody at 20 mg/kg was sufficient to provide convincing benefit as determined by the disease parameters analyzed. When treated after Day 2, animals still developed weight loss but recovered in approximately 4 days. Two weeks after virus exposure, more infectious virus was detected in the lungs of hamsters receiving antibody early (Day -1 or 1) than day 2 or later. Day 2 (or later) treatment of exposed animals occurred at a time when viral burden in the lungs was already remarkably high. CYP, by itself, does not induce weight loss or clinical signs of disease.

[00330] Example 14. Immunity conferred by SARS-CoV-2 and ACE2 antibodies

[00331] Antibodies described in Examples 4-6 are used to confer immunity in a subject. A subject is passively immunized with a SARS-CoV-2 or ACE2 antibody. The subject is then exposed to SARS-CoV-2 after immunization with the SARS-CoV-2 or ACE2 antibody. Exposure can be within a few days or within a few months. The subject can also receive the SARS-CoV-2 or ACE2 antibody immediately following exposure with SARS-CoV-2. Although the subject is exposed to SARS-CoV-2, the subject has developed an immunity against SARS-CoV-2 and infection is prevented.

[00332] Example 15. Sequences

[00333] Tables 19-41 show exemplary sequences for CDRH1-H3 and CDRL1-L3 as well as variant heavy chains and variant light chains for the SARS-CoV-2 and ACE2 variants.

Table 19. ACE2 VHH Variable Heavy Chain CDRs

Variant	SEQ ID NO	CDRH1	SEQ ID NO	CDRH2	SEQ ID NO	CDRH3
4-1	1	RTFSDDTMG	51	GGISWSGGNTYYA	101	CATDPPLFW
4-2	2	RTFGDYIMG	52	AAINWSAGYTAYA	102	CARASPNTGWHFDRW
4-3	3	RTFSDDAMG	53	AAINWSGGTTRYA	103	CATDPPLFW

4-4	4	RTFGDYIMG	54	AAINWIAGYTADA	104	CAEPSNTGWHFDHW
4-5	5	RTFGDDTMG	55	AAINWSGGNTYYA	105	CATDPPLFW
4-6	6	RTFGDDTMG	56	AAINWTGGYTPYA	106	CATDPPLFW
4-7	7	RTFGDYIMG	57	AAINWSGGYTAYA	107	CATASPNTGWHFDHW
4-8	8	RTFGDYIMG	58	GGINWSGGYTYA	108	CATDPPLFW
4-9	9	RTFGDYIMG	59	AAINWSGGYTHYA	109	CATDPPLFW
4-10	10	RTFSDDTMG	60	AAIHWSGSSTRYA	110	CATDPPLFW
4-11	11	RTFGDYAMG	61	APINWSGGSTYYA	111	CATDPPLFW
4-12	12	RTFGDDTMG	62	AAINWSGGNTPYA	112	CATDPPLFW
4-13	13	RTFGDDTMG	63	AAINWSGDNTHYA	113	CATDPPLFW
4-14	14	RTFSDDTMG	64	AAINWSGGTTRYA	114	CATDPPLFW
4-15	15	RTFSDDTMG	65	AAINWSGDSTYYA	115	CATDPPLFW
4-16	16	RTFSDYTMG	66	AAINWSGGYTYA	116	CATDPPLFW
4-17	17	RTFGDDTMG	67	AAINWSGGNTDYA	117	CATDPPLFW
4-18	18	RTFGDYIMG	68	AAINWSGGYTPYA	118	CATDPPLFW
4-19	19	RTFSDDTMG	69	AAINWSGGSTYYA	119	CATDPPLFW
4-20	20	RTFGDDIMG	70	AAIHWSAGYTRYA	120	CATDPPLFWGHVDLW
4-21	21	RTFSDDTMG	71	AGMTWSGSSTFYA	121	CATDPPLFW
4-22	22	RTFGDYIMG	72	AAINWSGDNTHYA	122	CATDPPLFW
4-23	23	RTFSDDAMG	73	AGISWNGGSIYYA	123	CATDPPLFW
4-24	24	RTFSDYTMG	74	AAINWSGGTTYA	124	CATDPPLFW
4-25	25	GTFSRYAMG	75	SAVDSGGSTYYA	125	CAASPSLRS AWQW
4-26	26	RTFSDDTMG	76	AAVNWSGGSTYYA	126	CATDPPLFW
4-27	27	RTFGDYIMG	77	AAINWSAGYTAYA	127	CARATPNTGWHFDHW
4-28	28	RTFGDDTMG	78	AAINWNGGNTHYA	128	CATDPPLFW
4-29	29	RTFGDDTMG	79	AAINWSGGYTYA	129	CATDPPLFW
4-30	30	RTFGDYTMG	80	AAINWTGGYTYA	130	CATDPPLFW
4-31	31	RTFGDYIMG	81	AAINWSAGYTAYA	131	CATASPNTGWHFDHW
4-32	32	FTFDDYEMG	82	AAISWRGGTTYA	132	CAADRRGLASTRAGDYDW
4-33	33	FTFSRHDMG	83	AGINWESGSTNYA	133	CAADRGVYGGRWYRTSQY TW

4-34	34	RTFGDYIMG	84	AAINWSADYTAYA	134	CATDPPLFCWHFDHW
4-35	35	QLANFASYAMG	85	AAITRSGSSTVYA	135	CATTMNPNNPRW
4-36	36	RTFGDYIMG	86	AAINWSAGYTAYA	136	CATAPPLFCWHFDHW
4-37	37	RTFGDYGMG	87	ATINWSGALTHYA	137	CATLPFYDFWSGYTGYYY MDVW
4-38	38	RTFSDDTMG	88	AAITWSGGRTRYA	138	CATDRPLFW
4-39	39	RTFSNAAMG	89	ARILWTGASRYA	139	CATTENPNPRW
4-40	40	RTFSDDTMG	90	AGINWSGNGVYYA	140	CATDPPLFW
4-41	41	RTFGDYIMG	91	AAINWSGGTTPYA	141	CATDPPLFCCHVDLW
4-42	42	RTFGDDTMG	92	AAINWSGGYTPYA	142	CATDPPLFWGHVDLW
4-43	43	RTFSDDTMG	93	AAINWSGGSTDYA	143	CATDPPLFW
4-44	44	RTFGDYIMG	94	AAINWSAGYTAYA	144	CATARPNTGWHFDHW
4-45	45	RTFSDDAMG	95	AAINWSGGSTRYA	145	CATDPPLFW
4-46	46	RTFGDYIMG	96	AAINWSAGYTPYA	146	CATDPPLFWGHVDLW
4-47	47	FTFGDYVMG	97	AAINWNAGYTAYA	147	CAKASPNTGWHFDHW
4-48	48	RTFSDDAMG	98	GRINWSGGNTYYA	148	CATDPPLFW
4-49	49	RTFGDYIMG	99	AAINWSAGYTAYA	149	CARASPNTGWHFDHW
4-50	50	GTFSNSGMG	100	AVVNWSGRRTYA	150	CAVPWMDYNRRDW

Table 20. SARS-CoV-2 S1 Variable Heavy Chain CDRs

Variant	SEQ ID NO	CDRH1	SEQ ID NO	CDRH2	SEQ ID NO	CDRH3
2-1	151	FTFSNYATD	166	SIISGSGGATYYA	181	CAKGGYCSDTCWWEYWLDPW
2-2	152	FTFSRHAMN	167	SGISGSGDETYA	182	CARDLPASYDSSGYWYHNGMDVW
2-3	153	FTFSDFAMA	168	SAISGSGDITYA	183	CAREADCLPSPWYLDLW
2-4	154	FTFSDFAMA	169	SAITGTGDITYA	184	CAREADGLHSPW
2-5	155	FTFSDFAMA	170	SAISGSGDITYA	185	CAREADGLHSPWHFDLW
2-6	156	FTFSDFAMA	171	SAISGSGDITYA	186	CAREADGLHSPWHFDLW
2-7	157	FTFSDFAMA	172	SAITGSGDITYA	187	CAREADGLHSPWHFDLW
2-8	158	FTFSDFAMA	173	SAISGSGDITYA	188	CAREADGLHSPWHFDLW
2-9	159	FTFPRYAMS	174	STISGSGSTTYA	189	CARLIDAFDIW

2-10	160	FTFSAFAMG	175	SAITASGDITYYA	190	CARQSDGLPSPWHFDLG
2-11	161	FTFSNYPMN	176	STISGSGGNTFYA	191	CVRHDEYSFDYW
2-12	162	FTFSDYPMN	177	STISGSGGITYYA	192	CVRHDEYSFDYW
2-13	163	FTFSDYPMN	178	SAISGSGDNTYYA	193	CVRHDEYSFDYW
2-14	164	FTFSDYPMN	179	SAITGSGDITYYA	194	CVRHDEYSFDYW
2-15	165	FTFSDYPMN	180	STISGSGGITYYA	195	CVRHDEYSFDYW

Table 21. SARS-CoV-2 S1 Variable Light Chain CDRs

Variant	SEQ ID NO	CDRL1	SEQ ID NO	CDRL2	SEQ ID NO	CDRL3
2-1	196	RASQSIHRFLN	211	AASNLHS	226	CQQSYGLPPTF
2-2	197	RASQTINTYLN	212	SASTLQS	227	CQQSYSTFTF
2-3	198	RASQNIHTYLN	213	AASTFAK	228	CQQSYSAPPYTF
2-4	199	RASQSIDTYLN	214	AASALAS	229	CQQSYSAPPYTF
2-5	200	RASQSIHTYLN	215	AASALAS	230	CQQSYSAPPYTF
2-6	201	RASQSIDTYLN	216	AASALAS	231	CQQSYSAPPYTF
2-7	202	RASQSIDTYLN	217	AASALAS	232	CQQSYSAPPYTF
2-8	203	RASQSIDTYLN	218	AASALAS	233	CQQSYSAPPYTF
2-9	204	RASQRIGTYLN	219	AASNLEG	234	CQQNYSTTWTF
2-10	205	RASQSIHISLN	220	LASPLAS	235	CQQSYSAPPYTF
2-11	206	RASQSIGNNYLN	221	GVSSLQS	236	CQQSHSAPLTF
2-12	207	RASQSIDNYLN	222	GVSALQS	237	CQQSHSAPPYFF
2-13	208	RASQSIDTYLN	223	GASALES	238	CQQSHSAPPYFF
2-14	209	RASQSIDTYLN	224	GVSALQS	239	CQQSYSAPPYFF
2-15	210	RASQSIDNYLN	225	GVSALQS	240	CQQSHSAPLTF

Table 22. ACE2 Variable Heavy Chain CDRs

Variant	SEQ ID NO	CDRH1	SEQ ID NO	CDRH2	SEQ ID NO	CDRH3
3-1	241	FMFGNYAMS	256	AAISGSGGSTYYA	271	CAKDRGYSSSWYGGFDYW
3-2	242	FTFRSHAMN	257	SAISGSGGSTNYA	272	CARGLKFWLPSAFDIW
3-3	243	FTFRNYAMA	258	SGISGSGGTYYG	273	CARGTRFLEWSLPLDVW

3-4	244	FTFRNHAMA	259	SGISGSGGTTYG	274	CARGTRFLQWSLPLDVW
3-5	245	FTITNYAMS	260	SGISGSGAGTYA	275	CARHAWWKGAGFFDHW
3-6	246	FTIPNYAMS	261	SGISGAGASTYA	276	CARHTWWKGAGFFDHW
3-7	247	FTIPNYAMS	262	SGISGSGASTYA	277	CARHTWWKGAGFFDHW
3-8	248	FTITNYAMS	263	SGISGSGASTYA	278	CARHTWWKGAGFFDHW
3-9	249	FTITNYAMS	264	SGISGSGAGTYA	279	CARHTWWKGAGFFDHW
3-10	250	FTFRSHAMS	265	SSISGGGASTYA	280	CARVKYLTSSGWPRPYFDNW
3-11	251	FTIRNYAMS	266	SSISGGGASTYA	281	CARVKYLTSSGWPRPYFDNW
3-12	252	FTFRSHAMS	267	SSISGGGASTYA	282	CARVKYLTSSGWPRPYFDNW
3-13	253	FTFRSHAMS	268	SSISGGGASTYA	283	CARVKYLTSSGWPRPYFDNW
3-14	254	FTFRSYAMS	269	SSISGGGASTYA	284	CARVKYLTSSGWPRPYFDNW
3-15	255	FTFSAYSMS	270	SAISGSGGSRYA	285	CGRSKWPQANGAFDIW

Table 23. ACE2 Variable Light Chain CDRs

Name	SEQ ID NO	CDRL1	SEQ ID NO	CDRL2	SEQ ID NO	CDRL3
3-1	286	RASQTIYSYLN	301	ATSTLQG	316	CQHRGTF
3-2	287	RTSQSINTYLN	302	GASNVQS	317	CQQSYRIPRTF
3-3	288	RASRSISRYLN	303	AASSLQA	318	CQQSYSSLLTF
3-4	289	RASRSIRRYLN	304	ASSSLQA	319	CQQSYSTLLTF
3-5	290	RASQSIGRYLN	305	AASSLKS	320	CQQSYSLPRTF
3-6	291	RASQSIGKYL	306	ASSSLQS	321	CQQSYSPPTF
3-7	292	RASQSIGRYLN	307	ASSSLQS	322	CQQSYSLPRTF
3-8	293	RASQSIGRYLN	308	AASSLKS	323	CQQSYSLPLTF
3-9	294	RASQSIGRYLN	309	AASSLKS	324	CQQSYSLPRTF
3-10	295	RASQSIRKYL	310	ASSTLQR	325	CQQSLSTPPTF
3-11	296	RASQSIGKYL	311	ASSTLQR	326	CQQSLSPPTF
3-12	297	RASQSIGKYL	312	ASSTLQR	327	CQQSLSTPPTF
3-13	298	RASQSIGKYL	313	ASSTLQR	328	CQQSFSPPTF
3-14	299	RASQSIGKYL	314	ASSTLQR	329	CQQSFSTPPTF
3-15	300	RASQNIKTYLN	315	AASKLQS	330	CQQSYSTSPTF

Table 24. SARS-CoV-2 S1 Variable Heavy Chain CDRs

Name	SEQ ID NO	CDRH1	SEQ ID NO	CDRH2	SEQ ID NO	CDRH3
2-1	331	FTFSNYATD	358	SIISGSGGATYYA	385	CAKGGYCSDTCWWEYWLDPW
2-10	332	FTFSAFAMG	359	SAITASGDITYYA	386	CARQSDGLPSPWHFDLG
2-5	333	FTFSDFAMA	360	SAISGSGDITYYA	387	CAREADGLHSPWHFDLW
2-2	334	FTFSRHAMN	361	SGISGSGDETYYA	388	CARDLPASYDSSGGYYWHNGMDVW
2-4	335	FTFSDFAMA	362	SAISGSGDITYYA	389	CAREADGLHSPWHFDLW
2-6	336	FTFSNYPMN	363	STISGSGGNTFYA	390	CVRHDEYSFDYW
2-11	337	FTFSDFAMA	364	SAITGSGDITYYA	391	CAREADGLHSPWHFDLW
2-12	338	FTFSYPMN	365	STISGSGGITYYA	392	CVRHDEYSFDYW
2-13	339	FTFSYPMN	366	SAISGSGDNTYYA	393	CVRHDEYSFDYW
2-14	340	FTFSDFAMA	367	SAITGTGDITYYA	394	CAREADGLHSPW
2-7	341	FTFSYPMN	368	SAITGSGDITYYA	395	CVRHDEYSFDYW
2-8	342	FTFSDFAMA	369	SAISGSGDITYYA	396	CAREADGLHSPWHFDLW
2-15	343	FTFSDFAMA	370	SAISGSGDITYYA	397	CAREADGLHSPWHFDLW
2-9	344	FTFPRYAMS	371	STISGSGSTTYA	398	CARLIDAFDIW
2-16	345	FTFSSYAMS	372	SVISGSGGSTYYA	399	CAREGYRDYLYWFDLW
2-17	346	FTFSNYAMS	373	SAISGSAGSTYYA	400	CARVRQGLRRTWYYFDYW
2-18	347	FTFSSYAMY	374	SAISGSAGSTYYA	401	CARDTNDFWSGYSIFDPW
2-19	348	FTFSSYTMS	375	SVISGSGGSTYYA	402	CAREGYRDYLYWFDLW
2-2	349	FTFSSYDMS	376	SVISGSGGSTYYA	403	CAKGPLVGWYFDLW
2-21	350	FTFPRYAMS	377	STISGSGSTTYA	404	CARLIDAFDIW
2-22	351	FTFTTYALS	378	SGISGSGDETYYA	405	CTTGDDFWSGGNWFDPW
2-23	352	FTFSRHAMN	379	SGITGSGDETYYA	406	CARDLPASYDSSGGYYWHNGMDVW
2-24	353	FVFSSYAMS	380	SAISGSGGSSYYA	407	CARVGGGYWYGIDVW
2-25	354	FTLSSYVMS	381	SGISGGGASTYYA	408	CARGYSRNWYPSWFDPW
2-26	355	FTFSTYAMS	382	SSIGSGGSTTYA	409	CAGGWYLDYW
2-27	356	FTYSNYAMT	383	SAISGSSGSTYYA	410	CASLCIVDPFDIW
2-28	357	FTFSNYPMN	384	STISGSGGNTFYA	411	CVRHDEYSFDYW

Table 25. SARS-CoV-2 S1 Variable Light Chain CDRs

Name	SEQ ID NO	CDRL1	SEQ ID NO	CDRL2	SEQ ID NO	CDRL3
2-1	412	RASQSIHRFLN	439	AASNLHS	466	CQQSYGLPPTF
2-10	413	RASQSIHISLN	440	LASPLAS	467	CQQSYSAPPYTF
2-5	414	RASQSIHTYLN	441	AASALAS	468	CQQSYSAPPYTF
2-2	415	RASQTINTYLN	442	SASTLQS	469	CQQSYSTFTF

2-4	416	RASQSIDTYLN	443	AASALAS	470	CQQSYSAPPYTF
2-6	417	RASQSIGNLYN	444	GVSSLQS	471	CQQSHSAPLTF
2-11	418	RASQSIDTYLN	445	AASALAS	472	CQQSYSAPPYTF
2-12	419	RASQSIDNYLN	446	GVSALES	473	CQQSHSAPPYFF
2-13	420	RASQSIDTYLN	447	GASALES	474	CQQSHSAPPYFF
2-14	421	RASQSIDTYLN	448	AASALAS	475	CQQSYSAPPYTF
2-7	422	RASQSIDTYLN	449	GVSALES	476	CQQSYSAPPYFF
2-8	423	RASQSIDTYLN	450	AASALAS	477	CQQSYSAPPYTF
2-15	424	RASQSIDNYLN	451	GVSALES	478	CQQSHSAPLTF
2-9	425	RASQRIGTYLN	452	AASNLEG	479	CQQNYSTTWTF
2-16	426	TGTSSDVGSYDLVS	453	EGNKRPS	480	CCSYAGSSVVF
2-17	427	TGTSSDVGSYNLVS	454	EGSKRPS	481	CCSYAGSLYVF
2-18	428	TGTSSDIGSYNLVS	455	EGTKRPS	482	CCSYAGSRTYVF
2-19	429	TGTSTDVGSYNLVS	456	EGTKRPS	483	CCSYAGSYTSVVF
2-2	430	TGTSSNVGSYNLVS	457	EGTKRPS	484	CCSYAGSSSFVVF
2-21	431	RASQSIHTYLN	458	AASALAS	485	CQQSYSAPPYTF
2-22	432	RASQSIHTYLN	459	AASALAS	486	CQQSYSAPPYTF
2-23	433	RASQTINTFLN	460	SASTLQS	487	CQQSYSTFTF
2-24	434	RASQTIRTYLN	461	DASTLQR	488	CQQSYRTPPWTF
2-25	435	RSSQSISSYLN	462	GASRLRS	489	CQQGYSAPWTF
2-26	436	RASQSIGSLN	463	AESRLHS	490	CQQSYSPQTF
2-27	437	RASRSISTYLN	464	AASNLQG	491	CQQSHSIPRTF
2-28	438	RASQSIHTYLN	465	AASALAS	492	CQQSYSAPPYTF

Table 26. SARS-CoV-2 S1 Variant Sequences Variable Heavy Chain

Name	SEQ ID NO	Amino Acid Sequence
2-1	493	EVQLLES GGGGLVQP GGSRLRLSCAASGFTFSNYATDWVRQAPGKGLEWVSIISGS GGATYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGGYCSDTC WWEYWLDPWGQGTLVTVSS
2-10	494	EVQLLES GGGGLVQP GGSRLRLSCAASGFTFSAFAMGWVRQAPGKGLEWVSAITAS GDITYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARQSDGLPSPWH FDLGGQGTLVTVSS
2-5	495	EVQLLES GGGGLVQP GGSRLRLSCAASGFTFSDFAMAWVRQAPGKGLEWVSAISGS GDITYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREADGLHSPW HFDLWGQGTLVTVSS
2-2	496	EVQLLES GGGGLVQP GGSRLRLSCAASGFTFSRHAMNWVRQAPGKGLEWVSGISG SGDEYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDLPASYD SSGYWHNGMDVWGQGTLVTVSS
2-4	497	EVQLLES GGGGLVQP GGSRLRLSCAASGFTFSDFAMAWVRQAPGKGLEWVSAISGS GDITYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREADGLHSPW

		HFDLWGQGLTVTVSS
2-6	498	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYPMNWVRQAPGKGLEWVSTISGS GGNTFYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCVRHDEYSFDYW GQGLTVTVSS
2-11	499	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDFAMAWVRQAPGKGLEWVSAITGS GDITYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREADGLHSPW HFDLWGQGLTVTVSS
2-12	500	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDFPMNWVRQAPGKGLEWVSTISGS GGITFYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCVRHDEYSFDYW GQGLTVTVSS
2-13	501	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDFPMNWVRQAPGKGLEWVSAISGS GDNTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCVRHDEYSFDYW GQGLTVTVSS
2-14	502	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDFAMAWVRQAPGKGLEWVSAITG TGDITYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREADGLHSP WGQGLTVTVSS
2-7	503	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDFPMNWVRQAPGKGLEWVSAITGS GDITYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCVRHDEYSFDYW GQGLTVTVSS
2-8	504	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDFAMAWVRQAPGKGLEWVSAISGS GDITYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREADGLHSPW HFDLWGQGLTVTVSS
2-15	505	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDFAMAWVRQAPGKGLEWVSAISGS GDITYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREADGLHSPW HFDLWGQGLTVTVSS
2-9	506	EVQLLESGGGLVQPGGSLRLSCAASGFTFPRYAMSWVRQAPGKGLEWVSTISGS GSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARLIDAFDIWGQ GTLTVTVSS
2-16	507	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISGS GGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREGYRDYLWY FDLWGQGLTVTVSS
2-17	508	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGS AGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARVRQGLRRTW YFDYWGGQGLTVTVSS
2-18	509	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMYWVRQAPGKGLEWVSAISGS AGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDTNDFWSGY SIFDPWGQGLTVTVSS
2-19	510	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYTMSWVRQAPGKGLEWVSVISGS GGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREGYRDYLWY FDLWGQGLTVTVSS
2-2	511	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVSVISGS GGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGPLVGWYFD LWGQGLTVTVSS
2-21	512	EVQLLESGGGLVQPGGSLRLSCAASGFTFPRYAMSWVRQAPGKGLEWVSTISGS GSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARLIDAFDIWGQ GTLTVTVSS
2-22	513	EVQLLESGGGLVQPGGSLRLSCAASGFTFTTYALSWVRQAPGKGLEWVSGISGS GDETYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTTGDDFWSGGN WFDPWGQGLTVTVSS
2-23	514	EVQLLESGGGLVQPGGSLRLSCAASGFTFSRHAMNWVRQAPGKGLEWVSGITG SGDETYADSVKGRFTISRDN SKNTLYLQMNSLKAEDTAVYYCARDLPASYDD SSGYWHNGMDVWGQGLTVTVSS
2-24	515	EVQLLESGGGLVQPGGSLRLSCAASGFVSSYAMSWVRQAPGKGLEWVSAISGS GGSSYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARVGGGYWYGI DVWGQGLTVTVSS

2-25	516	EVQLLESGGGLVQPGGSLRLSCAASGFTLSSYVMSWVRQAPGKGLEWVSGISGG GASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGYSRNWYPS WFDPWGQGT LVT VSS
2-26	517	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSSIGGS GSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAGGWYLDYWG QGT LVT VSS
2-27	518	EVQLLGSGGGLVQPGGSLRLSCAASGFTYSNYAMTWVRQAPGKGLEWVSAISG SSGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCASLCIVDPFDI WGQGT LVT VSS
2-28	519	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYPMNWVRQAPGKGLEWVSTISGS GGNTFYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCVRHDEYSFDYW GQGT LVT VSS

Table 27. SARS-CoV-2 S1 Variant Sequences Variable Light Chain

Name	SEQ ID NO	Amino Acid Sequence
2-1	520	DIQMTQSPSSLSASVGDRVITITCRASQSIHRFLN WYQQKPGKAPKLLIYAASN LHS GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYGLPP-TFGQGTKVEIK
2-10	521	DIQMTQSPSSLSASVGDRVITITCRASQSIHISLN WYQQKPGKAPKLLIYLASPLASG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSY SAPPYTFGQGTKVEIK
2-5	522	DIQMTQSPSSLSASVGDRVITITCRASQSIHTYLN WYQQKPGKAPKLLIYAASALAS GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSY SAPPYTFGQGTKVEIK
2-2	523	DIQMTQSPSSLSASVGDRVITITCRASQTINTYLN WYQQKPGKAPKLLIYASATLQS GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTFTFGQGTKVEIK
2-4	524	DIQMTQSPSSLSASVGDRVITITCRASQSIDTYLN WYQQKPGKAPKLLIYAASALAS GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSY SAPPYTFGQGTKVEIK
2-6	525	DIQMTQSPSSLSASVGDRVITITCRASQSIDTYLN WYQQKPGKAPKLLIYAASALAS GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSY SAPPYTFGQGTKVEIK
2-11	526	DIQMTQSPSSLSASVGDRVITITCRASQSIGN YLN WYQQKPGKAPKLLIYGVSSLQS GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHSAPLTFGQGTKVEIK
2-12	527	DIQMTQSPSSLSASVGDRVITITCRASQSIDNYLN WYQQKPGKAPKLLIYGVSA LQS GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHSAPPYFFGQGTKVEIK
2-13	528	DIQMTQSPSSLSASVGDRVITITCRASQSIDTYLN WYQQKPGKAPKLLIYGASALES GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHSAPPYFFGQGTKVEIK
2-14	529	DIQMTQSPSSLSASVGDRVITITCRASQSIDTYLN WYQQKPGKAPKLLIYGVSA LQS GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSY SAPPYFFGQGTKVEIK
2-7	530	DIQMTQSPSSLSASVGDRVITITCRASQSIDTYLN WYQQKPGKAPKLLIYAASALAS GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSY SAPPYTFGQGTKVEIK
2-8	531	DIQMTQSPSSLSASVGDRVITITCRASQSIDTYLN WYQQKPGKAPKLLIYAASALAS GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSY SAPPYTFGQGTKVEIK
2-15	532	DIQMTQSPSSLSASVGDRVITITCRASQSIDNYLN WYQQKPGKAPKLLIYGVSA LQS GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHSAPLTFGQGTKVEIK
2-9	533	DIQMTQSPSSLSASVGDRVITITCRASQRI GTYLN WYQQKPGKAPKLLIYAASNLE GGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQNYSTTWTFGQGTKVEIK
2-16	534	DIQMTQSPSSLSASVGDRVITITCTGTSSDVGSYDLVSWYQQKPGKAPKLLIYEGN KRPSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCCSYAGSSVVFQGTKVEIK
2-17	535	DIQMTQSPSSLSASVGDRVITITCTGTSSDVGSNLVSWYQQKPGKAPKLLIYEGSK RPSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCCSYAGSLYVFQGTKVEIK
2-18	536	DIQMTQSPSSLSASVGDRVITITCTGTSSDIGSYNLVSWYQQKPGKAPKLLIYEGTK RPSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCCSYAGSRTYVFQGTKVEIK
2-19	537	DIQMTQSPSSLSASVGDRVITITCTGTSTDVGSYNLVSWYQQKPGKAPKLLIYEGT KRPSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCCSYAGSYTSVVFQGTKVEIK

2-2	538	DIQMTQSPSSLSASVGDRVITICTGTSSNVGSYNLVSQYQKPGKAPKLLIYEGT KRPSGVPSRFGSGSGTDFTLTISSLQPEDFATYYCCSYAGSSSFVFGQGTKVEIK
2-21	539	DIQMTQSPSSLSASVGDRVITICRASQSIHTYLNWYQKPGKAPKLLIYAASALAS GVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYAPPYTFGQGTKVEIK
2-22	540	DIQMTQSPSSLSASVGDRVITICRASQSIHTYLNWYQKPGKAPKLLIYAASALAS GVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYAPPYTFGQGTKVEIK
2-23	541	DIQMTQSPSSLSASVGDRVITICRASQTINTFLNWYQKPGKAPKLLIYASATLQS GVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYSTFTFGGGTKVEIK
2-24	542	DIQMTQSPSSLSASVGDRVITICRASQTIRTYLNWYRQKPGKAPKLLIYDASTLQR GVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYRTPPWTFGGGTKVEIK
2-25	543	DIQMTQSPSSLSASVGDRVITICRSSQSISSYLNWYQKPGKAPKLLIYGASRLRSG VPSRFGSGSGTDFTLTISSLQPEDFATYYCQQGYAPWTFGGGTKVEIK
2-26	544	DIQMTQSPSSLSASVGDRVITICRASQSIGSLNWYQKPGKAPKLLIYAESRLHS GVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYSPPTFGGGTKVEIK
2-27	545	DIQMTQSPSSLSASVGDRVITICRASRSISTYLNWYQKPGKAPKLLIYAASNQGG GVPSRLSGSGSGTDFTLTISSLQPEDFATYYCQQSHSIPRTFGGGTKVEIK
2-28	546	DIQMTQSPSSLSASVGDRVITICRASQSIHTYLNWYQKPGKAPKLLIYAASALAS GVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYAPPYTFGQGTKVEIK

Table 28. ACE2 Variable Heavy Chain CDRs

Name	SEQ ID NO	CDRH1	SEQ ID NO	CDRH2	SEQ ID NO	CDRH3
3-10	547	FTFRSHAMS	576	SSISGGGASTYYA	605	CARVKYLTSSSGWPRPYFDNW
3-4	548	FTFSAYSMS	577	SAISGSGSRYA	606	CGRSKWPQANGAFDIW
3-7	549	FMFGNYAMS	578	AAISGSGGSTYYA	607	CAKDRGYSSSWYGGFDYW
3-1	550	FTFRNHAMA	579	SGISGSGGTYYG	608	CARGTRFLQWSLPLDVW
3-5	551	FTIPNYAMS	580	SGISGAGASTYYA	609	CARHTWWKGAGFFDHW
3-6	552	FTFRNYAMA	581	SGISGSGGTYYG	610	CARGTRFLEWSLPLDVW
3-15	553	FTIRNYAMS	582	SSISGGGASTYYA	611	CARVKYLTSSSGWPRPYFDNW
3-3	554	FTIPNYAMS	583	SGISGSGASTYYA	612	CARHTWWKGAGFFDHW
3-11	555	FTITNYAMS	584	SGISGSGAGTYA	613	CARHAWWKAGAGFFDHW
3-8	556	FTFRSHAMS	585	SSISGGGASTYYA	614	CARVKYLTSSSGWPRPYFDNW
3-2	557	FTITNYAMS	586	SGISGSGASTYYA	615	CARHTWWKGAGFFDHW
3-12	558	FTFRSHAMN	587	SAISGSGGSTNYA	616	CARGLKFLEWLPFAFDIW
3-14	559	FTFRSHAMS	588	SSISGGGASTYYA	617	CARVKYLTSSSGWPRPYFDNW
3-9	560	FTFRSYAMS	589	SSISGGGASTYYA	618	CARVKYLTSSSGWPRPYFDNW
3-13	561	FTITNYAMS	590	SGISGSGAGTYA	619	CARHTWWKGAGFFDHW
3-16	562	FTFTNFAMS	591	SAISGRGGGTYYA	620	CARDAHGYYYDSSGYDDW
3-17	563	FTFRSYPMS	592	STISGSGGITYA	621	CAKGVYGSTVTTCW
3-18	564	FTLTSYAMS	593	SAISGSGVDITYA	622	CARPTNWGFYDW
3-19	565	FTFINYAMS	594	STISTSGGNTYYA	623	CARADSNWASSAYW
3-2	566	FPFSTYAMS	595	SGISVSGGFTYYA	624	CARDPYSYGYYYYYGMDVW

3-21	567	FTFSTYAMG	596	SGISGGGVSTYYA	625	CARARNWGSPSDYW
3-22	568	FIFSDYAMT	597	SAISGSAFYA	626	CARDATYSSSWYNWFDPW
3-23	569	FTFSDYAMT	598	SDISGSGGSTYYA	627	CARGTVTSFDFW
3-24	570	FTFSIYAMG	599	SFISGSGGSTYYA	628	CAKDYHSASWFSAADYW
3-25	571	FTFASYAMT	600	SAISESGGSTYYA	629	CAREGQEYSSGSSYFDYW
3-26	572	FTFSEYAMS	601	SAITGSGGSTYYG	630	CARGSQTPYCGGDCPETFDYW
3-27	573	FTFDDYAMS	602	SGISGGGTSTYYA	631	CARDLYSSGWYGFDFW
3-28	574	FTFNYYAMN	603	SAISGSGVSTYYA	632	CARDNYDFWSGYTNNWFDPW
3-29	575	FTFTNHAMS	604	SAISGSGSNIYYA	633	CARDSLSVTMGRGVVTTYYYYGMDFW

Table 29. ACE2 Variant Sequences Variable Light Chain

Name	SEQ ID NO	CDRL1	SEQ ID NO	CDRL2	SEQ ID NO	CDRL3
3-10	634	RASQSIRKYLN	663	ASSTLQR	692	CQQSLSTPFTF
3-4	635	RASQNIKTYLN	664	AASKLQS	693	CQQSYSTSPFTF
3-7	636	RASQTIYSYLN	665	ATSTLQG	694	CQHRGTF
3-1	637	RASRSIRRYLN	666	ASSSLQA	695	CQQSYSTLLTF
3-5	638	RASQSIGKYLN	667	ASSSLQS	696	CQQSYSPPTF
3-6	639	RASRSISRYLN	668	AASSLQA	697	CQQSYSSLTF
3-15	640	RASQSIGKYLN	669	ASSTLQR	698	CQQSLSPPTF
3-3	641	RASQSIGRYLN	670	ASSSLQS	699	CQQSYSLPRTF
3-11	642	RASQSIGRYLN	671	AASSLKS	700	CQQSYSLPRTF
3-8	643	RASQSIGKYLN	672	ASSTLQR	701	CQQSLSTPFTF
3-2	644	RASQSIGRYLN	673	AASSLKS	702	CQQSYSLPLTF
3-12	645	RTSQSINTYLN	674	GASNVQS	703	CQQSYRIPRTF
3-14	646	RASQSIGKYLN	675	ASSTLQR	704	CQQSFSPPTF
3-9	647	RASQSIGKYLN	676	ASSTLQR	705	CQQSFSTPPTF
3-13	648	RASQSIGRYLN	677	AASSLKS	706	CQQSYSLPRTF
3-16	649	RASQIIGSYLN	678	TTSNLQS	707	CQQSYITPWTF
3-17	650	RASQSISRYIN	679	EASSLES	708	CQQSHITPLTF
3-18	651	RASQSIYTYLN	680	SASNLHS	709	CQQSDTTPWTF
3-19	652	RASQSIATYLN	681	GASSLEG	710	CQQTFFSPPTF
3-2	653	RASQNINTYLN	682	SASSLQS	711	CQQSSLTPWTF
3-21	654	RASQGIATYLN	683	YASNLQS	712	CQQSYSTRFTF
3-22	655	RASERISNYLN	684	TASNLES	713	CQQSYTPPRTF
3-23	656	RASQSISSSLN	685	AASRLQD	714	CQQSYSTPRSF
3-24	657	RASQSISSHLN	686	RASTLQS	715	CQQTYNTPQTF

3-25	658	RASQSISSYLI	687	AASRLHS	716	CQQGYNTPRTF
3-26	659	RASPSISTYLN	688	TASRLQT	717	CQQTYSTPSSF
3-27	660	RASQNIAYLN	689	GASGLQS	718	CQQSHSPITF
3-28	661	RASQSIGTYLN	690	AASNLHS	719	CQESYSAPYTF
3-29	662	RASQSIOPYLN	691	KASSLQS	720	CQQSSSTPYTF

Table 30. ACE2 Variant Sequences Variable Heavy Chain

Name	SEQ ID NO	Amino Acid Sequence
3-10	721	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSHAMSWVRQAPGKGLEWVS SISGGGASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR VKYLTSSGWPRPYFDNWGQGTLTVSS
3-4	722	EVQLLESGGGLVQPGGSLRLSCAASGFTFSAYSMSWVRQAPGKGLEWVS AISGSGGSRYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGRS KWPQANGAFDIWGQGTLTVSS
3-7	723	EVQLLESGGGLVQPGGSLRLSCAASGFMFGNYAMSWVRQAPGKGLEWV AAISGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCA KDRGYSSSWYGGFDYWGQGTLTVSS
3-1	724	EVQLLESGGGLVQPGGSLRLSCAASGFTFRNHAMAWVRQAPGKGLEWV SGISGSGGTYYGDSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR GTRFLQWSLPLDVWGQGTLTVSS
3-5	725	EVQLLESGGGLVQPGGSLRLSCAASGFTIPNYAMSWVRQAPGKGLEWVS GISGAGASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR HTWWKGAGFFDHWGQGTLTVSS
3-6	726	EVQLLESGGGLVQPGGSLRLSCAASGFTFRNYAMAWVRQAPGKGLEWV SGISGSGGTYYGDSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR GTRFLEWSLPLDVWGQGTLTVSS
3-15	727	EVQLLESGGGLVQPGGSLRLSCAASGFTIRNYAMSWVRQAPGKGLEWVS SISGGGASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR VKYLTSSGWPRPYFDNWGQGTLTVSS
3-3	728	EVQLLESGGGLVQPGGSLRLSCAASGFTIPNYAMSWVRQAPGKGLEWVS GISGSGASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR HTWWKGAGFFDHWGQGTLTVSS
3-11	729	EVQLLESGGGLVQPGGSLRLSCAASGFTITNYAMSWVRQAPGKGLEWVS GISGSGAGTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR HAWWKAGFFDHWGQGTLTVSS
3-8	730	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSHAMSWVRQAPGKGLEWVS SISGGGASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR VKYLTSSGWPRPYFDNWGQGTLTVSS
3-2	731	EVQLLESGGGLVQPGGSLRLSCAASGFTITNYAMSWVRQAPGKGLEWVS GISGSGASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR HTWWKGAGFFDHWGQGTLTVSS
3-12	732	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSHAMNWSVRQAPGKGLEWV SAISGSGGSTNYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR GLKFLEWLPSAFDIWGQGTLTVSS
3-14	733	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSHAMSWVRQAPGKGLEWVS SISGGGASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR VKYLTSSGWPRPYFDNWGQGTLTVSS
3-9	734	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSYAMSWVRQAPGKGLEWVS SISGGGASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR VKYLTSSGWPRPYFDNWGQGTLTVSS
3-13	735	EVQLLESGGGLVQPGGSLRLSCAASGFTITNYAMSWVRQAPGKGLEWVS

		GISGSGAGTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR HTWWKGAGFFDHWGQGLTVTVSS
3-16	736	EVQLLESGGGLVQPGGSLRLSCAASGFTFTNFAMSWVRQAPGKGLEWVS AISGRGGTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR DAHGYYYDSSGYDDWGQGLTVTVSS
3-17	737	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSYPMSWVRQAPGKGLEWVS TISGSGGITYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKG VYGSTVTTCHWGQGLTVTVSS
3-18	738	EVQLLESGGGLVQPGGSLRLSCAASGFTLTSYAMSWVRQAPGKGLEWVS AISGSGVDITYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR PTNWGFDYWGQGLTVTVSS
3-19	739	EVQLLESGGGLVQPGGSLRLSCAASGFTFINYAMSWVRQAPGKGLEWVS TISTSGGNTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARA DSNWASSAYWGQGLTVTVSS
3-2	740	EVQLLESGGGLVQPGGSLRLSCAASGFPFSTYAMSWVRQAPGKGLEWVS GISVSGGFTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR DPYSYGYYYYYGMDVWGQGLTVTVSS
3-21	741	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMGWVRQAPGKGLEWVS GISGGGVSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR ARNWGPSDYWGQGLTVTVSS
3-22	742	EVQLLESGGGLVQPGGSLRLSCAASGFIFSDYAMTWVRQAPGKGLEWVS AISGSAFYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDAT YSSSWYNWFDPWGQGLTVTVSS
3-23	743	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMTWVRQAPGKGLEWVS DISGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR GTVTSFDFWGQGLTVTVSS
3-24	744	EVQLLESGGGLVQPGGSLRLSCAASGFTFSIYAMGWVRQAPGKGLEWVS FISGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKD YHSASWFSAADYWGQGLTVTVSS
3-25	745	EVQLLESGGGLVQPGGSLRLSCAASGFTFASYAMTWVRQAPGKGLEWVS AISESGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARE GQEYSSGSSYFDYWGQGLTVTVSS
3-26	746	EVQLLESGGGLVQPGGSLRLSCAASGFTFSEYAMSWVRQAPGKGLEWVS AITGSGGSTYYGDSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR GSQTPYCGGDCPETFDYWGQGLTVTVSS
3-27	747	EVQLLESGGGLVQPGGSLRLSCAASGFTFDDYAMSWVRQAPGKGLEWV SGISGGGTSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR DLYSSGWYGFYWGQGLTVTVSS
3-28	748	EVQLLESGGGLVQPGGSLRLSCAASGFTFNYYAMNWVRQAPGKGLEWV SAISGSGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR DNYDFWSGYYTNWFDPWGQGLTVTVSS
3-29	749	EVQLLESGGGLVQPGGSLRLSCAASGFTFTNHAMSWVRQAPGKGLEWVS AISGSGSNIYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARD SLSVTMGRGVVTTYYYGMDFWGQGLTVTVSS

Table 31. ACE2 Variant Sequences Variable Light Chain

Name	SEQ ID NO	Amino Acid Sequence
3-10	750	DIQMTQSPSSLSASVGDRTITCRASQSIRKYLNWYQQKPGKAPKLLIYASST LQRGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSLSTPFTFGGGTKVEIK
3-4	751	DIQMTQSPSSLSASVGDRTITCRASRSIRRYLNWYQQKPGKAPKLLIYASSSL QAGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTLLTFGQGTKVEIK
3-7	752	DIQMTQSPSSLSASVGDRTITCRASQSIGRYLNWYQQKPGKAPKLLIYASSSL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSLPRTFGQGTKVEIK

3-1	753	DIQMTQSPSSLSASVGDRVITITCRASQTIYSYLNWYQQKPGKAPKLLIYATST LQGGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHRGTFGQGTKVEIK
3-5	754	DIQMTQSPSSLSASVGDRVITITCRASQSIGRYLNWYQQKPGKAPKLLIYAASS LKSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSLPRTFGQGTKVEIK
3-6	755	DIQMTQSPSSLSASVGDRVITITCRASQSIGKYNWYQQKPGKAPKLLIYASSS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSPFTFGQGTKVEIK
3-15	756	DIQMTQSPSSLSASVGDRVITITCRASQNIKTYLNWYQQKPGKAPKLLIYAASK LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTSPFTFGQGTKVEIK
3-3	757	DIQMTQSPSSLSASVGDRVITITCRASRSISRYLNWYQQKPGKAPKLLIYAASSL QAGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSSLLTFGQGTKVEIK
3-11	758	DIQMTQSPSSLSASVGDRVITITCRASQSIGKYNWYQQKPGKAPKLLIYASST LQRGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSLSPFTFGQGTKVEIK
3-8	759	DIQMTQSPSSLSASVGDRVITITCRASQSIGRYLNWYQQKPGKAPKLLIYAASS LKSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSLPLTFGQGTKVEIK
3-2	760	DIQMTQSPSSLSASVGDRVITITCRTSQSINTYLNWYQQKPGKAPKLLIYGASN VQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYRIPRTFGQGTKVEIK
3-12	761	DIQMTQSPSSLSASVGDRVITITCRASQSIGKYNWYQQKPGKAPKLLIYASST LQRGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSLSTPFTFGQGTKVEIK
3-14	762	DIQMTQSPSSLSASVGDRVITITCRASQSIGKYNWYQQKPGKAPKLLIYASST LQRGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSFSTPFTFGQGTKVEIK
3-9	763	DIQMTQSPSSLSASVGDRVITITCRASQSIGRYLNWYQQKPGKAPKLLIYAASS LKSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSLPRTFGQGTKVEIK
3-13	764	DIQMTQSPSSLSASVGDRVITITCRASQSIGKYNWYQQKPGKAPKLLIYASST LQRGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSFSPFTFGQGTKVEIK
3-16	765	DIQMTQSPSSLSASVGDRVITITCRASQIIGSYLNWYQQKPGKAPKLLIYTSTNL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYITPWTFGQGTKVEIK
3-17	766	DIQMTQSPSSLSASVGDRVITITCRASQISRYINWYQQKPGKAPKLLIYEASSL ESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHITPLTFGQGTKVEIK
3-18	767	DIQMTQSPSSLSASVGDRVITITCRASQSIYTYLNWYQQKPGKAPKLLIYSASN LHSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSDTTPWTFGQGTKVEIK
3-19	768	DIQMTQSPSSLSASVGDRVITITCRASQSIATYLNWYQQKPGKAPKLLIYGASS LEGGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQTFSSPFTFGQGTKVEIK
3-2	769	DIQMTQSPSSLSASVGDRVITITCRASQNINTYLNWYQQKPGKAPKLLIYSASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSSLTPWTFGQGTKVEIK
3-21	770	DIQMTQSPSSLSASVGDRVITITCRASQGIATYLNWYQQKPGKAPKLLIYASN LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTRFTFGQGTKVEIK
3-22	771	DIQMTQSPSSLSASVGDRVITITCRASERISNYLNWYQQKPGKAPKLLIYTASN LESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYTPPRTFGQGTKVEIK
3-23	772	DIQMTQSPSSLSASVGDRVITITCRASQSISSSLNWYQQKPGKAPKLLIYAASRL QDGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPRSFQGTKVEIK
3-24	773	DIQMTQSPSSLSASVGDRVITITCRASQSISSHLNWYQQKPGKAPKLLIYRASTL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQTYNTPQTFGQGTKVEIK
3-25	774	DIQMTQSPSSLSASVGDRVITITCRASQSISSYLIWYQQKPGKAPKLLIYAASRL HSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGYNTPRTFGQGTKVEIK
3-26	775	DIQMTQSPSSLSASVGDRVITITCRASPSISTYLNWYQQKPGKAPKLLIYTASRL QTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQTYSTPSSFGQGTKVEIK
3-27	776	DIQMTQSPSSLSASVGDRVITITCRASQNIKYNWYQQKPGKAPKLLIYGASG LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHSPITFGQGTKVEIK
3-28	777	DIQMTQSPSSLSASVGDRVITITCRASQSIGTYLNWYQQKPGKAPKLLIYAASN LHSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQESYSAPYTFGQGTKVEIK
3-29	778	DIQMTQSPSSLSASVGDRVITITCRASQSIPLYLNWYQQKPGKAPKLLIYKASSL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSSSTPYTFGQGTKVEIK

Table 32. ACE2 Variable Heavy Chain CDRs

Name	SEQ ID NO	CDRH1	SEQ ID NO	CDRH2	SEQ ID NO	CDRH3
4-51	779	PGTAIMG	920	ARISTSGGSTKYA	1062	CARTTVTTPLIW
4-52	780	RSFSNSVMG	921	ARITWNGGSTYYA	1063	CATTENPNPRW
4-53	781	RTFGDDTMG	922	AAVSWSGSGVYYA	1064	CATDPPLFW
4-54	782	RTFS DARMG	923	GAVSWSGGTTVYA	1065	CATTEDPYPRW
4-49	783	RTFGDYIMG	924	AAINWSAGYTAYA	1066	CARASPNTGWHFDHW
4-55	784	SGLSINAMG	925	AAISWSGGSTYTAY A	1067	CAAYQAGWGDW
4-39	785	RTFSNAAMG	926	ARILWTGASRNYA	1068	CATTENPNPRW
4-56	786	FSLDYYGMG	927	AAISWNGDFTAYA	1069	CAKRANPTGAYFDYW
4-33	787	FTFSRHDMG	928	AGINWESGSTNYA	1070	CAADRGVYGGRWYRTSQYT W
4-57	788	LTFRNYAMG	929	AAIGSGGYTDYA	1071	CAVKPGWVARDPSQYNW
4-25	789	GTFSRYAMG	930	SAVDSGGSTYYA	1072	CAASPSLRS AWQW
4-58	790	FTLDYYDMG	931	AAVTWSGGSTYYA	1073	CAADRRGLASTRAADYDW
4-59	791	RTFGDYIMG	932	AAINWSAGYTPYA	1074	CATAPPLFCWHFDLW
4-6	792	RTFGDDIMG	933	AAIHWSAGYTRYA	1075	CATDPPLFWGHVDLW
4-61	793	RTFGDYIMG	934	AAINWSADYTPYA	1076	CATAPPNTGWHFDHW
4-3	794	RTFGDYIMG	935	AAINWSAGYTAYA	1077	CATATPNTGWHFDHW
4-62	795	RTFSDDTMG	936	AAINWSGGSTDYA	1078	CATDPPLFW
4-43	796	RTFGDDTMG	937	AGINWSGGNTYYA	1079	CATDPPLFW
4-5	797	RTFGDYIMG	938	AAINWTGGYTSYA	1080	CATDPPLFW
4-42	798	RTFGDDTMG	939	AAINWSGGNTYYA	1081	CATDPPLFW
4-63	799	RTFS DYTMG	940	AAINWSGGYTYA	1082	CATDPPLFW
4-6	800	RTFGDYGMG	941	ATINWSGALTHYA	1083	CATLPFYDFWSGYYTGYYY MDVW
4-40	801	RTFSDDTMG	942	AGVTWSGSSTFYA	1084	CATDPPLFW
4-21	802	RTFSDDIMG	943	AAISWSGGNTHYA	1085	CATDPPLFW
4-64	803	RTFGDYIMG	944	AAINWSAGYTAYA	1086	CATASPNTGWHFDHW
4-47	804	FTFDDDYVM G	945	AAVSGSGDDTYA	1087	CAADRRGLASTRAADYDW
4-65	805	RTFGDYIMG	946	AAINWSAGYTAYA	1088	CATEPPLSCWHFDLW
4-18	806	RTFGDYIMG	947	AAINWSGGYTPYA	1089	CATAPPNTGWHFDHW
4-66	807	RTFGDDTMG	948	AAINWSAGYTPYA	1090	CATDPPLFCCHFDLW
4-36	808	RTFSDDTMG	949	AAISWSGGTTRYA	1091	CATDPPLFW
4-67	809	RTFSDDTMG	950	AAINWSGDSTYYA	1092	CATDPPLFW
4-16	810	RTFSDDTMG	951	AAINWSGGTTRYA	1093	CATDPPLFW
4-11	811	RTFSDDAMG	952	AAIHWSGSSTRYA	1094	CATDPPLFW

4-68	812	RTFSDDTMG	953	GTINWSGGSTYYA	1095	CATDPPLFW
4-34	813	RTFGDYIMG	954	AAINWSGGYTPYA	1096	CATDPPLFW
4-28	814	RTFGDDTMG	955	AAINWNGGNTHYA	1097	CATDPPLFW
4-69	815	RTFSDDAMG	956	AAINWSGGTTRYA	1098	CATDPPLFW
4-7	816	RTFGDYIMG	957	AAINWSAGYTPYA	1099	CATDPPLFWGHVDLW
4-71	817	RTFSDDTMG	958	ASINWSGGSTYYA	1100	CATDPPLFW
4-23	818	RTFSDDAMG	959	AGISWNGGSIYYA	1101	CATDPPLFW
4-9	819	FTFDDYEMG	960	AAISWRGGTTYA	1102	CAADDRGLASTRAGDYDW
4-72	820	RTFGDDTMG	961	AAINWSGGYTPYA	1103	CATDPPLFWGHVDLW
4-73	821	RTFSDDAMG	962	AAINWSGGSTRYA	1104	CATDPPLFW
4-29	822	VTLDDYAMG	963	AVINWSGGSTDYA	1105	CARGGGWVPSSTSESLNWFDRW
4-41	823	RTFGDYIMG	964	AAINWSGGTTPYA	1106	CATDPPLFCCHVDLW
4-74	824	LTFSDDTMG	965	AAVSWSGGNTYYA	1107	CATDPPLFW
4-75	825	RTFGDDTMG	966	AAINWTGGYTPYA	1108	CATDPPLFW
4-31	826	RTFGDYIMG	967	ATINWTAGYTYA	1109	CATDPPLFCWHFDHW
4-32	827	RTFGDDTMG	968	AAINWSGGNTDYA	1110	CATDPPLFW
4-15	828	RTFGDYTMG	969	AAINWSGGNTYYA	1111	CATDPPLFW
4-14	829	RTFSDDTMG	970	AGINWSGNGVYYA	1112	CATDPPLFW
4-76	830	RTFGDYAMG	971	APINWSGGSTYYA	1113	CATDPPLFW
4-50	831	GTFSSNGMG	972	AVVNWSGRRTYA	1114	CAVPWMDYNRRDW
4-17	832	QLANFASYA MG	973	AAITRSGSSTVYA	1115	CATTMNPNNPRW
4-37	833	RTFSDDIMG	974	AAINWTGGSTYYA	1116	CATDPPLFW
4-44	834	RTFGDYIMG	975	AAINWSAGYTAYA	1117	CATARPNTGWHFDHW
4-77	835	RTFSDDTMG	976	GSINWSGGSTYYA	1118	CATDPPLFW
4-78	836	RTFSDDTMG	977	AGMTWSGSSTFYA	1119	CATDPPLFW
4-79	837	RTFGDYIMG	978	AAINWSGDYTDYA	1120	CATDPPLFW
4-8	838	RTFGDYIMG	979	GGINWSGGYTYA	1121	CATDPPLFW
4-81	839	RTFSDDTMG	980	AAVNWSGGSTYYA	1122	CATDPPLFW
4-82	840	RTFGDYAMG	981	AAINWSGGYTRYA	1123	CATDPPLFW
4-83	841	RTFGDDTMG	982	AAINWSGGYTPYA	1124	CATDPPLFW
4-35	842	RTFGDYIMG	983	AAINWSAGYTAYA	1125	CARASPNTGWHFDRW
4-45	843	RTFGDYIMG	984	AAINWSGGYTHYA	1126	CATDPPLFW
4-84	844	RTFSDDTMG	985	AAITWSGGRTRYA	1127	CATDRPLFW
4-85	845	RTFGDYIMG	986	AAINWSGGYTAYA	1128	CATASPNTGWHFDHW
4-86	846	RTFSDDTMG	987	AAIHWSGSSTRYA	1129	CATDPPLFW

4-87	847	RTFSDYTMG	988	AAINWSGGTTYA	1130	CATDPPLFW
4-88	848	RTFGDDTMG	989	AAINWSGDNTHYA	1131	CATDPPLFW
4-89	849	FAFGDNWIG	990	ASISSGGTTAYA	1132	CAHRGGWLRPWGYW
4-9	850	RTFSDDAMG	991	GRINWSGGNTYYA	1133	CATDPPLFW
4-91	851	RTFSDDTMG	992	GGISWSGGNTYYA	1134	CATDPPLFW
4-92	852	RTFSDDTMG	993	AAINWSGGSTYYA	1135	CATDPPLFW
4-46	853	RTFGDDTMG	994	AAINWSGGYTYA	1136	CATDPPLFW
4-20	854	RTFGDYIMG	995	AAINWSADYTAYA	1137	CATDPPLFCWHFDHW
4-93	855	RTFSDDAMG	996	AAINWSGSSTYYA	1138	CATDPPLFW
4-4	856	RTFGDYIMG	997	AAINWIAGYTADA	1139	CAEPSNTGWHFDHW
4-2	857	RTFGDDTMG	998	AAINWSGGNTPYA	1140	CATDPPLFW
4-94	858	RTFSDDTMG	999	AAINWSGDNTHYA	1141	CATDPPLFW
4-95	859	RTFGDYIMG	1000	AAINWSAGYTAYA	1142	CATAPPLFCWHFDHW
4-12	860	FTFGDYVMG	1001	AAINWNAGYTAYA	1143	CAKASPNTGWHFDHW
4-30	861	RTFGDYTMG	1002	AAINWTGGYTYA	1144	CATDPPLFW
4-27	862	RTFGDYIMG	1003	AAINWSAGYTAYA	1145	CARATPNTGWHFDHW
4-22	863	RTFGDYIMG	1004	AAINWSGDNTHYA	1146	CATDPPLFW
4-96	864	RTFGDYIMG	1005	AAINWSAGYTPYA	1147	CATDPPLFCCHFDHW
4-97	865	RTFGDYIMG	1006	AAINWSAGYTAYA	1148	CATAPNTGWHFDHW
4-98	866	FTWGDYTMG	1007	AAINWSGGNTYYA	1149	CAADRRGLASTRAADYDW
4-99	867	IPSTLRAMG	1008	AAVSSLGPFTRYA	1150	CAAKPGWVARDPSQYNW
4-100	868	FSFDDDYVM G	1009	AAINWSGGSTYYA	1151	CAADRRGLASTRAADYDW
4-101	869	RTFSNAAMG	1010	ARILWTGASRSYA	1152	CATTENPNPRW
4-102	870	GTFGVYHMG	1011	AAINMSGDDSAYA	1153	CAILVGPGQVEFDHW
4-103	871	FTFSSYYMG	1012	ARISGSTFYA	1154	CAALPFVCPSGSYSDYGDEY DW
4-104	872	RTFSGDIMG	1013	GRINWSGGNTYYA	1155	CPTDPPLFW
4-105	873	STLRDYAMG	1014	AAITWSGGSTAYA	1156	CASLLAGDRYFDYW
4-106	874	FTFDDYTMG	1015	AAITDNGGSKYYA	1157	CAADRRGLASTRAADYDW
4-107	875	GTFSSYGMG	1016	AAINWSGASTYYA	1158	CARDWRDRTWGNSLDYW
4-108	876	FSFDDDYVM G	1017	AAISWSEDNTYYA	1159	CAADRRGLASTRAADYDW
4-109	877	FSFDDDYVM G	1018	AAVSGSGDDTYA	1160	CAADRRGLASTRAADYDW
4-110	878	NIAAINVMG	1019	AAISASGRRTDYA	1161	CARRVYYDSSGPPGVTFDI W
4-111	879	IITSRYVMG	1020	AAISTGGSTIYA	1162	CARQDSSSPYFDYW
4-112	880	FSFDDDYVM G	1021	AAISNSGLSTYYA	1163	CAADRRGLASTRAADYDW

4-113	881	SISSINVMG	1022	ATMRWSTGSTYYA	1164	CAQVRVGRFFGLRTPSWYE W
4-114	882	LTFILYRMG	1023	AAINNFGTKYA	1165	CARTHYDFWSGYTSRTPNYF DYW
4-115	883	GTFSVYHMG	1024	AAISWSGGSTAYA	1166	CAAVNTWTSPSFDSW
4-116	884	RAFSTYGMG	1025	AGINWSGDTPTYA	1167	CAREVGPPPGYFDLW
4-117	885	RTFSDIAMG	1026	ASINWGGGNTYYA	1168	CAAKGIWDYLGRRDFGDW
4-118	886	RTFSSARMG	1027	AAISWSGDNTHYA	1169	CATTENPNPRW
4-119	887	FAFSSYAMG	1028	ATINGDDYTYA	1170	CVATPGGYGLW
4-120	888	ITFRRHDMG	1029	AAIRWSSSSTVYA	1171	CAADRGVYGRWYRTSQYT W
4-121	889	TAASFNPMG	1030	AAITSGGSTNYA	1172	CAAIAYEEGVYRWDW
4-122	890	NINIINYMG	1031	AAIHWNGDSTAYA	1173	CASGPPYSNYFAYW
4-123	891	FTFDDYAMG	1032	AAISGSGGSTAYA	1174	CAKIMGSGRPYFDHW
4-124	892	NIFTRNVMG	1033	AAITSSGSTNYA	1175	CARPSSDLQGGVDYW
4-125	893	RTFSSIAMG	1034	ASINWGGGNTIYA	1176	CAAKGIWDYLGRRDFGDW
4-126	894	IPSTLRAMG	1035	AAVSSLGPFTRYA	1177	CAAKPGWVARDPSEYNW
4-127	895	FTLDDSAMG	1036	AAITNGGSTYYA	1178	CARFARGSPYFDW
4-128	896	SISSFNAMG	1037	AAIDWDGSTAYA	1179	CARGGGYYGSGSFYEW
4-129	897	NIFSDNIIG	1038	AYYTSGGSIDYA	1180	CARGTAVGRPPPGMDVW
4-130	898	SISSIGAMG	1039	AAISSGSSTVYA	1181	CARVPPGQAYFDSW
4-131	899	FTFDDYGMG	1040	ATITWSGDSTYYA	1182	CAKGGSWYYDSSGYGRW
4-132	900	RTFSNYTMG	1041	SAISWSTGSTYYA	1183	CAADRYGPPWYDW
4-133	901	STNYMG	1042	AAISMSGDDTIYA	1184	CARIGLRGRYFDLW
4-134	902	GTFSVGMG	1043	AVINWSGARTYYA	1185	CAVPWMDYNRRDW
4-135	903	RIFTNTAMG	1044	AAINWSGGSTAYA	1186	CARTSGSYSFDYW
4-136	904	EEFSDHWMG	1045	GAIHWSGGRTYYA	1187	CAADRRGLASTRAADYDW
4-137	905	RTFSSIAMG	1046	AAINWSGARTAYA	1188	CAAKGIWDYLGRRDFGDW
4-138	906	STSSLRTMG	1047	AAISSRDGSTIYA	1189	CARDSSSPYFDYW
4-139	907	GGTFGSYAM G	1048	AAISIASGASGGTTN YA	1190	CATTMNPNNPRW
4-140	908	RTFSNAAMG	1049	ARITWNGGSTFYA	1191	CATTENPNPRW
4-141	909	IILSDNAMG	1050	AAISWLGESTYYA	1192	CAADRRGLASTRAADYDW
4-142	910	RTFGDYIMG	1051	AAINWNGGYTAYA	1193	CATTSPNTGWHYYRW
4-143	911	FNFNWYPMG	1052	AAISWTGVSTYTAY A	1194	CARWGPAGGSPGLVGFD YW
4-144	912	SIRSVSVMG	1053	AAISWSGVGTAYA	1195	CAAYQRGWGDW
4-145	913	MTFRLYAMG	1054	GAINWLSESTYYA	1196	CAAKPGWVARDPSEYNW
4-146	914	RTFSDDAMG	1055	AAINWSGGSTYYA	1197	CATDPPLFW

4-147	915	GTFSVYAMG	1056	AAISMSGDDAAYA	1198	CAKISKDDGGKPRGAFFDSW
4-148	916	FALGYIAMG	1057	AAISSRDGSTAYA	1199	CARLATGPQAYFHHW
4-149	917	FNLDDYAMG	1058	AAISWDGGATAYA	1200	CARVGRGTAFDSW
4-150	918	NTFSGGFMG	1059	ASIRSGARTYYA	1201	CAQVRVGGFFGLRTTPSWYE W
4-151	919	SIRSINIMG	1060	AAISWSGGSTVYA	1202	CASLLAGDRYFDYW

Table 33. ACE2 Variant Sequences Variable Heavy Chain

Name	SEQ ID	Amino Acid Sequence
4-51	1203	EVQLVESGGGLVQPGGSLRLSCAASGPGTAIMGWFRQAPGKEREVARISTSGGSTK YADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARTTVTTPPLIWGQGTLVTV SS
4-52	1204	EVQLVESGGGLVQPGGSLRLSCAASGRSFSNSVMGWFRQAPGKEREVARITWNNGS TYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATTENPNPRWGQGTLVT VSS
4-53	1205	EVQLVESGGGLVQPGGSLRLSCAASGRFTGDDTMGWFRQAPGKEREFVAAVSWSGS GVYYADSVKGRFTITADNSKNTAYLQMNSLKPENTAVYYCATDPPLFWGQGTLVTV SS
4-54	1206	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDARMGWFRQAPGKEREFVAVSWSGG TTVYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATTEDPYPRWGQGTLV TVSS
4-49	1207	EVQLVESGGGLVQPGGSLRLSCAASGRFTGDYIMGWFRQAPGKERESVAAINWSAG YTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARASPNTGWHFDHWG QGTLVTVSS
4-55	1208	EVQLVESGGGLVQPGGSLRLSCAASGSGLSINAMGWFRQAPGKERESVAAISWSGG TYTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAYQAGWGDWGGQT LVTVSS
4-39	1209	EVQLVESGGGLVQPGGSLRLSCAASGRFTSNAAMGWFRQAPGKEREFVARILWTGA SRNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATTENPNPRWGQGTLV TVSS
4-56	1210	EVQLVESGGGLVQPGGSLRLSCAASGFSLDYGMGWFRQAPGKERESVAAISWNGD FTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAKRANPTGAYFDYWGQ GTLVTVSS
4-33	1211	EVQLVESGGGLVQPGGSLRLSCAASGFTSRHDMGWFRQAPGKEREFVAGINWESGS TNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADRGVYGGRWYRTSQ YTWGQGTLVTVSS
4-57	1212	EVQLVESGGGLVQPGGSLRLSCAASGLTFRNYAMGWFRQAPGKEREFVAAIGSGGY TDYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAVKPGWVARDPSQYNW GQGTLVTVSS
4-25	1213	EVQLVESGGGLVQPGGSLRLSCAASGGTFSRYAMGWFRQAPGKEREWVSAVDSGGS TYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAASPSLRSWQWGQGTL VTVSS
4-58	1214	EVQLVESGGGLVQPGGSLRLSCAASGFTLDYYDMGWFRQAPGKEREFVAAVTWSGG STYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADRRGLASTRAADYD WGQGTLVTVSS
4-59	1215	EVQLVESGGGLVQPGGSLRLSCAASGRFTGDYIMGWFRQAPGKEREFVAAINWSAG YTPYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATAPPLFCWHFDLWGQ GTLVTVSS
4-6	1216	EVQLVESGGGLVQPGGSLRLSCAASGRFTGDDIMGWFRQAPGKEREFVAAIHWSAG YTRYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGHVDLWGQ GTLVTVSS

4-61	1217	EVQLVESGGGLVQPGGSLRLSCAASGRFTFGDYIMGWFRQAPGKEREIVAAINWSADY TPYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATAPPNTGWHFDHWGQG TLVTVSS
4-3	1218	EVQLVESGGGLVQPGGSLRLSCAASGRFTFGDYIMGWFRQAPGKEREIVAAINWSAGY TAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATATPNTGWHFDHWGQ GTLVTVSS
4-62	1219	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDTMGWFRQAPGKEREFVAAINWSGG STDYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTVS S
4-43	1220	EVQLVESGGGLVQPGGSLRLSCAASGRFTGDDTMGWFRQAPGKEREFVAGINWSGG NTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTV SS
4-5	1221	EVQLVESGGGLVQPGGSLRLSCAASGRFTFGDYIMGWFRQAPGKEREFVAAINWTGG YTSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTVS S
4-42	1222	EVQLVESGGGLVQPGGSLRLSCAASGRFTGDDTMGWFRQAPGKERECVAAINWSGG NTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTV SS
4-63	1223	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDYTMGWFRQAPGKEREFVAAINWSGG YTTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTV SS
4-6	1224	EVQLVESGGGLVQPGGSLRLSCAASGRFTFGDYGMGWFRQAPGKEREFVATINWSGA LTHYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATLPFYDFWSGYYTG YYMDVWGQGTLVTVSS
4-40	1225	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDTMGWFRQAPGKEREFVAGVTWSGS STFYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTVS S
4-21	1226	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDIMGWFRQAPGKEREFVAAISWSGGN THYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTVSS
4-64	1227	EVQLVESGGGLVQPGGSLRLSCAASGRFTFGDYIMGWFRQAPGKERESVAAINWSAG YTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATASPNTGWHFDHWG QGTLVTVSS
4-47	1228	EVQLVESGGGLVQPGGSLRLSCAASGFTFDDDYVMGWFRQAPGKEREFVAAVSGSG DDTTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADRRGLASTRAADY DWGQGTLVTVSS
4-65	1229	EVQLVESGGGLVQPGGSLRLSCAASGRFTFGDYIMGWFRQAPGKEREFVAAINWSAG YTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATEPPLSCWHFDLWGQ GTLVTVSS
4-18	1230	EVQLVESGGGLVQPGGSLRLSCAASGRFTFGDYIMGWFRQAPGKEREIVAAINWSGGY TPYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATAPPNTGWHFDHWGQG TLVTVSS
4-66	1231	EVQLVESGGGLVQPGGSLRLSCAASGRFTGDDTMGWFRQAPGKEREIVAAINWSAG YTPYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFCCHFDLWGQ GTLVTVSS
4-36	1232	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDTMGWFRQAPGKEREFVAAISWSGGT TRYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTVSS
4-67	1233	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDTMGWFRQAPGKEREFVAAINWSGD STYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTVS S
4-16	1234	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDTMGWFRQAPGKEREFVAAINWSGG TTRYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTVS S
4-11	1235	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDAMGWFRQAPGKEREFVAAIHWSSG TRYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTVSS

4-68	1236	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDTMGWFRQAPGKERELVGTINWSGGS TYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTVSS
4-34	1237	EVQLVESGGGLVQPGGSLRLSCAASGRFTFGDYIMGWFRQAPGKEREFVAAINWSGG YTPYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTVS S
4-28	1238	EVQLVESGGGLVQPGGSLRLSCAASGRFTGDDTMGWFRQAPGKERELVAAINWNGG NTHYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTV SS
4-69	1239	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDAMGWFRQAPGKEREFVAAINWSGG TTRYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTVS S
4-7	1240	EVQLVESGGGLVQPGGSLRLSCAASGRFTFGDYIMGWFRQAPGKERESVAAINWSAG YTPYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGHVDLWGQ GTLVTVSS
4-71	1241	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDTMGWFRQAPGKEREWVASINWSGG STYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTVS S
4-23	1242	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDAMGWFRQAPGKEREFVAGISWNGG SIYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTVS S
4-9	1243	EVQLVESGGGLVQPGGSLRLSCAASGFTFDDYEMGWFRQAPGKEREFVAAISWRGG TTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADRRGLASTRAGDYD WGQGTLVTVSS
4-72	1244	EVQLVESGGGLVQPGGSLRLSCAASGRFTGDDTMGWFRQAPGKEREFVAAINWSGG YTPYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGHVDLWGQ GTLVTVSS
4-73	1245	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDAMGWFRQAPGKEREFVAAINWSGG STRYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTVS S
4-29	1246	EVQLVESGGGLVQPGGSLRLSCAASGVTLDYAMGWFRQAPGKEREFVAVINWSGG STDYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGGGWVPSSTSESLN WYFDRWGQGTLVTVSS
4-41	1247	EVQLVESGGGLVQPGGSLRLSCAASGRFTFGDYIMGWFRQAPGKERESVAAINWSGGT TPYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFCCHVDLWGQG TLVTVSS
4-74	1248	EVQLVESGGGLVQPGGSLRLSCAASGLTFSDDTMGWFRQAPGKEREFVAAVSWSGG NTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTV SS
4-75	1249	EVQLVESGGGLVQPGGSLRLSCAASGRFTGDDTMGWFRQAPGKEREFVAAINWTGG YTPYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTVS S
4-31	1250	EVQLVESGGGLVQPGGSLRLSCAASGRFTFGDYIMGWFRQAPGKEREFVATINWTAG YTTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFCWHFDHWGQ GTLVTVSS
4-32	1251	EVQLVESGGGLVQPGGSLRLSCAASGRFTGDDTMGWFRQAPGKEREFVAAINWSGG NTDYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTV SS
4-15	1252	EVQLVESGGGLVQPGGSLRLSCAASGRFTFGDYTMGWFRQAPGKEREFVAAINWSGG NTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTV SS
4-14	1253	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDTMGWFRQAPGKEREFVAGINWSGN GVYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTV SS
4-76	1254	EVQLVESGGGLVQPGGSLRLSCAASGRFTFGDYAMGWFRQAPGKERELVAPINWSGG STYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTVS

		S
4-50	1255	EVQLVESGGGLVQPGGSLRLSCAASGGTFSNSGMGWFRQAPGKERELVAVVNWSGR RTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAVPWMDYNRRDWGQG TLVTVSS
4-17	1256	EVQLVESGGGLVQPGGSLRLSCAASGQLANFASYAMGWFRQAPGKEREFVAAITRSG SSTVYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATTMNPNPWRWGQGT LTVSS
4-37	1257	EVQLVESGGGLVQPGGSLRLSCAASGRTFSDDIMGWFRQAPGKEREFVAAINWTGGS TYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTVSS
4-44	1258	EVQLVESGGGLVQPGGSLRLSCAASGRTFGDYIMGWFRQAPGKEREIFVAAINWSAGY TAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATARPNTGWHFDHWGQ GTLVTVSS
4-77	1259	EVQLVESGGGLVQPGGSLRLSCAASGRTFSDDTMGWFRQAPGKEREWVGSINWSGG STYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTVS S
4-78	1260	EVQLVESGGGLVQPGGSLRLSCAASGRTFSDDTMGWFRQAPGKEREFVAGMTWSGS STFYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTVS S
4-79	1261	EVQLVESGGGLVQPGGSLRLSCAASGRTFGDYIMGWFRQAPGKERECVAAINWSGD YTDYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTV SS
4-8	1262	EVQLVESGGGLVQPGGSLRLSCAASGRTFGDYIMGWFRQAPGKEREFVGGINWSGG YTTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTV SS
4-81	1263	EVQLVESGGGLVQPGGSLRLSCAASGRTFSDDTMGWFRQAPGKEREFVAAVNWSGG STYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTVS S
4-82	1264	EVQLVESGGGLVQPGGSLRLSCAASGRTFGDYAMGWFRQAPGKEREFVAAINWSGG YTRYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTV SS
4-83	1265	EVQLVESGGGLVQPGGSLRLSCAASGRTFGDDTMGWFRQAPGKEREFVAAINWSGG YTPYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTVS S
4-35	1266	EVQLVESGGGLVQPGGSLRLSCAASGRTFGDYIMGWFRQAPGKERESVAAINWSAG YTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARASPNTGWHFDRWG QGTLVTVSS
4-45	1267	EVQLVESGGGLVQPGGSLRLSCAASGRTFGDYIMGWFRQAPGKEREFVAAINWSGG YTHYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTV SS
4-84	1268	EVQLVESGGGLVQPGGSLRLSCAASGRTFSDDTMGWFRQAPGKEREFVAAITWSGG RTRYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDRPLFWGQGTLVTV SS
4-85	1269	EVQLVESGGGLVQPGGSLRLSCAASGRTFGDYIMGWFRQAPGKERESVAAINWSGG YTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATASPNTGWHFDHWG QGTLVTVSS
4-86	1270	EVQLVESGGGLVQPGGSLRLSCAASGRTFSDDTMGWFRQAPGKEREFVAAIHWSSG TRYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTVSS
4-87	1271	EVQLVESGGGLVQPGGSLRLSCAASGRTFSDYTMGWFRQAPGKEREWVAAINWSGG TTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTVS S
4-88	1272	EVQLVESGGGLVQPGGSLRLSCAASGRTFGDDTMGWFRQAPGKEREFVAAINWSGD NTHYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTV SS
4-89	1273	EVQLVESGGGLVQPGGSLRLSCAASGFAGDNWIGWFRQAPGKEREWVASISSGGTT AYADNVKGRFTIADNSKNTAYLQMNSLKPEDTAVYYCAHRGGWLRPWGYWGQGT

		LVTVSS
4-9	1274	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDAMGWFRQAPGKEREFVGRINWSGG NTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTV SS
4-91	1275	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDTMGWFRQAPGKEREFVGGISWSGG NTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTV SS
4-92	1276	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDTMGWFRQAPGKEREFVAAINWSGG STYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTVS S
4-46	1277	EVQLVESGGGLVQPGGSLRLSCAASGRFTGDDTMGWFRQAPGKEREFVAAINWSGG YTTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTV SS
4-20	1278	EVQLVESGGGLVQPGGSLRLSCAASGRFTGDYIMGWFRQAPGKEREFVAAINWSAD YTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFCWHFDHWGQ GTLVTVSS
4-93	1279	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDAMGWFRQAPGKEREFVAAINWSGSS TYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTVSS
4-4	1280	EVQLVESGGGLVQPGGSLRLSCAASGRFTGDYIMGWFRQAPGKEREMVAAINWIAG YTADADSVRRLFTITADNNKNTAHLMMNLLKPENTAVYYCAEPSNTGWHFDHWG QGTLVTVSS
4-2	1281	EVQLVESGGGLVQPGGSLRLSCAASGRFTGDDTMGWFRQAPGKEREFVAAINWSGG NTPYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTVS S
4-94	1282	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDTMGWFRQAPGKEREFVAAINWSGD NTHYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTV SS
4-95	1283	EVQLVESGGGLVQPGGSLRLSCAASGRFTGDYIMGWFRQAPGKEREIFVAAINWSAGY TAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATAPPLFCWHFDHWGQG TLVTVSS
4-12	1284	EVQLVESGGGLVQPGGSLRLSCAASGFTGDYVMGWFRQAPGKEREIFVAAINWNAG YTAYADSVRGLFTITADNSKNTAYLQMNSLKPEDTAVYYCAKASPNTGWHFDHWG QGTLVTVSS
4-30	1285	EVQLVESGGGLVQPGGSLRLSCAASGRFTGDYTMGWFRQAPGKEREFVAAINWTGG YTTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTV SS
4-27	1286	EVQLVESGGGLVQPGGSLRLSCAASGRFTGDYIMGWFRQAPGKEREIFVAAINWSAGY TAYADSVKGLFTITADNSKNTAYLQMNILKPEDTAVYYCARATPNTGWHFDHWGQG TLVTVSS
4-22	1287	EVQLVESGGGLVQPGGSLRLSCAASGRFTGDYIMGWFRQAPGKEREFVAAINWSGD NTHYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTLVTV SS
4-96	1288	EVQLVESGGGLVQPGGSLRLSCAASGRFTGDYIMGWFRQAPGKEREIFVAAINWSAGY TPYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFCCHFDHWGQG TLVTVSS
4-97	1289	EVQLVESGGGLVQPGGSLRLSCAASGRFTGDYIMGWFRQAPGKERESVAAINWSAG YTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATAPPNTGWHFDHWG QGTLVTVSS
4-98	1290	EVQLVESGGGLVQPGGSLRLSCAASGFTWGDYTMGWFRQAPGKEREFVAAINWSGG NTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADRRGLASTRAADYD WGQGTLVTVSS
4-99	1291	EVQLVESGGGLVQPGGSLRLSCAASGIPSTLRAMGWFRQAPGKEREFVAAVSSLGPFT RYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAKPGWVARDPSQYNWG QGTLVTVSS

4-100	1292	EVQLVESGGGLVQPGGSLRLSCAASGFSFDDDYVMGWFRQAPGKEREVFAAINWSG GSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADRRGLASTRAADY DWGQGTTLTVSS
4-101	1293	EVQLVESGGGLVQPGGSLRLSCAASGRTFSNAAMGWFRQAPGKEREVVARILWTGA SRSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATTENPNPRWGQGTTLT VSS
4-102	1294	EVQLVESGGGLVQPGGSLRLSCAASGGTFGVYHMGWFRQAPGKEREVFAAINMSGD DSAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAILVGPQVEFDHWGQ GTLTVTVSS
4-103	1295	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMGWFRQAPGKEREVARI-- SGSTFYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAALPFVCPSPGSYSDY GDEYDWGQGTTLTVSS
4-104	1296	EVQLVESGGGLVQPGGSLRLSCAASGRTFSGDFMGWFRQAPGKEREVGRINWSGG NTYYADSVRGLFTITADNNKNTAYLMMNLLKPEDTAVYYCPTDPLFWGLGTLTVT SS
4-105	1297	EVQLVESGGGLVQPGGSLRLSCAASGSLRDYAMGWFRQAPGKERESVAAITWSGG STAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCASLLAGDRYFDYWGQG TLTVTVSS
4-106	1298	EVQLVESGGGLVQPGGSLRLSCAASGFTFDDYTMGWFRQAPGKEREVFAAITDNNGS KYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADRRGLASTRAADYD WGQGTTLTVTVSS
4-107	1299	EVQLVESGGGLVQPGGSLRLSCAASGGTFSSYGMGWFRQAPGKEREVFAAINWSGA STYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARDWRDRTWGNSLDY WGQGTTLTVTVSS
4-108	1300	EVQLVESGGGLVQPGGSLRLSCAASGFSFDDDYVMGWFRQAPGKEREVFAAISWSE DNTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADRRGLASTRAADY DWGQGTTLTVTVSS
4-109	1301	EVQLVESGGGLVQPGGSLRLSCAASGFSFDDDYVMGWFRQAPGKEREVFAAVSGSG DDTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADRRGLASTRAADY DWGQGTTLTVTVSS
4-110	1302	EVQLVESGGGLVQPGGSLRLSCAASGNIAAINVMGWFRQAPGKEREVFAAISASGRR TDYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARRVYYDSSGPPGVTF DIWGQGTTLTVTVSS
4-111	1303	EVQLVESGGGLVQPGGSLRLSCAASGIITSRYVMGWFRQAPGKEREVFAAISTGGSTI YADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARQDSSSPYFDYWGQGTTLV TVSS
4-112	1304	EVQLVESGGGLVQPGGSLRLSCAASGFSFDDDYVMGWFRQAPGKEREVFAAISNSGL STYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADRRGLASTRAADYD WGQGTTLTVTVSS
4-113	1305	EVQLVESGGGLVQPGGSLRLSCAASGSISSINVMGWFRQAPGKEREVATMRWSTGS TYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAQVRGFFGPLRTTPSWY EWGQGTTLTVTVSS
4-114	1306	EVQLVESGGGLVQPGGSLRLSCAASGLTFILYRMGWFRQAPGKEREVFAAINNFGTT KYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARTHYDFWSGYTSRTPNY FDYWGQGTTLTVTVSS
4-115	1307	EVQLVESGGGLVQPGGSLRLSCAASGGTFVYHMGWFRQAPGKEREVFAAISWSGG STAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAVNTWTSPSFDSWGQ GTLTVTVSS
4-116	1308	EVQLVESGGGLVQPGGSLRLSCAASGRAFSYGMGWFRQAPGKEREVAGINWSGD TPYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAREVGPPPGYFDLWGQ GTLTVTVSS
4-117	1309	EVQLVESGGGLVQPGGSLRLSCAASGRTFSDIAMGWFRQAPGKEREVFAASINWGGGN TYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAKGIWDYLGRRDFGD WGQGTTLTVTVSS
4-118	1310	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSARMGWFRQAPGKEREVFAAISWSGDN

		THYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATTENPNPRWGQGLTVTVSS
4-119	1311	EVQLVESGGGLVQPGGSLRLSCAASGFAFSSYAMGWFRQAPGKEREWVATINGDDY TYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCVATPGGYGLWGQGLTVTVSS
4-120	1312	EVQLVESGGGLVQPGGSLRLSCAASGITFRRHDMGWFRQAPGKEREFVAAIRWSSSS TVYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADRGVYGGRWYRTSQ YTWGQGLTVTVSS
4-121	1313	EVQLVESGGGLVQPGGSLRLSCAASGTAASFNPMGWFRQAPGKEREFVAAITSGGST NYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAIAEYEGVYRWDWGQG TLTVTVSS
4-122	1314	EVQLVESGGGLVQPGGSLRLSCAASGNINIINMGWFRQAPGKEREGVAAIHWNGDS TAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCASGPPYSNYFAYWGQGT LTVTVSS
4-123	1315	EVQLVESGGGLVQPGGSLRLSCAASGFTFDDYAMGWFRQAPGKERESVAAISGSGGS TAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAKIMGSGRPYFDHWGQG TLTVTVSS
4-124	1316	EVQLVESGGGLVQPGGSLRLSCAASGNIFTRNVMGWFRQAPGKEREFVAAITSSGST NYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARPSSDLQGGVDYWGQGT LTVTVSS
4-125	1317	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSIAMGWFRQAPGKEREFVASINWGGGN TIYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAKGIWDYLGRRDFGDW GQGLTVTVSS
4-126	1318	EVQLVESGGGLVQPGGSLRLSCAASGIPSTLRAMGWFRQAPGKEREFVAAVSSLGPFT RYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAKPGWVARDPSEYNWG QGLTVTVSS
4-127	1319	EVQLVESGGGLVQPGGSLRLSCAASGFTLDDSAMGWFRQAPGKEREWVAAITNGGS TYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARFARGSPYFDWQGT LTVTVSS
4-128	1320	EVQLVESGGGLVQPGGSLRLSCAASGSISSFNAMGWFRQAPGKERESVAAIDWDGST AYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGGGYYGSGSFEYWGQ GTLTVTVSS
4-129	1321	EVQLVESGGGLVQPGGSLRLSCAASGNIFSDNIIGWFRQAPGKEREMVAYYTSGGSID YADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGTAVGRPPPGGMDVWG QGLTVTVSS
4-130	1322	EVQLVESGGGLVQPGGSLRLSCAASGSISSIGAMGWFRQAPGKEREGVAAISSGSST VYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARVPPGQAYFDSWGQGLT VTVSS
4-131	1323	EVQLVESGGGLVQPGGSLRLSCAASGFTFDDYGMGWFRQAPGKERELVATITWSGD STYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAKGGSWYYDSSGYGR WGQGLTVTVSS
4-132	1324	EVQLVESGGGLVQPGGSLRLSCAASGRTFSNYTMGWFRQAPGKEREWVSAISWSTGS TYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADRYGPPWYDWGQGT LTVTVSS
4-133	1325	EVQLVESGGGLVQPGGSLRLSCAASGSTNYMGWFRQAPGKEREGVAAISMSGDDTIY ADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARIGLRGRYFDLWGQGLTVT VSS
4-134	1326	EVQLVESGGGLVQPGGSLRLSCAASGGTFSSVGMGWFRQAPGKERELVAVINWSGA RTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAVPWMDYNRRDWGQG TLTVTVSS
4-135	1327	EVQLVESGGGLVQPGGSLRLSCAASGRIFTNTAMGWFRQAPGKEREGVAAINWSGGS TAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARTSGSYSFDYWGQGLT VTVSS
4-136	1328	EVQLVESGGGLVQPGGSLRLSCAASGEEFSDHWMGWFRQAPGKEREFVGAIHWSGG RTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADRRGLASTRAADYD

		WGQGLTVTVSS
4-137	1329	EVQLVESGGGLVQPGGSLRLSCAASGRFTSSIAMGWFRQAPGKEREFVAAINWSGAR TAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAKGIWDYLGRRDFGD WGQGLTVTVSS
4-138	1330	EVQLVESGGGLVQPGGSLRLSCAASGSTSSLRTMGWFRQAPGKEREGVAAISSRDGS TIYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARDSSSPYFDYWGQGLT TVTVSS
4-139	1331	EVQLVESGGGLVQPGGSLRLSCAASGGGTFGSYAMGWFRQAPGKEREFVAAISIASG ASGGTTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATTMNPNPWRWGQ GTLTVTVSS
4-140	1332	EVQLVESGGGLVQPGGSLRLSCAASGRFTSNAAMGWFRQAPGKEREFVARITWNGG STFYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATTENPNPRWGQGLTVT VSS
4-141	1333	EVQLVESGGGLVQPGGSLRLSCAASGIILSDNAMGWFRQAPGKEREFVAAISWLGEST YYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADRRGLASTRAADYDW GQGLTVTVSS
4-142	1334	EVQLVESGGGLVQPGGSLRLSCAASGRFTFGDYIMGWFRQAPGKERESVAAINWNGG YTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATTSPTGWHYRWG QGLTVTVSS
4-143	1335	EVQLVESGGGLVQPGGSLRLSCAASGFNFNWYPMGWFRQAPGKERESVAAISWTGV STYTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARWGPGPAGGSPGL VGFDYWGQGLTVTVSS
4-144	1336	EVQLVESGGGLVQPGGSLRLSCAASGSIRSVSMGWFRQAPGKEREA VAAISWSGVG TAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAYQRGWGDWGQGLTV TVSS
4-145	1337	EVQLVESGGGLVQPGGSLRLSCAASGMTFRLYAMGWFRQAPGKEREFVGAINWLSE STYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAKPGWVARDPSEYNW GQGLTVTVSS
4-146	1338	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDAMGWFRQAPGKEREFVAAINWSGG STYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTMTV TVSS
4-147	1339	EVQLVESGGGLVQPGGSLRLSCAASGGTFSVYAMGWFRQAPGKEREGVAAISMSGD DAAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAKISKDDGGKPRGAFF DSWGQGLTVTVSS
4-148	1340	EVQLVESGGGLVQPGGSLRLSCAASGFALGYAMGWFRQAPGKERESVAAISSRDGS TAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARLATGPQAYFHHWGQG TLTVTVSS
4-149	1341	EVQLVESGGGLVQPGGSLRLSCAASGFNLDDYAMGWFRQAPGKERESVAAISWDGG ATAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARVGRGTAFDSWGQG TLTVTVSS
4-150	1342	EVQLVESGGGLVQPGGSLRLSCAASGNTFSGGFMGWFRQAPGKEREFVASIRSGART YYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAQVRGFFGLRTPSWYE WGQGLTVTVSS
4-151	1343	EVQLVESGGGLVQPGGSLRLSCAASGSIRSINIMGWFRQAPGKEREA VAAISWSGGST VYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCASLLAGDRYFDYWGQGLT TVTVSS

Table 34. SARS-CoV-2 S1 Variable Heavy Chain CDRs

Name	SEQ ID NO	CDRH1	SEQ ID NO	CDRH2	SEQ ID NO	CDRH3
5-1	1344	GTFSSIGMG	1524	AAISWDGGATAYA	1704	CAKEDVGKPFDW
5-2	1345	LRFDDYAMG	1525	AIKFSGGTTDYA	1705	CASWDGLIGLDAYEYDW

5-3	1346	SIFSIDVMG	1526	AGISWSGDSTLYA	1706	CAAFDGYTGSDW
5-4	1347	FTLADYAMG	1527	AVITCSGGSTDYA	1707	CAADDCYIGCGW
5-5	1348	RTFSSIAMG	1528	AEITEGGISPSGDNIY YA	1708	CAAELHSSDYTSPGAESDYG W
5-6	1349	PTFSSYAMMG	1529	AAINNFGTTKYA	1709	CAASASDYGLGLELFHDEYN W
5-7	1350	STGYMG	1530	AAIHSGGSTNYA	1710	CATVATALIW
5-8	1351	RPFSEYTMG	1531	SSIHWGGRGTNYA	1711	CAAELHSSDYTSPGAYAW
5-9	1352	LTLSTYGMG	1532	AHIPRSTYSPYYA	1712	CAAIGDGAVW
5-10	1353	FTFNNHNMG	1533	AAISSYSHTAYA	1713	CALQPFASNYRW
5-11	1354	GIYRVMG	1534	ASISSGGGINYA	1714	CAAESWGRQW
5-12	1355	YTDSNLWMG	1535	AINRSTGSTSYA	1715	CATSGSGSPNW
5-13	1356	FTFDYYTMG	1536	AAIRSSGGLFYA	1716	CAAYLDGYSGSW
5-14	1357	GIFSINVMG	1537	SAIRWNGGNTAYA	1717	CAGFDGYTGSDW
5-15	1358	FTFDGAAMG	1538	ATIRWTNSTDYA	1718	CARGRYGIVERW
5-16	1359	RTHSIYPMG	1539	AAIHSGGATVYA	1719	CAARRWIPPGPIW
5-17	1360	PTFSIYAMG	1540	AGIRWSDVYTQYA	1720	CALDIDYRDW
5-18	1361	LTFDDNIHVM G	1541	AAIHWSSGGSTIYA	1721	CAADVYPQDYGLGYVEGK MYYGMDW
5-19	1362	LTLDDYYAMG	1542	ASINWSGGSTYYA	1722	CAAYGSGEFDW
5-20	1363	RTIVPYTMG	1543	AAISPSAFTEYA	1723	CAARRWGYDW
5-21	1364	GTFTTYHMG	1544	AHISTGGATNYA	1724	CATFPAIVTDSYDLGNDW
5-22	1365	FTFNVFAMG	1545	AAINWSDSRTDYA	1725	CASGSDNRARELSRYEYVW
5-23	1366	SIFSIDVMG	1546	AAISWSGESTLYA	1726	CAAFDGYSGSDW
5-24	1367	FTFSSYSMG	1547	AAISSYSHTAYA	1727	CALQPFASNYRW
5-25	1368	NTFSINVMG	1548	AAIHWSGDSTLYA	1728	CAAFDGYSGNHW
5-26	1369	RTISSYIMG	1549	ARIYTGGDTIYA	1729	CAARTSYNGRYDYIDDYSW
5-27	1370	RANSINWMG	1550	ATITPGGNTNYA	1730	CAAAAGSTWYGTLYEYDW
5-28	1371	GTFSVFAMG	1551	AEITAGGSTYYA	1731	CAVDGPFGW
5-29	1372	FTFDDYPMG	1552	ASVLRGGYTWYA	1732	CAKDWATGLAW
5-30	1373	FALGYAMG	1553	AGIRWTDAYTEYA	1733	CAADVSPSYGSRWYW
5-31	1374	RTLDIHVMG	1554	AVINWTGESTLYA	1734	CAAFDGYTGNYW
5-32	1375	FTPDNYAMG	1555	AALGWSGVTTYHY YA	1735	CASDESDAANW
5-33	1376	FTFDDYAMG	1556	ATIMWSGNNTYYA	1736	CATNDDDV
5-34	1377	RTFSRYIMG	1557	AAISWSGGDNTYYA	1737	CAAYRIVVGGTSPGDWRW
5-35	1378	PTFSIYAMG	1558	AGISWNGGSTNYA	1738	CALRRRFGGQEW
5-36	1379	RTFSLNAMG	1559	AAISCGGGSTYA	1739	CAADNDMGYCSW
5-37	1380	STFSINAMG	1560	GGISRSATTNYA	1740	CAADGVPEYSDYASGPVW

5-38	1381	RTFSMHAMG	1561	ASISSQGRRTNYA	1741	CAAQVRNGSDYLPIDW
5-39	1382	VTLDLYAMG	1562	AGIRWTDAYTEYA	1742	CAVDIDYRDW
5-40	1383	LPFTINVMG	1563	AAIHWSSGLTTFYA	1743	CAELDGYFFAHW
5-41	1384	RAFSNYAMG	1564	AWINNRGTDDYADS GSTYYA	1744	CASTDDYGVWD
5-42	1385	FTPDDYAMG	1565	ASIGYSGRSNSYNY YA	1745	CAIAHGSSTYNW
5-43	1386	FTLNYYGMG	1566	AAITSGGAPHYA	1746	CASAYDRGIGYDW
5-44	1387	LPFSTKSMG	1567	AAIHWSSGLTSYA	1747	CAADRAADFFAQRDEYDW
5-45	1388	RTFSINAMG	1568	AAISWSGESTQYA	1748	CAAFDGGSGTQW
5-46	1389	EEFSDHWMG	1569	AAIHWSSGDSTHRNY A	1749	CATVGITLNW
5-47	1390	FTFGSYDMG	1570	TAINWSGARTAYA	1750	CAARSVYSYEYNW
5-48	1391	LPLDLYAMG	1571	AGIRWSDAYTEYA	1751	CALDIDYRHW
5-49	1392	RTSTVNGMG	1572	ASISQSGAATAYA	1752	CAADRTYSYSTGYW
5-50	1393	FSLDYYGMG	1573	AAITSGGTPHYA	1753	CASAYNPGIGYDW
5-51	1394	RPNSINWMG	1574	ATITPGGNTNYA	1754	CAAAAGTTWYGTLYEYDW
5-52	1395	EKFSDHWMG	1575	ATITFSGARTAYA	1755	CAALIKPSSTDRIFEW
5-53	1396	LTVVPYAMG	1576	AAIRRSVNTNYA	1756	CAARRWGYHYW
5-54	1397	TTFNFNVMG	1577	AVISWTGESTLYA	1757	CAAFDGYTGRDW
5-55	1398	IDVNRNAMG	1578	AAITWSGGWRYYA	1758	CATTFGDAGIPDQYDFGW
5-56	1399	RTFSSNMG	1579	ARIFGGDRTLYA	1759	CADINGDW
5-57	1400	GTFSMGWIR	1580	GCIGWITYYA	1760	CAPFGW
5-58	1401	CTLDYYAMG	1581	AGIRWTDAYTEYA	1761	CAADVSPSYGGRWYW
5-59	1402	LTFSLYRMC	1582	SCISNIDGSTYYA	1762	CAADLLGDSYEPSSGFGW
5-60	1403	RSFSSHRMG	1583	AAIMWSGSHRNYA	1763	CAAIAEEGVYRWDW
5-61	1404	RIIVPNTMG	1584	TGISPSAFTEYA	1764	CAAHGWGCHW
5-62	1405	SIFIISMG	1585	TGINWSGGSTTYA	1765	CAASAIGSGALRRFEYDW
5-63	1406	FSLDYYDMG	1586	AALGWSGGSTDYA	1766	CAAGNGGRYGIVERW
5-64	1407	TSISNRVMG	1587	ARIYTGGDTLYA	1767	CAARKIYRSLSYGYDYDW
5-65	1408	NIDRLYAMG	1588	AAIDSDGSTDYA	1768	CAALIDYGLGFPIEW
5-66	1409	NTFTINVMG	1589	AAINWNGGTTLTYA	1769	CAAFDGYSGIDW
5-67	1410	FNVNDYAMG	1590	AGITSSVGVNTNYA	1770	CAADIFFVNW
5-68	1411	FTFDHYTMG	1591	AAISGSENVTSYA	1771	CAAEPYIPVRTMRHMTFLT W
6-1	1412	RTFGNYNMG	1592	ATINSLGGTSYA	1772	CARVDYYMDVW
6-2	1413	FTMSSSWMG	1593	TVISGVGTSYA	1773	CARGPDSSGYGFDYW
6-3	1414	FTFSPSWMG	1594	ATINEYGGRNYA	1774	CARVDRDFDYW
6-4	1415	FTRDYYTMG	1595	AAISRSGSLTSYA	1775	CANLAYDSSGYDYW

6-5	1416	RTFTMG	1596	ASTNSAGSTNYA	1776	CTTVDQYFDYW
6-6	1417	TTLDYYAMG	1597	AAISWSGGSTAYA	1777	CAREDDYDSSGYSW
6-7	1418	FTFSSYWMG	1598	ATINWSGVTAYA	1778	CARADDYFDYW
6-8	1419	FTLSGIWMG	1599	AIITTGGRTTYA	1779	CAGYSTFGSSSAYYYYSMD VG
6-9	1420	FTFDYYAMG	1600	SAIDSEGRTSYA	1780	CARWGPFDIW
6-10	1421	SIASIHAMG	1601	AAISRSGGFGSYA	1781	CARDDKYDSSGYPAYFQH W
6-11	1422	LAFNAYAMG	1602	ATIGWSGANTYYA	1782	CASDPPGW
6-12	1423	STYTTYSMG	1603	AAISGSENVTSYA	1783	CARVDDYMDVW
6-13	1424	LTFNDYAMG	1604	AHIPRSTYSPYYA	1784	CAFLVGPQGVDPHGAFDVW
6-14	1425	ITFRFKAMG	1605	AAVSWDGRNTYYA	1785	CASDYYYMDVW
6-15	1426	STVLINAMG	1606	AAVRWSDDYTYA	1786	CAKEGRAGSLDYW
6-16	1427	FTFDDAAMG	1607	AHISWSGGSTYYA	1787	CATFGATVTATNDAFDIW
6-17	1428	NTGSTGYMG	1608	AGVINDGSTVYA	1788	CARLATSHQDGTGYLFDYW
6-18	1429	LTFRNYAMG	1609	AGMMWSGGTTTYA	1789	CAREGYYDSSGYLNYFDY W
6-19	1430	SILSIAVMG	1610	AAISPSAVTYYA	1790	CAIGYYDSSGYFDYW
6-20	1431	STLPYHAMG	1611	AAITWNGASTSYA	1791	CARDRYDYDTSASYFESETW
6-21	1432	TLFKINAMG	1612	AAITSSGSNIDYTY A	1792	CARSNTGWYSFDYW
6-22	1433	RTFSEVVMG	1613	ATIHSSGSTSYA	1793	CVRVTSDYSMSDW
6-23	1434	SIFSMNTMG	1614	ALINRSGGGINYA	1794	CVRLSSGYYDFDYW
6-24	1435	FTLDYYAMG	1615	AAINWSGDNTHYA	1795	CARAPFYCTTTKCQDNYYY MDVW
6-25	1436	LTFGTYYTMG	1616	AAISRFGSTYYA	1796	CARGGDYDFWSVDYMDVW
6-26	1437	DTFSTSWMG	1617	ATINTGGGTNYA	1797	CARVTTSFDYW
6-27	1438	ITFRFKAMG	1618	ASISRSGTYYA	1798	CATDYSAFDMW
6-28	1439	DTYGSYWMG	1619	ATITSDDRNTYA	1799	CARVTSSLSGMDVW
6-29	1440	YTLKNYYAM G	1620	AAIWTGESTLDA	1800	CAREGYYDSSGYYW
6-30	1441	FAFGDSWMG	1621	ATINWSGVTAYA	1801	CARADGYFDYW
6-31	1442	DTFSANRMG	1622	ASITWSSANTYYA	1802	CATFNWNDEGFDFW
6-32	1443	FTLDYYDMG	1623	ALISWSGGSTYYA	1803	CATDFYGWGTRERDAFDIW
6-33	1444	TFQRINHMG	1624	ATINTGGQPNYA	1804	CASLIAAQDYFDYW
6-34	1445	SAFRSNAMG	1625	AHISWSSKSTYYA	1805	CATYCSSTSCFDYW
6-35	1446	FTLAYYAMG	1626	AAISMSGDDTIYA	1806	CARELGYSSTVWPW
6-36	1447	FDFSVSWMG	1627	TAITWSGDSTNYA	1807	CASLLHTGPSGGNYFDYW
6-37	1448	HTFSTSWMG	1628	ATINSLGGTNYA	1808	CARVSSGDYGMVW
6-38	1449	NTFSGGFMG	1629	AVISSLSKSYA	1809	CAKVDSDYDYW

6-39	1450	FTFSPSWMG	1630	AAISWSGGSTAYA	1810	CHGLGEGDPYGDYEGYFDLW
6-40	1451	FTFSDYWMG	1631	ARVWWNGGSAYYA	1811	CAREVLRQQVVLDDYW
6-41	1452	FTFSTSWMG	1632	ASINEYGGRNYA	1812	CAGLHYYYDSSGYNPTEYYGMDVW
6-42	1453	DTYGSYWMG	1633	AVITSGGSTNYA	1813	CTHVQNSYYYAMDVW
6-43	1454	RTFSSYAMMG	1634	ASVNWDASQINYA	1814	CTTLGAVYFDSSGYHDFDYW
6-44	1455	GTFGVYHMG	1635	GRITWTDGSTYYA	1815	CFGLELVYDMTFDYW
6-45	1456	NMF SINAMG	1636	TLISWSSGRTSYA	1816	CASLG YCSGGSCFDYW
6-46	1457	LTFSAMG	1637	ALIRRDGSTIYA	1817	CAALGILFGYDAFDIW
6-47	1458	RTFSMHAMG	1638	ASITYGGNINYA	1818	CAKEGYDYDSTGYRTYFQQW
6-48	1459	FTVS NYAMG	1639	ASVNWSGGTTSYA	1819	CATTGTVTLGYW
6-49	1460	STVLINAMG	1640	AAISWSPGRD TYA	1820	CARDCSGGSCYSGDYW
6-50	1461	FSFDRWAMG	1641	ASLATGGNTNYA	1821	CARVTNYDAFDIW
6-51	1462	YTYSSYVMG	1642	AAISRFGSTYYA	1822	CARDSGEHFWDSGYIDHW
6-52	1463	DTYGSYWMG	1643	AAITSGGSTVYA	1823	CARVDSRFDYW
6-53	1464	ISINTNVMG	1644	AAISTGSVTIYA	1824	CARVDDFGYFDLW
6-54	1465	FEFENHWMG	1645	AHITAGGLSNYA	1825	CGRHWGIYDSSGFSSFDYW
6-55	1466	FTMSSSWMG	1646	ARITSGGSTGYA	1826	CASVDGYFDYW
6-56	1467	NIFRSNMG	1647	AGITWNGD TTYA	1827	CARALGVTYQFDYW
6-57	1468	LTFDHSMG	1648	AAVPLSGNTYYA	1828	CASFSGGPADF DYW
6-58	1469	RAVSTYAMG	1649	AAISGSENVTSYA	1829	CLSVTGD TEDYGVFDTW
6-59	1470	ISGSVFSRTPMG	1650	SSIYSDGSNTYYA	1830	CAHWSWELGDWFDPW
6-60	1471	DTYGSYWMG	1651	ATISQSGAATAYA	1831	CAGLLRYS GTTYDAFDVW
6-61	1472	DTYGSYWMG	1652	AAINWSGGSTNYA	1832	CAGLGWNYMDYW
6-62	1473	STFSGNWMG	1653	AVISWTGGSTYYA	1833	CATHNSLSGFDYW
6-63	1474	QTFNMG	1654	AAIGSGGSTSYA	1834	CWRLGNDYFDYW
6-64	1475	IPSIHAMG	1655	AAINWSHGVTYYA	1835	CGGGYGYHFDYW
6-65	1476	LPFSTLHMG	1656	ASLSIFGATGYA	1836	CWMYYYYDSSGYGNYYYGMDVW
6-66	1477	LTFSLFAMG	1657	AAISSGGSTDYA	1837	CARGNTKYYYDSSGYSSAFDYW
6-67	1478	SFSNYAMG	1658	AAISSSGALTSYA	1838	CWIVGPGPLDGMDVW
6-68	1479	FTLSDRAMG	1659	AHITAGGLSNYA	1839	CVHLASQTGAGYFDLW
6-69	1480	GTFSSVGMG	1660	AGISRSGGTYYA	1840	CARYDFWSGYPYW
6-70	1481	FNLDDYADM G	1661	AAIGWGGGSTRYA	1841	CAREILWFGEFGEPNVW
6-71	1482	ITFSNDAMG	1662	AIITSSDTNDTTNYA	1842	CARLHYDSSGYFDYW
6-72	1483	STLSINAMG	1663	AAIDWSGGSTAYA	1843	CARDSSATRTGPDYW

6-73	1484	HTFSGYAMG	1664	AVITREGSTYYA	1844	CARLGGEFDFYW
6-74	1485	FAFGDSWMG	1665	AAITSGGSTDYA	1845	CARGLLWFGELFGYW
6-75	1486	GTFSTYWMG	1666	AAISRSGGNTYYA	1846	CVRHSGTDGDSSFDYW
6-76	1487	LAFDFDGMG	1667	AAINSGGSTYYA	1847	CARFFRAHDYW
6-77	1488	FTFDRSWMG	1668	AAVTEGGTTSYA	1848	CARADYDFDYW
6-78	1489	RTYDAMG	1669	ASVTSGGYTHYA	1849	CAKFRKIVGATELDYW
6-79	1490	SISSIDYMG	1670	SWISSSDGSTYYA	1850	CARSPFSQIYYYYYMDVW
6-80	1491	GTFSFYNMG	1671	AFISNGGTSYA	1851	CAVVAMRMVTTEGPDVLDV W
6-81	1492	FIGNYHAMG	1672	AAVTWSGGTTNYA	1852	CAREGYYYDSSGYPYYFDY W
6-82	1493	SSLDAYGMG	1673	AAISWGGGSIYYA	1853	CARLSQGMVALDYW
6-83	1494	SIASIHAMG	1674	AAITWSGAITSYA	1854	CAKDGGYGELHYGMEVW
6-84	1495	FTPDDYAMG	1675	AAINSGGSYTYA	1855	CARDRGPW
6-85	1496	GTFSVFAMG	1676	SAINWSGGSLLYA	1856	CALFGDFDYW
6-86	1497	PISGINRMG	1677	AVITSNGRPSYA	1857	CVRLSSGYFDFDYW
6-87	1498	TSIMVGAMG	1678	AIIRGDGRTSYA	1858	CARFAGWDAFDIW
6-88	1499	RTFSTHWMG	1679	AVINWSGGSIYYA	1859	CARLSSDGYNYFDFW
6-89	1500	TIFASAMG	1680	AVVNWNWSSTVYA	1860	CTTVDQYFNYW
6-90	1501	FPFSIWPMG	1681	AAVRWSSTYYA	1861	CATGECDDGGSCSLAYW
6-91	1502	RTFGNYAMG	1682	ASISSSGVSKHYA	1862	CVRFGSSWARDLDQW
6-92	1503	FLFDSYASMG	1683	ATIWRRGNTYYANY A	1863	CTETGTAAW
6-93	1504	LPFSTKSMG	1684	AAISMSGLTSYA	1864	CLKVLGGDYEADNWFDFYW
6-94	1505	NIFRIETMG	1685	AGIIRSGGETLYA	1865	CARSLYYDRSGSYFDFYW
6-95	1506	IPSSIRAMG	1686	AVIRWTGGSTYYA	1866	CARDIGYYDSSGYNDGGF DYW
6-96	1507	FTLSGNWMG	1687	AIITSGGRTNYA	1867	CAGHATFGGSSSSYYGMD VW
6-97	1508	FTFSSLAMG	1688	AAITWSGDITNYA	1868	CLRLSSSGFDHW
6-98	1509	TFGHYAMG	1689	AAINWSSRSTVYA	1869	CAKSDGLMGELRSASAFDIW
6-99	1510	IPFRSRTMG	1690	AGISRSGASTAYA	1870	CTHANDYGDYW
6-100	1511	GTFSTSWMG	1691	AHITAGGLSNYA	1871	CARLLVREDWYFDLW
6-101	1512	GTFSLFAMG	1692	AAISWTGDSTYYKY YA	1872	CAYNNSSGEYW
6-102	1513	SSFSAYAMG	1693	SAIDSEGTTTYA	1873	CAGDYNFWSGFDHW
6-103	1514	RTSSPIAMG	1694	AVRWSDDYTYA	1874	CAKKLGGYYAFDIW
6-104	1515	LTFNQYTMG	1695	ASITDGGSTYYA	1875	CARDSRYMDVW
6-105	1516	PTFSSMG	1696	AAISWDGGATAYA	1876	CAIEIVVGGIYW
6-106	1517	IPSTLRAMG	1697	AATSWSGGSKYYA	1877	CATDLYYMDVW

6-107	1518	GVGFSVTNM G	1698	AVISSSSSTNYA	1878	CTTFNWNDEGFDYW
6-108	1519	GTFGSYGMG	1699	AAIRWSGGITYYA	1879	CARERYWNPLPYYYYGMD VW
6-109	1520	GTFSTYAMG	1700	ASIDWSGLTSYA	1880	CARGPFYMYCSGTKCYSTN WFDPW
6-110	1521	PIYAVNRMG	1701	AGIWRSGGHRDYA	1881	CARGEIDILTYWYDYW
6-111	1522	FTFSNYWMG	1702	GGISRSVSTSYA	1882	CTTLYYYYDSSGYSFDAFDI W
6-112	1523	GTFSAYHMG	1703	TIIDNGGPTSYA	1883	CTALLYFDNSGYNFDPFDI W

Table 35. SARS-CoV-2 S1 Variant Variably Heavy Chain

Name	SEQ ID NO	Amino Acid Sequence
5-1	1884	EVQLVESGGGLVQPGGSLRLSCAASGGTFSSIGMGWFRQAPGKEREFVAAISWD GGATAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAKEDVGKPFDW GQGLTVTVSS
5-2	1885	EVQLVESGGGLVQPGGSLRLSCAASGLRFDDYAMGWFRQAPGKERELVAIKFSG GTTDYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCASWDGLIGLDAYE YDWGQGLTVTVSS
5-3	1886	EVQLVESGGGLVQPGGSLRLSCAASGSIFSIDVMGWFRQAPGKEREFVAGISWSG DSTLYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAFDGYTGSDWG QGLTVTVSS
5-4	1887	EVQLVESGGGLVQPGGSLRLSCAASGFTLADYAMGWFRQAPGKEREFVAVITCS GGSTDYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADDCYIGCGW GQGLTVTVSS
5-5	1888	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSIAMGWFRQAPGKERELVAEITEGG ISPSGDNIIYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAELHSSDY TSPGAESDYGWGQGLTVTVSS
5-6	1889	EVQLVESGGGLVQPGGSLRLSCAASGPTFSSYAMMGWFRQAPGKEREWVAAIN NFGTTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAASASDYGLGL ELFHDEYNWQGLTVTVSS
5-7	1890	EVQLVESGGGLVQPGGSLRLSCAASGSTGYMGWFRQAPGKEREFVAAIHSGGST NYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATVATALIWGQGLTV TVSS
5-8	1891	EVQLVESGGGLVQPGGSLRLSCAASGRPFSEYTMGWFRQAPGKEREFVSSIHWG GRGTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAELHSSDYTSP GAYAWGQGLTVTVSS
5-9	1892	EVQLVESGGGLVQPGGSLRLSCAASGLTLSTYMGWFRQAPGKEREFVAHIPRST YSPYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAIGDGA VWGQG TLTVTVSS
5-10	1893	EVQLVESGGGLVQPGGSLRLSCAASGFTFNNHNMGWFRQAPGKEREFVAAISSY SHTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCALQPFASNYRW GQGLTVTVSS
5-11	1894	EVQLVESGGGLVQPGGSLRLSCAASGGIYRVMGWFRQAPGKERELVASISSGGGI NYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAESWGRQWGQGLTV TVSS
5-12	1895	EVQLVESGGGLVQPGGSLRLSCAASGYTDSNLWMGWFRQAPGKEREFVAINRST GSTSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATSGSGSPNWGQG TLTVTVSS
5-13	1896	EVQLVESGGGLVQPGGSLRLSCAASGFTFDYYTMGWFRQAPGKEREFVAAIRSS GGLFYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAYLDGYSGSWG

		QGTLVTVSS
5-14	1897	EVQLVESGGGLVQPGGSLRLSCAASGGIFSINVMGWFRQAPGKEREWVSAIRWN GGNTAYADSVKGRFTITADNSKNTAYLQMNSLKPEDTAVYYCAGFDGYTGSDW QGTLVTVSS
5-15	1898	EVQLVESGGGLVQPGGSLRLSCAASGFTFDGAAMGWFRQAPGKEREFVATIRWT NSTDYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGRYGIVERWG QGTLVTVSS
5-16	1899	EVQLVESGGGLVQPGGSLRLSCAASGRTHSIYPMGWFRQAPGKERELVAAIHSG GATVYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAARRWIPPPIWG QGTLVTVSS
5-17	1900	EVQLVESGGGLVQPGGSLRLSCAASGPTFSIYAMGWFRQAPGKEREFVAGIRWS DVYTQYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCALDIDYRDWQG GTLVTVSS
5-18	1901	EVQLVESGGGLVQPGGSLRLSCAASGLTFDDNIHVMGWFRQAPGKEREFVAAIH WSGGSTIYADSVKGRFTINADNSKNTAYLQMNSLKPEDTAVYYCAADVYPQDY GLGYVEGKMYYGMDWGQGTTLVTVSS
5-19	1902	EVQLVESGGGLVQPGGSLRLSCAASGLTDYYAMGWFRQAPGKEREWVASINW SGGSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAYGSGEFDW QGTLVTVSS
5-20	1903	EVQLVESGGGLVQPGGSLRLSCAASGRITVPYTMGWFRQAPGKERELVAAISPSA FTEYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAARRWGYDWGQGT LTVTVSS
5-21	1904	EVQLVESGGGLVQPGGSLRLSCAASGGTFTTYHMGWFRQAPGKEREFVAHISTG GATNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATFPAIVTDSYD LGNDWGQGTTLVTVSS
5-22	1905	EVQLVESGGGLVQPGGSLRLSCAASGFTFNVFAMGWFRQAPGKEREFVAAINWS DSRTDYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCASGSDNRARELS RYEYVWGQGTTLVTVSS
5-23	1906	EVQLVESGGGLVQPGGSLRLSCAASGSIFSIDVMGWFRQAPGKEREFVAAISWSG ESTLYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAFDGYSGSDWGQ GTLVTVSS
5-24	1907	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMGWFRQAPGKEREFVAAISSYS HTAYADSVKGRFTIADNSKNTAYLQMNSLKPEDTAVYYCALQPFGASSYRWGQ GTLVTVSS
5-25	1908	EVQLVESGGGLVQPGGSLRLSCAASGNTF SINVMGWFRQAPGKEREFVAAIHS GDSTLYADSGKGRFTIADNNKNTAYLQMISLKPEDTAVYYCAAFDGYSGNHWG QGTLVTVSS
5-26	1909	EVQLVESGGGLVQPGGSLRLSCAASGRTISSYIMGWFRQAPGKERELVARIYTG DTIYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAARTSYNGRYDYID DYSWGQGTTLVTVSS
5-27	1910	EVQLVESGGGLVQPGGSLRLSCAASGRANSINWMGWFRQAPGKEREFVATITPG GNTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAAGSTWYGT YEYDWGQGTTLVTVSS
5-28	1911	EVQLVESGGGLVQPGGSLRLSCAASGGTFSVFAMGWFRQVPGKERELVAEITAG GSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAVDGPFGWGQGT LTVTVSS
5-29	1912	EVQLVESGGGLVQPGGSLRLSCAASGFTFDDYPMGWFRQAPGKEREGVASVLRG GYTWYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAKDWTGLAWG QGTLVTVSS
5-30	1913	EVQLVESGGGLVQPGGSLRLSCAASGFALGYAMGWFRQAPGKEREFVAGIRW TDAYTEYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADVSPSYGSR WYWGQGTTLVTVSS
5-31	1914	EVQLVESGGGLVQPGGSLRLSCAASGRTLDIHVMGWFRQAPGKEREFVAVINWT GESTLYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAFDGYTGNYW QGTLVTVSS

5-32	1915	EVQLVESGGGLVQPGGSLRLSCAASGFTPDNYAMGWFRQAPGKEREFVAALGW SGVTTHYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCASDESDAAN WGQGLTVTVSS
5-33	1916	EVQLVESGGGLVQPGGSLRLSCAASGFTFDDYAMGWFRQAPGKERELVATIMW SGNTTYYADSVRRRFIIRDNNNKNTAHLQMNSLKPEDTAVYYCATNDDDVWGQ GTLTVTVSS
5-34	1917	EVQLVESGGGLVQPGGSLRLSCAASGRTFSRYIMGWFRQAPGKEREFVAAISWSG GDNTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAYRIVVGGTSP GDWRWGQGLTVTVSS
5-35	1918	EVQLVESGGGLVQPGGSLRLSCAASGPTFSIYAMGWFRQAPGKERELVAGISWN GGSTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCALRRRFGGQEW GQGLTVTVSS
5-36	1919	EVQLVESGGGLVQPGGSLRLSCAASGRTFSLNAMGWFRQAPGKERELVAAISCG GGSTYADNGKGRFTIITDNSKNTAYLQMMNLKPEDTAAYYCAADNDMGYCSW GQGLTVTVSS
5-37	1920	EVQLVESGGGLVQPGGSLRLSCAASGSTFSINAMGWFRQAPGKEREFVGGISRS ATTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADGVPEYSDYAS GPVWGQGLTVTVSS
5-38	1921	EVQLVESGGGLVQPGGSLRLSCAASGRTFSMHAMGWFRQAPGKERELVASISSQ GRNTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAA EVRNGSDYLPI DWGQGLTVTVSS
5-39	1922	EVQLVESGGGLVQPGGSLRLSCAASGVTLDLYAMGWFRQAPGKEREFVAGIRW TDAYTEYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAVDIDYRDWG QGLTVTVSS
5-40	1923	EVQLVESGGGLVQPGGSLRLSCAASGLPFTINVMGWFRQAPGKEREFVAAIHS GLTTFYADSVKGLFTITEDNSKNTAHLMMNLLKPEDTAVYYCAELDGYFFAHWG QGLTVTVSS
5-41	1924	EVQLVESGGGLVQPGGSLRLSCAASGRAFSNYAMGWFRQAPGKEREFVAWINN RGTTDYADSGSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCASTD DYGVDWGQGLTVTVSS
5-42	1925	EVQLVESGGGLVQPGGSLRLSCAASGFTPDDYAMGWFRQAPGKEREFVASIGYS GRNSYNYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAIAHGSSTY NWGQGLTVTVSS
5-43	1926	EVQLVESGGGLVQPGGSLRLSCAASGFTLNYYGMGWFPQAPGKEREFVAAITSG GAPHYADSVKGRFTINADNSKNTAYLQMNSLKPEDTAVYYCASAYDRGIGYDW GQGLTVTVSS
5-44	1927	EVQLVESGGGLVQPGGSLRLSCAASGLPFSTKSMGWFRQAPGKEREFVAAIHS GLTSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADRAADFFAQRD EYDWGQGLTVTVSS
5-45	1928	EVQLVESGGGLVQPGGSLRLSCAASGRTFSINAMGWFPQAPGKERELVAAISWSG ESTQYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAFDGGSGTQWG QGLTVTVSS
5-46	1929	EVQLVESGGGLVQPGGSLRLSCAASGEEFSDHWMGWFRQAPGKEREFVAAIHW SGDSTHRNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATVGITLNW GQGLTVTVSS
5-47	1930	EVQLVESGGGLVQPGGSLRLSCAASGFTFGSYDMGWFRQAPGKEREFVTAINWS GARTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAARSVYSYEYN WGQGLTVTVSS
5-48	1931	EVQLVESGGGLVQPGGSLRLSCAASGLPLDLYAMGWFPAPGKELEFVAGIRWS DAYTEYADSVKGRFTINADNSKNPANLQMNSLKPEDTAVYYCALDIDYRHWGQ GTLTVTVSS
5-49	1932	EVQLVESGGGLVQPGGSLRLSCAASGRTSTVNGMGWFRQAPGKEREFVASISQS GAATAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADRTYSYSTG YYWGQGLTVTVSS
5-50	1933	EVQLVESGGGLVQPGGSLRLSCAASGFSLDYYGMGWFRQAPGKEREFVAAITSG

		GTPHYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCASAYNPGIGYDWG QGTLTVSS
5-51	1934	EVQLVESGGGLVQPGGSLRLSCAASGRPN SINWMGWFRQAPGKERQFVATITPG GNTNYADSVKGRFTISADNSKNTAYLLMNSLKPEDTAVYYCAAAGTTWYGT YEYDWGQGTLTVSS
5-52	1935	EVQLVESGGGLVQPGGSLRLSCAASGEKFS DHWMGWFRQAPGKEREFVATITFS GARTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAALIKPSSTRIF EEWGQGTLTVSS
5-53	1936	EVQLVESGGGLVQPGGSLRLSCAASGLTVVPYAMGWFRQAPGKEREFVAAIRRS AVTNYADSVKGRFTIADNSKNTAYLLMNSLKPEDTAVYYCAARRWGYHYWGQ GTLTVSS
5-54	1937	EVQLVESGGGLVQPGGSLRLSCAASGTTFNFNVMGWFRQAPGKERELVAVISWT GESTLYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAFDGYTGRDW QGTLTVSS
5-55	1938	EVQLVESGGGLVQPGGSLRLSCAASGIDVNRNAMGWFRQAPGKEREFVAAITWS GGWRYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATTFGDAGIPDQ YDFGWQGTLTVSS
5-56	1939	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSNMGWFRQAPGKEREFVARIFGGD RTLYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCADINGDWGQGTLV TVSS
5-57	1940	EVQLVESGGGLVQPGGSLRLSCAASGGTFSMGWIRWVPQAQGKELEFMGCIGWI TYYADYAKSRFSLFTDNADNTKNPPNMHMNPQKPEDTAVYYCAPFGWGQGLV TVSS
5-58	1941	EVQLVESGGGLVQPGGSLRLSCAASGCTLDYYAMGWFRQAPGKEREFVAGIRW TDAYTEYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADVSPSYGGR WYWGQGTLTVSS
5-59	1942	EVQLVESGGGLVQPGGSLRLSCAASGLTFSLYRMCWFRQAPGKEREEVSCISNID GSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADLLGDSYEPS SGFGWGQGTLTVSS
5-60	1943	EVQLVESGGGLVQPGGSLRLSCAASGRSFSHRMGWFRQAPGKEREFVAAIMWS GSHRNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAIAEYEGVYR WDWGQGTLTVSS
5-61	1944	EVQLVESGGGLVQPGGSLRLSCAASGRIIVPNTMGWFRQAPGKERERVGTGISPAF TEYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAHGWGCHWGQGL TVSS
5-62	1945	EVQLVESGGGLVQPGGSLRLSCAASGSIFIISMGWFRQAPGKEHEFTGINWSSGS TTYADSVKGRFTINADNSKNTAYLQMNSLKPEDTAVYYCAASAIGSGALRRFEY DWQGQGLTVSS
5-63	1946	EVQLVESGGGLVQPGGSLRLSCAASGSFLDYYDMGWFRQAPGKEREFVAALGW SGGSTDYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRYGIV ERWGQGTLTVSS
5-64	1947	EVQLVESGGGLVQPGGSLRLSCAASGTSISNRVMGWFRQAPGKERELVARIYTG GDTLYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAARKIYRSLSYYG DYDWQGQGLTVSS
5-65	1948	EVQLVESGGGLVQPGGSLRLSCAASGNIDRLYAMGWFRQAPGKEREGVAAIDSD GSTDYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAALIDYGLGFPIEW QGTLTVSS
5-66	1949	EVQLVESGGGLVQPGGSLRLSCAASGNTFTINVMGWFRQAPGKEREFVAAINWN GGTTLYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAFDGYSGIDWG QGTLTVSS
5-67	1950	EVQLVESGGGLVQPGGSLRLSCAASGFNVNDYAMGWFRQAPGKEREFVAGITSS VGVNTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADIFFVNWGR GTLTVSS
5-68	1951	EVQLVESGGGLVQPGGSLRLSCAASGFTFDHYTMGWFRQAPGKEREFVAAISGS ENVTSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAEPYIPVRTMR

		HMTFLTWGQGLTVTVSS
6-1	1952	EVQLVESGGGLVQPGGSLRLSCAASGRTFGNYNMGWFRQAPGKEREVATINSL GGTSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARVDYYMDVWG QGTLTVTVSS
6-2	1953	EVQLVESGGGLVQPGGSLRLSCAASGFTMSSSWMGWFRQAPGKEREVTVISGV GTSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGPDSSGYGFDYW QGTLTVTVSS
6-3	1954	EVQLVESGGGLVQPGGSLRLSCAASGFTFSPSWMGWFRQAPGKEREVATINEY GGRNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARVDRDFDYWGQ GTLTVTVSS
6-4	1955	EVQLVESGGGLVQPGGSLRLSCAASGFTRDYTMGWFRQAPGKEREVAAISRS GSLTSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCANLAYDSSGY DYWGQGTLTVTVSS
6-5	1956	EVQLVESGGGLVQPGGSLRLSCAASGRTFTMGWFRQAPGKEREVASTNSAGST NYADSVNGRFTISADNSKNTAYLQMNSLKPEDTAVYYCTTVDQYFDYWQGTL TVTVSS
6-6	1957	EVQLVESGGGLVQPGGSLRLSCAASGTTLDDYYAMGWFRQAPGKERELVAAISWS GGSTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAREDYDSSGYS WGQGTLTVTVSS
6-7	1958	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMGWFRQAPGKEREVATINWS GVTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARADDYFDYWQG GTLTVTVSS
6-8	1959	EVQLVESGGGLVQPGGSLRLSCAASGFTLSGIWMGWFLQAPGKEHEFVAIHTTG RTTYADSVKGRFTSSSDNSKNTAYLQMNLLKPEDTAEYYCAGYSTFGSSAYYY YSMDVGVWGQGTLTVTVSS
6-9	1960	EVQLVESGGGLVQPGGSLRLSCAASGFTFDYYAMGWFRQAPGKEREVSAIDSE GRTSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARWGPFDIWGGT LTVTVSS
6-10	1961	EVQLVESGGGLVQPGGSLRLSCAASGSIAHAMGWFRQAPGKEREVAAISRSG GFGSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARDKYYDSSGYP AYFQHWQGTLTVTVSS
6-11	1962	EVQLVESGGGLVQPGGSLRLSCAASGLAFNAYAMGWFRQAPGKEREEVATIGW SGANTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCASDPPGWGQG TLTVTVSS
6-12	1963	EVQLVESGGGLVQPGGSLRLSCAASGSTYTTYSMGWFRQAPGKEREVAAISGSE NVTSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARVDDYMDVWG QGTLTVTVSS
6-13	1964	EVQLVESGGGLVQPGGSLRLSCAASGLTFNDYAMGWFRQAPGKEREVVAHIPRS TYSPPYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAFLVGPQGV DHGAFDVWGQGTLTVTVSS
6-14	1965	EVQLVESGGGLVQPGGSLRLSCAASGITFRFKAMGWFRQAPGKEREVAAVSWD GRNTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCASDYYYMDVW QGTLTVTVSS
6-15	1966	EVQLVESGGGLVQPGGSLRLSCAASGSTVLINAMGWFRQAPGKEREVAAVRWS DDYTTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAKEGRAGSLDY WGQGTLTVTVSS
6-16	1967	EVQLVESGGGLVQPGGSLRLSCAASGFTFDDAAMGWFRQAPGKEREVVAHISWS GGSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATFGATVTATND AFDIWGQGTLTVTVSS
6-17	1968	EVQLVESGGGLVQPGGSLRLSCAASGNTGSTGYMGWFRQAPGKEREMVAGVIN DGSTVYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARLATSHQDGTG YLFYDWQGTLTVTVSS
6-18	1969	EVQLVESGGGLVQPGGSLRLSCAASGLTFRNYAMGWFRQAPGKEREFIAGMMW SGGTTTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAREGYYYDSSG YLNIFYDWQGTLTVTVSS

6-19	1970	EVQLVESGGGLVQPGGSLRLSCAASGSILSIAMGWFRQAPGKEREFVAAISPSA VTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAIGYYDSSGYFDY WGQGLTVTVSS
6-20	1971	EVQLVESGGGLVQPGGSLRLSCAASGSTLPYHAMGWFRQAPGKEREFVAAITWN GASTSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARDRYDTSASY FESETWGQGLTVTVSS
6-21	1972	EVQLVESGGGLVQPGGSLRLSCAASGTLFKINAMGWFRQAPGKEREFVAAITSSG SNIDYTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARSNTGWYSF DYWGQGLTVTVSS
6-22	1973	EVQLVESGGGLVQPGGSLRLSCAASGRTFSEVVMGWFRQAPGKEREFVATIHSSG STSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCVRVTSDDYSMDSWG QGLTVTVSS
6-23	1974	EVQLVESGGGLVQPGGSLRLSCAASGSIFSMTMGWFRQAPGKEREFVALINRSG GGINYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCVRLSSGYDFFDYW GQGLTVTVSS
6-24	1975	EVQLVESGGGLVQPGGSLRLSCAASGFTLDYYAMGWFRQAPGKEREFVAAINWS GDNTHYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARAPFYCTTKC QDNYYYMDVWGQGLTVTVSS
6-25	1976	EVQLVESGGGLVQPGGSLRLSCAASGLTFGTMTMGWFRQAPGKEREFVAAISR GSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGGDYDFWSVD YMDVWGQGLTVTVSS
6-26	1977	EVQLVESGGGLVQPGGSLRLSCAASGDTFSTSWMGWFRQAPGKEREFVATINTG GGTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARVTTSFDYWGQ GTLTVTVSS
6-27	1978	EVQLVESGGGLVQPGGSLRLSCAASGITFRFKAMGWFRQAPGKEREFVASISRS TTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDYSAFDMWGQ TLTVTVSS
6-28	1979	EVQLVESGGGLVQPGGSLRLSCAASGDTYGSYWMGWFRQAPGKEREFVATITSD DRTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARVTSSLSGMDV WGQGLTVTVSS
6-29	1980	EVQLVESGGGLVQPGGSLRLSCAASGYTLKNYYAMGWFRQAPGKERXLVAII WTGESTLDADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAREGYDSSG YYWGQGLTVTVSS
6-30	1981	EVQLVESGGGLVQPGGSLRLSCAASGFAFGDSWMGWFRQAPGKEREFVATINWS GVTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARADGYFDYWGQ GTLTVTVSS
6-31	1982	EVQLVESGGGLVQPGGSLRLSCAASGDTFSANRMGWFRQAPGKEREFVASITWS SANTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATFNWNDEGFDF WGQGLTVTVSS
6-32	1983	EVQLVESGGGLVQPGGSLRLSCAASGFTLDYYDMGWFRQAPGKEREFVALISWS GGSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDFYGWGTRE RDAFDIWGQGLTVTVSS
6-33	1984	EVQLVESGGGLVQPGGSLRLSCAASGTFQRINHMGWFRQAPGKEREFVATINTG GQPNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCASLIAAQDYFDY WGQGLTVTVSS
6-34	1985	EVQLVESGGGLVQPGGSLRLSCAASGSAFRSNAMGWFRQAPGKEREFVAHISWS SKSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATYCSSTSCFDY WGQGLTVTVSS
6-35	1986	EVQLVESGGGLVQPGGSLRLSCAASGFTLAYYAMGWFRQAPGKEREFVAAISMS GDDTIYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARELGYSSTVWP WGQGLTVTVSS
6-36	1987	EVQLVESGGGLVQPGGSLRLSCAASGDFSVSWMGWFRQAPGKEREFVTAITWS GDSTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCASLLHTGPSGNN YFDYWGQGLTVTVSS
6-37	1988	EVQLVESGGGLVQPGGSLRLSCAASGHTFSTSWMGWFRQAPGKEREFVATINSL

		GGTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARVSSGDYGM DV WGQGT LVT VSS
6-38	1989	EVQLVESGGGLVQP GGSRLS CAASGNTFSGGFMGWFRQAPGKEREFVAVISSLS SKSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAKVDSGYDYWGQG TLVT VSS
6-39	1990	EVQLVESGGGLVQP GGSRLS CAASGFTFSPSWMGWFRQAPGKEREFVAAISWS GGSTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCHGLGEGDPYGD YEGYFDLWGQGT LVT VSS
6-40	1991	EVQLVESGGGLVQP GGSRLS CAASGFTFSDYWMGWFRQAPGKERELVARVW WNGGSAYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAREVLRQQV VLDYWGQGT LVT VSS
6-41	1992	EVQLVESGGGLVQP GGSRLS CAASGFTFSTSWMGWFRQAPGKEREFVASINEY GGRNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAGLHYYYDSSGY NPTEYYGMDVWGQGT LVT VSS
6-42	1993	EVQLVESGGGLVQP GGSRLS CAASGDTYGSYWMGWFRQAPGKEREFVAVITSG GSTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCTHVQNSYYAMD VWGQGT LVT VSS
6-43	1994	EVQLVESGGGLVQP GGSRLS CAASGRTFSSYAMMGWFRQAPGKEREFVASVN WDASQINYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCTTLGAVYFDS SGYHDYFDYWGQGT LVT VSS
6-44	1995	EVQLVESGGGLVQP GGSRLS CAASGGTFGVYHMGWFRQAPGKEREFGRITWT DGSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCFGLLEVYDMTFD YWGQGT LVT VSS
6-45	1996	EVQLVESGGGLVQP GGSRLS CAASGNMFSINAMGWFRQAPGKEREFVTLISWSS GRTSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCASLGYS CGSCFD YWGQGT LVT VSS
6-46	1997	EVQLVESGGGLVQP GGSRLS CAASGLTFSAMGWFRQAPGKEREFVALIRRDGST IYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAALGILFGYDAFDIWGQ GTLVT VSS
6-47	1998	EVQLVESGGGLVQP GGSRLS CAASGRTFSMHAMGWFRQAPGKERELVASITYG GNINYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAKEGYDYDSTGYRT YFQQWGQGT LVT VSS
6-48	1999	EVQLVESGGGLVQP GGSRLS CAASGFTVSNYAMGWFRQAPGKEREFVASVNW SGGTTSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATTGT VTLGYW GQGT LVT VSS
6-49	2000	EVQLVESGGGLVQP GGSRLS CAASGSTVLINAMGWFRQAPGKEREFVAAISWSP GRTDYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARD CSGGSCYSGD YWGQGT LVT VSS
6-50	2001	EVQLVESGGGLVQP GGSRLS CAASGFSFDRWAMGWFRQAPGKEREWVASLAT GGNTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARVTNYDAFDI WGQGT LVT VSS
6-51	2002	EVQLVESGGGLVQP GGSRLS CAASGYTYSSYVMGWFRQAPGKEREFVAAISRF GSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARDSGEHFWDSG YIDHWGQGT LVT VSS
6-52	2003	EVQLVESGGGLVQP GGSRLS CAASGDTYGSYWMGWFRQAPGKEREFVAAITS GGSTVYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARVDSRFDYWG QGT LVT VSS
6-53	2004	EVQLVESGGGLVQP GGSRLS CAASGISINTNVMGWFRQAPGKEREFVAAISTGS VTIYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARVDDFGYFDLWGQ GTLVT VSS
6-54	2005	EVQLVESGGGLVQP GGSRLS CAASGFEFENHWMGWFRQAPGKEREFVAHITA GGLSNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCGRHWGIYDSSGF SSFYDWGQGT LVT VSS
6-55	2006	EVQLVESGGGLVQP GGSRLS CAASGFTMSSSWMGWFRQAPGKEREFVARITSG GSTGYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCASVDGYFDYWGQ

		GTLVTVSS
6-56	2007	EVQLVESGGGLVQPGGSLRLSCAASGNIFRSNMGWFRQAPGKEREFVAGITWNG DTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARALGVTYQFDY WGQGLVTVSS
6-57	2008	EVQLVESGGGLVQPGGSLRLSCAASGLTFDDHSMGWFRQAPGKEREFVAAVPLS GNTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCASFSGGPADFDY WGQGLVTVSS
6-58	2009	EVQLVESGGGLVQPGGSLRLSCAASGRAVSTYAMGWFRQAPGKEREFVAAISGS ENVTSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCLSVTGDTEGYGV FDTWGQGLVTVSS
6-59	2010	EVQLVESGGGLVQPGGSLRLSCAASGISGSVFSRTPMGWFRQAPGKEREWVSSY SDGSNTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAHWSWELGD WFDPWGQGLVTVSS
6-60	2011	EVQLVESGGGLVQPGGSLRLSCAASGDTYGSYWMGWFRQAPGKEREFVATISQS GAATAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAGLLRYSGTY DAFDVWGQGLVTVSS
6-61	2012	EVQLVESGGGLVQPGGSLRLSCAASGDTYGSYWMGWFRQAPGKEREFVAAINW SGGSTNYADSVKGRFTITADNNKNTAYLQMNSLKPEDTAVYYCAGLGWNYMD YWGQGLVTVSS
6-62	2013	EVQLVESGGGLVQPGGSLRLSCAASGSTFSGNWMGWFRQAPGKEREFVAVISWT GGSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATHNSLSGFDYW GQGLVTVSS
6-63	2014	EVQLVESGGGLVQPGGSLRLSCAASGQTFNMGWFRQAPGKEREFVAAIGSGGST SYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCWRLGNDYFDYWGQGT LTVSS
6-64	2015	EVQLVESGGGLVQPGGSLRLSCAASGIPSIHAMGWFRQAPGKERELVAAINWSH GVTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCGGGYGYHFDYWG QGLVTVSS
6-65	2016	EVQLVESGGGLVQPGGSLRLSCAASGLPFSTLHMGWFRQAPGKEREFVASLSIFG ATGYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCWMYYYDSSGYGN YYYGMDVWGQGLVTVSS
6-66	2017	EVQLVESGGGLVQPGGSLRLSCAASGLTFSLFAMGWFRQAPGKERELVAAISSGG STDYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGNTKYYYDSSGY SSAFDYWGQGLVTVSS
6-67	2018	EVQLVESGGGLVQPGGSLRLSCAASGSFSNYAMGWFRQAPGKEREFVAAISSG ALTSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCWIVGPGPLDGMV WGQGLVTVSS
6-68	2019	EVQLVESGGGLVQPGGSLRLSCAASGFTLSDRAMGWFRQAPGKEREFVAHITAG GLSNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCVHLASQTGAGYFD LWGQGLVTVSS
6-69	2020	EVQLVESGGGLVQPGGSLRLSCAASGGTFSSVGMGWFRQAPGKEREFVAGISRS GGTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARYDFWSGYPYW GQGLVTVSS
6-70	2021	EVQLVESGGGLVQPGGSLRLSCAASGFNLDDYADMGWFRQAPGKEREFVAAIG WGGGSTRYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAREILWFGEF GEPNVWGQGLVTVSS
6-71	2022	EVQLVESGGGLVQPGGSLRLSCAASGITFSNDAMGWFRQAPGKEREFVAITSSDT NDTTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARLHYDSSGYF DYWGQGLVTVSS
6-72	2023	EVQLVESGGGLVQPGGSLRLSCAASGSTLSINAMGWFRQAPGKEREFVAAIDWS GGSTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARDSSATRTGPD YWGQGLVTVSS
6-73	2024	EVQLVESGGGLVQPGGSLRLSCAASGHTFSGYAMGWFRQAPGKEREFVAVITRE GSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARLGGEFDFYWG QGLVTVSS

6-74	2025	EVQLVESGGGLVQPGGSLRLSCAASGFAFGDSWMGWFRQAPGKERELVAAITSG GSTDYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGLLWFGELFGY WGQGLTLTVSS
6-75	2026	EVQLVESGGGLVQPGGSLRLSCAASGGTFSTYWMGWFRQAPGKEREFVAAISRS GGNTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCVRHSGTDGDSSF DYWGQGLTLTVSS
6-76	2027	EVQLVESGGGLVQPGGSLRLSCAASGLAFDFDGMGWFRQAPGKEREGVAAINSG GSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARFFRAHDYWGQ GTLTVSS
6-77	2028	EVQLVESGGGLVQPGGSLRLSCAASGFTFDRSWMGWFRQAPGKEREFVAAVTE GGTTSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARADYDFDYWG QGLTLTVSS
6-78	2029	EVQLVESGGGLVQPGGSLRLSCAASGRTYDAMGWFRQAPGKEREFVASVTSGG YTHYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAKFRKIVGATELD YWGQGLTLTVSS
6-79	2030	EVQLVESGGGLVQPGGSLRLSCAASGSISSIDYMGWFRQAPGKEREGVSWISSSD GSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARSPFSQIYYYYY MDVWGQGLTLTVSS
6-80	2031	EVQLVESGGGLVQPGGSLRLSCAASGGTFSFYNMGWFRQAPGKEREFVAFISGN GGTSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAVVAMRMVTTEG PDVLDVWGQGLTLTVSS
6-81	2032	EVQLVESGGGLVQPGGSLRLSCAASGFIGNYHAMGWFRQAPGKEREFVAAVTW SGGTTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAREGYYYDSSG YPYFFDYWGQGLTLTVSS
6-82	2033	EVQLVESGGGLVQPGGSLRLSCAASGSSLDAYGMGWFRQAPGKEREFVAAISWG GGSIYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARLSQGMVALDY WGQGLTLTVSS
6-83	2034	EVQLVESGGGLVQPGGSLRLSCAASGSIASIHAMGWFRQAPGKEREFVAAITWSG AITSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAKDGGYGELHYG MEVWGQGLTLTVSS
6-84	2035	EVQLVESGGGLVQPGGSLRLSCAASGFTPDDYAMGWFRQAPGKEREFVAAINSG GSYTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARDRGPWGQGT LTVSS
6-85	2036	EVQLVESGGGLVQPGGSLRLSCAASGGTFSVFAMGWFRQAPGKEREFVSAINWS GGSLLYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCALFGDFDYWGQ GTLTVSS
6-86	2037	EVQLVESGGGLVQPGGSLRLSCAASGPISGINRMGWFRQAPGKEREFVAVITSNG RPSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCVRLLSSGYDFDYWG QGLTLTVSS
6-87	2038	EVQLVESGGGLVQPGGSLRLSCAASGTSIMVGAMGWFRQAPGKEREFVAIIRGD GRTSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARFAGWDAFDIW GQGLTLTVSS
6-88	2039	EVQLVESGGGLVQPGGSLRLSCAASGRTFSTHWMGWFRQAPGKEREFVAVINWS GGSIIYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARLSSDGYNYFD FWGQGLTLTVSS
6-89	2040	EVQLVESGGGLVQPGGSLRLSCAASGTIFASAMGWFRQAPGKEHQFVAVVNW GSSTVYADNVKGRFTIADNSKNTAYLQMNSLKPEDTAVYYCTTVDQYFNYWG QGLTLTVSS
6-90	2041	EVQLVESGGGLVQPGGSLRLSCAASGFPFSIWPMGWFRQAPGKEREFVAAVRWS STYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATGECDDGGSCSLAY WGQGLTLTVSS
6-91	2042	EVQLVESGGGLVQPGGSLRLSCAASGRTFGNYAMGWFRQAPGKEREFVASISS GVSKHYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCVRFGSSWARDL DQWGQGLTLTVSS
6-92	2043	EVQLVESGGGLVQPGGSLRLSCAASGFLFDSYASMGWFRQAPGKEREFVATIWR

		RGNTYYANYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCTETGTAAW GQGLTVTVSS
6-93	2044	EVQLVESGGGLVQPGGSLRLSCAASGLPFSTKSMGWFRQAPGKEREVAAISMSG LTSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCLKVLGGDYEADNW FDYWGGQGLTVTVSS
6-94	2045	EVQLVESGGGLVQPGGSLRLSCAASGNIFRIETMGWFRQAPGKEREVAGIIRSGG ETLYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARSLEYDRSGSYF DYWGQGLTVTVSS
6-95	2046	EVQLVESGGGLVQPGGSLRLSCAASGIPSSIRAMGWFRQAPGKEREVAVIRWTG GSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARDIGYYDSSGYY NDGGFDYWGGQGLTVTVSS
6-96	2047	EVQLVESGGGLVQPGGSLRLSCAASGFTLSGNWMGWFRQAPGKEREVAAITSG GRITNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAGHATFGGSSSSY YGMMDVWGQGLTVTVSS
6-97	2048	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSLAMGWFRQAPGKEREVAAITWS GDITNYADSVKGRFTITADNSKNTAYLQMNSLKPEDTAVYYCLRLSSSGFDHWG QGLTVTVSS
6-98	2049	EVQLVESGGGLVQPGGSLRLSCAASGTFGHYAMGWFRQAPGKEREVAAINWSS RSTVYADSVKGRFTITADNSKNTAYLQMNSLKPEDTAVYYCAKSDGLMGELRSA SAFDIWGGQGLTVTVSS
6-99	2050	EVQLVESGGGLVQPGGSLRLSCAASGIPFRSRTMGWFRQAPGKEREVAGISRSR ASTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCTHANDYGDYWGQ GTLTVTVSS
6-100	2051	EVQLVESGGGLVQPGGSLRLSCAASGGTFSTSWMGWFRQAPGKEREFVAHITAG GLSNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARLLVREDWYFDL WGQGLTVTVSS
6-101	2052	EVQLVESGGGLVQPGGSLRLSCAASGGTFSLFAMGWFRQAPGKEREVAAISWT GDSTYYKYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAYNNSSGE YWGQGLTVTVSS
6-102	2053	EVQLVESGGGLVQPGGSLRLSCAASGSSFSAYAMGWFRQAPGKEREVSAIDSEG TTTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAGDYNFWSGFDHW GQGLTVTVSS
6-103	2054	EVQLVESGGGLVQPGGSLRLSCAASGRTSSPIAMGWFRQAPGKEREPVAVRWS DYTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAKKLGYYAFDI WGQGLTVTVSS
6-104	2055	EVQLVESGGGLVQPGGSLRLSCAASGLTFNQYTMGWFRQAPGKEREVASITDG GSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARDSRYMDVWGQ GTLTVTVSS
6-105	2056	EVQLVESGGGLVQPGGSLRLSCAASGPTFSSMGWFRQAPGKEREVAAISWDGG ATAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAIEIVVGGIYWGGQ TLTVTVSS
6-106	2057	EVQLVESGGGLVQPGGSLRLSCAASGIPSTLRAMGWFRQAPGKEREVAAATSW GGSKYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDLYMDVW GQGLTVTVSS
6-107	2058	EVQLVESGGGLVQPGGSLRLSCAASGGVGFSTNMGWFRQAPGKEREVAVISS SSSTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCTTFNWNDEGFDY WGQGLTVTVSS
6-108	2059	EVQLVESGGGLVQPGGSLRLSCAASGGTFGSYGMGWFRQAPGKEREVAAIRWS GGITYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARERYWNPLPY YGMMDVWGQGLTVTVSS
6-109	2060	EVQLVESGGGLVQPGGSLRLSCAASGGTFSTYAMGWFRQVPGKEREVASIDWS GLTSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGPFYMYCSGTK CYSTNWFDPWGQGLTVTVSS
6-110	2061	EVQLVESGGGLVQPGGSLRLSCAASGPIYAVNRMGWFRQAPGKEREVAGIWR GGHRDYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGEIDILTYW

		YDYWGQGTTLVTVSS
6-111	2062	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNYWMGWFRQAPGKEREFVGGISRS GVSTSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCTTLLYYYDSSGY SFDAFDIWGQGTTLVTVSS
6-112	2063	EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYHMGWFRQAPGKERELVTIIDNG GPTSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCTALLYFDNSGYN FDPFDIWGQGTTLVTGSS

Table 36. Reformatted SARS-CoV-2 S1 Variant Sequences

Name	SEQ ID NO	Amino Acid Sequence
2-H1	2064	EVQLLES GGGLVQPGGSLRLSCAASGFTFSNYATDWVRQAPGKGLEWVSIISGSG GATYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGGYCSSDTCW WEYWLDPWGQGTTLVTVSS
2-H2	2065	EVQLLES GGGLVQPGGSLRLSCAASGFTFSAFAMGWVRQAPGKGLEWVSAITASG DITYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARQSDGLPSPWHFD LGGQGTTLVTVSS
2-H3	2066	EVQLLES GGGLVQPGGSLRLSCAASGFTFSDFAMAWVRQAPGKGLEWVSAISGSG DITYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREADGLHSPWHFD LWGQGTTLVTVSS
2-H4	2067	EVQLLES GGGLVQPGGSLRLSCAASGFTFSRHAMNWVRQAPGKGLEWVSGISGSG DEYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDLPASYDSSGY YWHNGMDVWGQGTTLVTVSS
2-H5	2068	EVQLLES GGGLVQPGGSLRLSCAASGFTFSDFAMAWVRQAPGKGLEWVSAISGSG DITYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREADCLPSPWYLD LWGQGTTLVTVSS
2-H6	2069	EVQLLES GGGLVQPGGSLRLSCAASGFTFSDFAMAWVRQAPGKGLEWVSAISGSG DITYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREADGLHSPWHFD LWGQGTTLVTVSS
2-H7	2070	EVQLLES GGGLVQPGGSLRLSCAASGFTFSNYPMNWVRQAPGKGLEWVSTISGSG GNTFYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCVRHDEYSFDYWGQ GTLVTVSS
2-H8	2071	EVQLLES GGGLVQPGGSLRLSCAASGFTFSDFAMAWVRQAPGKGLEWVSAITGSG DITYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREADGLHSPWHFD LWGQGTTLVTVSS
2-H9	2072	EVQLLES GGGLVQPGGSLRLSCAASGFTFSDYPMNWVRQAPGKGLEWVSTISGSG GITFYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCVRHDEYSFDYWGQ GTLVTVSS
2-H10	2073	EVQLLES GGGLVQPGGSLRLSCAASGFTFSDYPMNWVRQAPGKGLEWVSAISGSG DNTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCVRHDEYSFDYWGQ GTLVTVSS
2-H11	2074	EVQLLES GGGLVQPGGSLRLSCAASGFTFSDFAMAWVRQAPGKGLEWVSAITGTG DITYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREADGLHSPWGQ GTLVTVSS
2-H12	2075	EVQLLES GGGLVQPGGSLRLSCAASGFTFSDYPMNWVRQAPGKGLEWVSAITGSG DITYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCVRHDEYSFDYWGQ GTLVTVSS
2-H13	2076	EVQLLES GGGLVQPGGSLRLSCAASGFTFSDFAMAWVRQAPGKGLEWVSAISGSG DITYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREADGLHSPWHFD LWGQGTTLVTVSS
2-H14	2077	EVQLLES GGGLVQPGGSLRLSCAASGFTFSDFAMAWVRQAPGKGLEWVSAISGSG DITYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREADGLHSPWHFD LWGQGTTLVTVSS

2-H15	2078	EVQLLESGGGLVQPGGSLRLSCAASGFTFPRYAMSWVRQAPGKGLEWVSTISGSG STYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARLIDAFDIWGQGT LTVSS
2-L1	2079	DIQMTQSPSSLSASVGDRVITITCRASQSIHRFLNWFYQQKPGKAPKLLIYAASNLHS GVPSRFGSGSGTDFTLTISLQPEDFATYYCQQSYGLPPTFGQGTKVEIK
2-L2	2080	DIQMTQSPSSLSASVGDRVITITCRASQSIHISLNWFYQQKPGKAPKLLIYLASPLASG VPSRFGSGSGTDFTLTISLQPEDFATYYCQQSYSAAPPYTFGQGTKVEIK
2-L3	2081	DIQMTQSPSSLSASVGDRVITITCRASQSIHTYLNWFYQQKPGKAPKLLIYAASALAS GVPSRFGSGSGTDFTLTISLQPEDFATYYCQQSYSAAPPYTFGQGTKVEIK
2-L4	2082	DIQMTQSPSSLSASVGDRVITITCRASQTINTYLNWFYQQKPGKAPKLLIYASATLQSG VPSRFGSGSGTDFTLTISLQPEDFATYYCQQSYSTFTFGQGTKVEIK
2-L5	2083	DIQMTQSPSSLSASVGDRVITITCRASQNIHTYLNWFYQQKPGKAPKLLIYAASSTFAK GVPSRFGSGSGTDFTLTISLQPEDFATYYCQQSYSAAPPYTFGQGTKVEIK
2-L6	2084	DIQMTQSPSSLSASVGDRVITITCRASQSIDTYLNWFYQQKPGKAPKLLIYAASALAS GVPSRFGSGSGTDFTLTISLQPEDFATYYCQQSYSAAPPYTFGQGTKVEIK
2-L7	2085	DIQMTQSPSSLSASVGDRVITITCRASQSIGNYNWFYQQKPGKAPKLLIYGVSSLQS GVPSRFGSGSGTDFTLTISLQPEDFATYYCQQSHSAPLTFGQGTKVEIK
2-L8	2086	DIQMTQSPSSLSASVGDRVITITCRASQSIDTYLNWFYQQKPGKAPKLLIYAASALAS GVPSRFGSGSGTDFTLTISLQPEDFATYYCQQSYSAAPPYTFGQGTKVEIK
2-L9	2087	DIQMTQSPSSLSASVGDRVITITCRASQSIDNYLNWFYQQKPGKAPKLLIYGVSAALQS GVPSRFGSGSGTDFTLTISLQPEDFATYYCQQSHSAPPYFFGQGTKVEIK
2-L10	2088	DIQMTQSPSSLSASVGDRVITITCRASQSIDTYLNWFYQQKPGKAPKLLIYGASALES GVPSRFGSGSGTDFTLTISLQPEDFATYYCQQSHSAPPYFFGQGTKVEIK
2-L11	2089	DIQMTQSPSSLSASVGDRVITITCRASQSIDTYLNWFYQQKPGKAPKLLIYAASALAS GVPSRFGSGSGTDFTLTISLQPEDFATYYCQQSYSAAPPYTFGQGTKVEIK
2-L12	2090	DIQMTQSPSSLSASVGDRVITITCRASQSIDTYLNWFYQQKPGKAPKLLIYGVSAALQS GVPSRFGSGSGTDFTLTISLQPEDFATYYCQQSYSAAPPYFFGQGTKVEIK
2-L13	2091	DIQMTQSPSSLSASVGDRVITITCRASQSIDTYLNWFYQQKPGKAPKLLIYAASALAS GVPSRFGSGSGTDFTLTISLQPEDFATYYCQQSYSAAPPYTFGQGTKVEIK
2-L14	2092	DIQMTQSPSSLSASVGDRVITITCRASQSIDNYLNWFYQQKPGKAPKLLIYGVSAALQS GVPSRFGSGSGTDFTLTISLQPEDFATYYCQQSHSAPLTFGQGTKVEIK
2-L15	2093	DIQMTQSPSSLSASVGDRVITITCRASQIRIGTYLNWFYQQKPGKAPKLLIYAASNLEG GVPSRFGSGSGTDFTLTISLQPEDFATYYCQQNYSTTWTFGQGTKVEIK
2-H16	2094	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISGSG STYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAREGYRDYLVYFD LWGQGTLLTVSS
2-H17	2095	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSA STYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARVRQGLRRTWYY FDYWGQGTLLTVSS
2-H18	2096	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMYWVRQAPGKGLEWVSAISGSA STYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDTNDFWSGYSIF DPWGQGTLLTVSS
2-H19	2097	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYTMSWVRQAPGKGLEWVSVISGSG STYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAREGYRDYLVYFD LWGQGTLLTVSS
2-H20	2098	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVSVISGSG STYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKGPLVGVYFDLW GQGTLLTVSS
2-L16	2099	DIQMTQSPSSLSASVGDRVITITCTGTSSDVGSYDLVSWYQQKPGKAPKLLIYEGNK RPSGVPSRFGSGSGTDFTLTISLQPEDFATYYCCSYAGSSVVFQGTKVEIK
2-L17	2100	DIQMTQSPSSLSASVGDRVITITCTGTSSDVGSNLSVSWYQQKPGKAPKLLIYEGSK RPSGVPSRFGSGSGTDFTLTISLQPEDFATYYCCSYAGSLYVFQGTKVEIK
2-L18	2101	DIQMTQSPSSLSASVGDRVITITCTGTSSDIGSYNLVSWYQQKPGKAPKLLIYEGTKR PSGVPSRFGSGSGTDFTLTISLQPEDFATYYCCSYAGSRTYVFQGTKVEIK

2-L19	2102	DIQMTQSPSSLSASVGDRTITCTGTSTDVGSYNLVSQYQKPGKAPKLLIYEGTK RPSGVPSRFSGSGSGTDFLTITSLQPEDFATYYCCSYAGSYTSVVFQGGTKVEIK
2-L20	2103	DIQMTQSPSSLSASVGDRTITCTGTSSNVGSYNLVSQYQKPGKAPKLLIYEGTK RPSGVPSRFSGSGSGTDFLTITSLQPEDFATYYCCSYAGSSSFVVFQGGTKVEIK

Table 37. Reformatted ACE2 Variant Sequences

Name	SEQ ID NO	Amino Acid Sequence
3-H1	2104	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSHAMSWVRQAPGKGLEWVSSISGGG ASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARVKYLTSSGWPR PYFDNWGGQGLTVTVSS
3-H2	2105	EVQLLESGGGLVQPGGSLRLSCAASGFTFSAYSMSWVRQAPGKGLEWVSAISGSG GSRYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGRSKWPQANGAFDI WGQGLTVTVSS
3-H3	2106	EVQLLESGGGLVQPGGSLRLSCAASGFMFGNYAMSWVRQAPGKGLEWVAISGS GGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDRGYSSSWYG GFDYWGGQGLTVTVSS
3-H4	2107	EVQLLESGGGLVQPGGSLRLSCAASGFTFRNHAMAWVRQAPGKGLEWVSGISGSG GTTYGDSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGTRFLQWSLPLD VWGQGLTVTVSS
3-H5	2108	EVQLLESGGGLVQPGGSLRLSCAASGFTIPNYAMSWVRQAPGKGLEWVSGISGAG ASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARHTWWKGAGFFD HWGQGLTVTVSS
3-H6	2109	EVQLLESGGGLVQPGGSLRLSCAASGFTFRNYAMAWVRQAPGKGLEWVSGISGSG GTTYGDSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGTRFLEWSLPLD VWGQGLTVTVSS
3-H7	2110	EVQLLESGGGLVQPGGSLRLSCAASGFTIRNYAMSWVRQAPGKGLEWVSSISGGG ASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARVKYLTSSGWPR PYFDNWGGQGLTVTVSS
3-H8	2111	EVQLLESGGGLVQPGGSLRLSCAASGFTIPNYAMSWVRQAPGKGLEWVSGISGSG ASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARHTWWKGAGFFD HWGQGLTVTVSS
3-H9	2112	EVQLLESGGGLVQPGGSLRLSCAASGFTITNYAMSWVRQAPGKGLEWVSGISGSG AGTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARHAWWKAGAGFF DHWGQGLTVTVSS
3-H10	2113	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSHAMSWVRQAPGKGLEWVSSISGGG ASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARVKYLTSSGWPR PYFDNWGGQGLTVTVSS
3-H11	2114	EVQLLESGGGLVQPGGSLRLSCAASGFTITNYAMSWVRQAPGKGLEWVSGISGSG ASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARHTWWKGAGFFD HWGQGLTVTVSS
3-H12	2115	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSHAMNWRQAPGKGLEWVSAISGSG GSTNYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGLKFWLPSAF DIWGQGLTVTVSS
3-H13	2116	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSHAMSWVRQAPGKGLEWVSSISGGG ASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARVKYLTSSGWPR PYFDNWGGQGLTVTVSS
3-H14	2117	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSYAMSWVRQAPGKGLEWVSSISGGG ASTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARVKYLTSSGWPR PYFDNWGGQGLTVTVSS
3-H15	2118	EVQLLESGGGLVQPGGSLRLSCAASGFTITNYAMSWVRQAPGKGLEWVSGISGSG AGTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARHTWWKGAGFFD HWGQGLTVTVSS

3-L1	2119	DIQMTQSPSSLSASVGDRVTTICRASQSIRKYLNWYQQKPGKAPKLLIYASSTLQRG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSLSTPFTFGQGTKVEIK
3-L2	2120	DIQMTQSPSSLSASVGDRVTTICRASQNIKTYLNWYQQKPGKAPKLLIYAASKLQS GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTSPFTFGQGTKVEIK
3-L3	2121	DIQMTQSPSSLSASVGDRVTTICRASQTIYSYLNWYQQKPGKAPKLLIYATSTLQGG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHRGTFGQGTKVEIK
3-L4	2122	DIQMTQSPSSLSASVGDRVTTICRASRSIRRYLNWYQQKPGKAPKLLIYASSSLQAG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTLLTFGQGTKVEIK
3-L5	2123	DIQMTQSPSSLSASVGDRVTTICRASQSIGKYLNWYQQKPGKAPKLLIYASSSLQSG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSPFTFGQGTKVEIK
3-L6	2124	DIQMTQSPSSLSASVGDRVTTICRASRSIRYLNWYQQKPGKAPKLLIYAASSLQAG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSSLTFGQGTKVEIK
3-L7	2125	DIQMTQSPSSLSASVGDRVTTICRASQSIGKYLNWYQQKPGKAPKLLIYASSTLQRG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSLSPFTFGQGTKVEIK
3-L8	2126	DIQMTQSPSSLSASVGDRVTTICRASQSIGRYLNWYQQKPGKAPKLLIYASSSLQSG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSLPRTFGQGTKVEIK
3-L9	2127	DIQMTQSPSSLSASVGDRVTTICRASQSIGRYLNWYQQKPGKAPKLLIYAASSLKSG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSLPRTFGQGTKVEIK
3-L10	2128	DIQMTQSPSSLSASVGDRVTTICRASQSIGKYLNWYQQKPGKAPKLLIYASSTLQRG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSLSTPFTFGQGTKVEIK
3-L11	2129	DIQMTQSPSSLSASVGDRVTTICRASQSIGRYLNWYQQKPGKAPKLLIYAASSLKSG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSLPLTFGQGTKVEIK
3-L12	2130	DIQMTQSPSSLSASVGDRVTTICRTSQSINTYLNWYQQKPGKAPKLLIYGASNVQS GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYRIPRTFGQGTKVEIK
3-L13	2131	DIQMTQSPSSLSASVGDRVTTICRASQSIGKYLNWYQQKPGKAPKLLIYASSTLQRG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSFSPFTFGQGTKVEIK
3-L14	2132	DIQMTQSPSSLSASVGDRVTTICRASQSIGKYLNWYQQKPGKAPKLLIYASSTLQRG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSFSTPFTFGQGTKVEIK
3-L15	2133	DIQMTQSPSSLSASVGDRVTTICRASQSIGRYLNWYQQKPGKAPKLLIYAASSLKSG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSLPRTFGQGTKVEIK
3-H16	2134	EVQLLESGGGLVQPGGSLRLSCAASGFTFTNFAMSWVRQAPGKGLEWVSAISGRG GGTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARD AHGYYYDSSG YDDWGQGLTVTVSS
3-H17	2135	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSYPMWSVRQAPGKGLEWVSTISGSG GITYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGVYGSTVTTC H WGQGLTVTVSS
3-H18	2136	EVQLLESGGGLVQPGGSLRLSCAASGFTLT SYAMSWVRQAPGKGLEWVSAISGSG VDTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARPTNWGF DYWGQ GTLTVTVSS
3-H19	2137	EVQLLESGGGLVQPGGSLRLSCAASGFTFINYAMSWVRQAPGKGLEWVSTISTSGG NTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARADSNWASSAYWG QGTLTVTVSS
3-H20	2138	EVQLLESGGGLVQPGGSLRLSCAASGF PFSTYAMSWVRQAPGKGLEWVSGISVSG GFTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDPYSYGYYYYY GMDVWGQGLTVTVSS
3-H21	2139	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMGWVRQAPGKGLEWVSGISGGG VSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARARNWGPSDYWG QGTLTVTVSS
3-H22	2140	EVQLLESGGGLVQPGGSLRLSCAASGFIFSDYAMTWVRQAPGKGLEWVSAISGSA FYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDATYSSSWYNW FDP WGQGLTVTVSS
3-H23	2141	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMTWVRQAPGKGLEWVSDISGSG GSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGTVTSFDFW GQ GTLTVTVSS

3-H24	2142	EVQLLESGGGLVQPGGSLRLSCAASGFTFSIYAMGWVRQAPGKGLEWVSFISGSGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDYHSASWFSAAADYWGQGT LTVTVSS
3-H25	2143	EVQLLESGGGLVQPGGSLRLSCAASGFTFASYAMTWVRQAPGKGLEWVSAISESGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREGQEYSSGSSYFDYWGQGT LTVTVSS
3-H26	2144	EVQLLESGGGLVQPGGSLRLSCAASGFTFSEYAMSWVRQAPGKGLEWVSAITGSGSTYYGDSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGSQTPYCGGDCPETFDYWGQGT LTVTVSS
3-H27	2145	EVQLLESGGGLVQPGGSLRLSCAASGFTFDDYAMSWVRQAPGKGLEWVSGISGGTSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDLYSSGWYGF DYWGQGT LTVTVSS
3-H28	2146	EVQLLESGGGLVQPGGSLRLSCAASGFTFNYYAMNWVRQAPGKGLEWVSAISGSGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDNYDFWSGYYTNWFDPWGQGT LTVTVSS
3-H29	2147	EVQLLESGGGLVQPGGSLRLSCAASGFTFTNHAMSWVRQAPGKGLEWVSAISGSGSNIYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDSL SVTMGRGVV TYYYYGMDFWGQGT LTVTVSS
3-L16	2148	DIQMTQSPSSLSASVGDRVTITCRASQIIGSYLNWYQQKPGKAPKLLIYTTSNLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYITPWF TFGQGTKVEIK
3-L17	2149	DIQMTQSPSSLSASVGDRVTITCRASQISRYINWYQQKPGKAPKLLIYEASSLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHITPLTFGQGTKVEIK
3-L18	2150	DIQMTQSPSSLSASVGDRVTITCRASQSIYTYLNWYQQKPGKAPKLLIYSASNLHSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSDTTPWTFGQGTKVEIK
3-L19	2151	DIQMTQSPSSLSASVGDRVTITCRASQSIATYLNWYQQKPGKAPKLLIYGASSLEGGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQTFSSPFTFGQGTKVEIK
3-L20	2152	DIQMTQSPSSLSASVGDRVTITCRASQNINTYLNWYQQKPGKAPKLLIYSASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSSLTPWTFGQGTKVEIK
3-L21	2153	DIQMTQSPSSLSASVGDRVTITCRASQGIATYLNWYQQKPGKAPKLLIYYASNLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTRFTFGQGTKVEIK
3-L22	2154	DIQMTQSPSSLSASVGDRVTITCRASERISNYLNWYQQKPGKAPKLLIYTASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYTPPRTFGQGTKVEIK
3-L23	2155	DIQMTQSPSSLSASVGDRVTITCRASQSISSSLNWYQQKPGKAPKLLIYAASRLQDGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPRSFQGTKVEIK
3-L24	2156	DIQMTQSPSSLSASVGDRVTITCRASQSISSHLNWYQQKPGKAPKLLIYRASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQTYNTPQTFGQGTKVEIK
3-L25	2157	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLIWYQQKPGKAPKLLIYAASRLHSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGYNTPRTFGQGTKVEIK
3-L26	2158	DIQMTQSPSSLSASVGDRVTITCRASPSISTYLNWYQQKPGKAPKLLIYTASRLQTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQTYSTPSSFGQGTKVEIK
3-L27	2159	DIQMTQSPSSLSASVGDRVTITCRASQNIKYLWYQQKPGKAPKLLIYGASGLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHSPITFGQGTKVEIK
3-L28	2160	DIQMTQSPSSLSASVGDRVTITCRASQSIGTYLNWYQQKPGKAPKLLIYAASNLHSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQESYSAPYTFGQGTKVEIK
3-L29	2161	DIQMTQSPSSLSASVGDRVTITCRASQISPYLNWYQQKPGKAPKLLIYKASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSSSTPYTFGQGTKVEIK

Table 38. Reformatted ACE2 Variant Sequences

Name	SEQ ID NO	Amino Acid Sequence
4-51	2162	EVQLVESGGGLVQPGGSLRLSCAASGPGTAIMGWFRQAPGKEREFVARISTSGGSTKYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARTT VTPPLIWGQGT LTVTVSS

4-52	2163	EVQLVESGGGLVQPGGSLRLSCAASGRSFSNSVMGWFRQAPGKEREVVARITWNG GSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATTENPNPRWGQG TLVTVSS
4-53	2164	EVQLVESGGGLVQPGGSLRLSCAASGRTFGDDTMGWFRQAPGKEREVVAASWS GSGVYYADSVKGRFTITADNSKNTAYLQMNSLKPENTAVYYCATDPPLFWGQGT LTVTVSS
4-54	2165	EVQLVESGGGLVQPGGSLRLSCAASGRTFSDARMGWFRQAPGKEREVVGAVSWS GGTTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATTEDPYPRWGQ GTLVTVSS
4-49	2166	EVQLVESGGGLVQPGGSLRLSCAASGRTFGDYIMGWFRQAPGKERESVAAINWSA GYTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARASPNTGWHFDH WGQGTTLVTVSS
4-55	2167	EVQLVESGGGLVQPGGSLRLSCAASGSGLSINAMGWFRQAPGKERESVAAISWSG GSTYTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAYQAGWGDW QGQGTTLVTVSS
4-39	2168	EVQLVESGGGLVQPGGSLRLSCAASGRTFSNAMGWFRQAPGKEREVVARILWT GASRNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATTENPNPRWGQ GTLVTVSS
4-56	2169	EVQLVESGGGLVQPGGSLRLSCAASGFSLDYYGMGWFRQAPGKERESVAAISWN GDFTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAKRANPTGAYFD YWQGTTLVTVSS
4-33	2170	EVQLVESGGGLVQPGGSLRLSCAASGFTFSRHDMGWFRQAPGKEREVAGINWES GSTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADRGVYGGRWY RTSQYTWGQGTTLVTVSS
4-57	2171	EVQLVESGGGLVQPGGSLRLSCAASGLTFRNYAMGWFRQAPGKEREVAAIGSG GYTDYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAVKPGWVARDPSQ YNWGQGTTLVTVSS
4-25	2172	EVQLVESGGGLVQPGGSLRLSCAASGGTFSRYAMGWFRQAPGKEREWVSAVDSG GSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAASPSLRSWQWG QGQGTTLVTVSS
4-58	2173	EVQLVESGGGLVQPGGSLRLSCAASGFTLDYYDMGWFRQAPGKEREVAAVTWS GGSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADRRGLASTRA ADYDWGQGTTLVTVSS
4-59	2174	EVQLVESGGGLVQPGGSLRLSCAASGRTFGDYIMGWFRQAPGKEREVAAINWSA GYTPYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATAPPLFCWHFDL WGQGTTLVTVSS
4-6	2175	EVQLVESGGGLVQPGGSLRLSCAASGRTFGDDIMGWFRQAPGKEREVAAIHWSA GYTRYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGHVDL WGQGTTLVTVSS
4-61	2176	EVQLVESGGGLVQPGGSLRLSCAASGRTFGDYIMGWFRQAPGKEREIVAAINWSA DYTPYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATAPNTGWHFDH WGQGTTLVTVSS
4-3	2177	EVQLVESGGGLVQPGGSLRLSCAASGRTFGDYIMGWFRQAPGKEREIVAAINWSA GYTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATATPNTGWHFDH WGQGTTLVTVSS
4-62	2178	EVQLVESGGGLVQPGGSLRLSCAASGRTFSDDTMGWFRQAPGKEREVAAINWS GGSTDYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LTVTVSS
4-43	2179	EVQLVESGGGLVQPGGSLRLSCAASGRTFGDDTMGWFRQAPGKEREVAGINWS GGNTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LTVTVSS
4-5	2180	EVQLVESGGGLVQPGGSLRLSCAASGRTFGDYIMGWFRQAPGKEREVAAINWT GGYTSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LTVTVSS
4-42	2181	EVQLVESGGGLVQPGGSLRLSCAASGRTFGDDTMGWFRQAPGKERECVAAINWS

		GGNTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LVTVSS
4-63	2182	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDYTMGWFRQAPGKEREFVAAINWS GGYTTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LVTVSS
4-6	2183	EVQLVESGGGLVQPGGSLRLSCAASGRFTFGDYMGWFRQAPGKEREFVATINWS GALTHYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATLPFYDFWSGY YTGYYMDVWGQGT LVTVSS
4-40	2184	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDTMGWFRQAPGKEREFVAGVTWS GSSTFYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LVTVSS
4-21	2185	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDIMGWFRQAPGKEREFVA AISWSG GNTHYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LVTVSS
4-64	2186	EVQLVESGGGLVQPGGSLRLSCAASGRFTFGDYIMGWFRQAPGKERESVAAINWSA GYTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATASPNTGWHFDH WGQGT LVTVSS
4-47	2187	EVQLVESGGGLVQPGGSLRLSCAASGFTFDDDYVMGWFRQAPGKEREFVA AVSG SGDDTTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADRRGLASTR AADYDWGQGT LVTVSS
4-65	2188	EVQLVESGGGLVQPGGSLRLSCAASGRFTFGDYIMGWFRQAPGKEREFVAAINWSA GYTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATEPPLSCWHFDL WGQGT LVTVSS
4-18	2189	EVQLVESGGGLVQPGGSLRLSCAASGRFTFGDYIMGWFRQAPGKEREIFVAAINWSG GYTPYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATAPNTGWHFDH WGQGT LVTVSS
4-66	2190	EVQLVESGGGLVQPGGSLRLSCAASGRFTGDDTMGWFRQAPGKEREIFVAAINWS AGYTPYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFCCHFDL WGQGT LVTVSS
4-36	2191	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDTMGWFRQAPGKEREFVA AISWSG GTTRYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LVTVSS
4-67	2192	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDTMGWFRQAPGKEREFVAAINWS GDSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LVTVSS
4-16	2193	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDTMGWFRQAPGKEREFVAAINWS GGTTRYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LVTVSS
4-11	2194	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDAMGWFRQAPGKEREFVA AIHWS GSSTRYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LVTVSS
4-68	2195	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDTMGWFRQAPGKERELVGTINWS GGSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LVTVSS
4-34	2196	EVQLVESGGGLVQPGGSLRLSCAASGRFTFGDYIMGWFRQAPGKEREFVAAINWSG GYTPYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LVTVSS
4-28	2197	EVQLVESGGGLVQPGGSLRLSCAASGRFTGDDTMGWFRQAPGKERELVAAINWN GGNTHYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LVTVSS
4-69	2198	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDAMGWFRQAPGKEREFVAAINWS GGTTRYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LVTVSS
4-7	2199	EVQLVESGGGLVQPGGSLRLSCAASGRFTFGDYIMGWFRQAPGKERESVAAINWSA GYTPYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGHVDL

		WGQGT LVT VSS
4-71	2200	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDTMGWFRQAPGKEREFVASINWS GGSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LVT VSS
4-23	2201	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDTMGWFRQAPGKEREFVAGISWN GGSIYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LVT VSS
4-9	2202	EVQLVESGGGLVQPGGSLRLSCAASGFTFDDYEMGWFRQAPGKEREFVAAISWR GGTTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADRRGLASTRA GDYDWGQGT LVT VSS
4-72	2203	EVQLVESGGGLVQPGGSLRLSCAASGRFTGDDTMGWFRQAPGKEREFVAAINWS GGYTPYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGHVD LWGQGT LVT VSS
4-73	2204	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDTMGWFRQAPGKEREFVAAINWS GGSTRYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LVT VSS
4-29	2205	EVQLVESGGGLVQPGGSLRLSCAASGVTLDYAMGWFRQAPGKEREFVAVINWS GGSTDYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGGGWVPSSTS ESLNWYFDRWGQGT LVT VSS
4-41	2206	EVQLVESGGGLVQPGGSLRLSCAASGRFTGDIYMGWFRQAPGKERESVAAINWSG GTPYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFCCHVDLW GQGT LVT VSS
4-74	2207	EVQLVESGGGLVQPGGSLRLSCAASGLTFSDTMGWFRQAPGKEREFVAAVSWS GGNTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LVT VSS
4-75	2208	EVQLVESGGGLVQPGGSLRLSCAASGRFTGDDTMGWFRQAPGKEREFVAAINWT GGYTPYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LVT VSS
4-31	2209	EVQLVESGGGLVQPGGSLRLSCAASGRFTGDIYMGWFRQAPGKEREFVATINWTA GYTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFCWHFDH WGQGT LVT VSS
4-32	2210	EVQLVESGGGLVQPGGSLRLSCAASGRFTGDDTMGWFRQAPGKEREFVAAINWS GGNTDYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LVT VSS
4-15	2211	EVQLVESGGGLVQPGGSLRLSCAASGRFTGDIYTMGWFRQAPGKEREFVAAINWS GGNTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LVT VSS
4-14	2212	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDTMGWFRQAPGKEREFVAGINWS GNGVYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LVT VSS
4-76	2213	EVQLVESGGGLVQPGGSLRLSCAASGRFTGDIYAMGWFRQAPGKERELVAPINWS GGSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LVT VSS
4-50	2214	EVQLVESGGGLVQPGGSLRLSCAASGGTFSNSGMGWFRQAPGKERELVAVVNWS GRRYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAVPWMDYNRRD WGQGT LVT VSS
4-17	2215	EVQLVESGGGLVQPGGSLRLSCAASGQLANFASYAMGWFRQAPGKEREFVAAIT RSGSTVYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATTMNPNP RWGQGT LVT VSS
4-37	2216	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDIMGWFRQAPGKEREFVAAINWTG GSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LVT VSS
4-44	2217	EVQLVESGGGLVQPGGSLRLSCAASGRFTGDIYMGWFRQAPGKEREIVAAINWSA GYTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATARPNTGWHFDH WGQGT LVT VSS

4-77	2218	EVQLVESGGGLVQPGGSLRLSCAASGRTFSDDTMGWFRQAPGKEREWVGSINWS GGSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LVTVSS
4-78	2219	EVQLVESGGGLVQPGGSLRLSCAASGRTFSDDTMGWFRQAPGKEREFVAGMTWS GSSTFYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTL VTVSS
4-79	2220	EVQLVESGGGLVQPGGSLRLSCAASGRTFGDYIMGWFRQAPGKERECVAAINWS GDYTDYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LVTVSS
4-8	2221	EVQLVESGGGLVQPGGSLRLSCAASGRTFGDYIMGWFRQAPGKEREFVGGINWSG GYTTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTL VTVSS
4-81	2222	EVQLVESGGGLVQPGGSLRLSCAASGRTFSDDTMGWFRQAPGKEREFVAAVNWS GGSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LVTVSS
4-82	2223	EVQLVESGGGLVQPGGSLRLSCAASGRTFGDYAMGWFRQAPGKEREFVAAINWS GGYTRYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LVTVSS
4-83	2224	EVQLVESGGGLVQPGGSLRLSCAASGRTFGDDTMGWFRQAPGKEREFVAAINWS GGYTPYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LVTVSS
4-35	2225	EVQLVESGGGLVQPGGSLRLSCAASGRTFGDYIMGWFRQAPGKERESVAAINWSA GYTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARASPNTGWHFDR WGQGTLVTVSS
4-45	2226	EVQLVESGGGLVQPGGSLRLSCAASGRTFGDYIMGWFRQAPGKEREFVAAINWSG GYTHYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTL VTVSS
4-84	2227	EVQLVESGGGLVQPGGSLRLSCAASGRTFSDDTMGWFRQAPGKEREFVAAITWSG GRTRYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDRPLFWGQGTL VTVSS
4-85	2228	EVQLVESGGGLVQPGGSLRLSCAASGRTFGDYIMGWFRQAPGKERESVAAINWSG GYTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATASPNTGWHFDH WGQGTLVTVSS
4-86	2229	EVQLVESGGGLVQPGGSLRLSCAASGRTFSDDTMGWFRQAPGKEREFVAAIHWS GSSTRYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTL VTVSS
4-87	2230	EVQLVESGGGLVQPGGSLRLSCAASGRTFSDYTMGWFRQAPGKEREWVAAINWS GGTTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LVTVSS
4-88	2231	EVQLVESGGGLVQPGGSLRLSCAASGRTFGDDTMGWFRQAPGKEREFVAAINWS GDNTHYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LVTVSS
4-89	2232	EVQLVESGGGLVQPGGSLRLSCAASGFAFGDNWIGWFRQAPGKEREWVASISSG TTAYADNVKGRFTIADNSKNTAYLQMNSLKPEDTAVYYCAHRGGWLRPWGYW GQGTLVTVSS
4-9	2233	EVQLVESGGGLVQPGGSLRLSCAASGRTFSDDAMGWFRQAPGKEREFVGRINWS GGNTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LVTVSS
4-91	2234	EVQLVESGGGLVQPGGSLRLSCAASGRTFSDDTMGWFRQAPGKEREFVGGISWSG GNTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGTL VTVSS
4-92	2235	EVQLVESGGGLVQPGGSLRLSCAASGRTFSDDTMGWFRQAPGKEREFVAAINWS GGSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LVTVSS
4-46	2236	EVQLVESGGGLVQPGGSLRLSCAASGRTFGDDTMGWFRQAPGKEREFVAAINWS

		GGYTTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LTVVSS
4-20	2237	EVQLVESGGGLVQPGGSLRLSCAASGRFTFGDYIMGWFRQAPGKEREFVAAINWSA DYTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFCWHFDH WGQGT LTVVSS
4-93	2238	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDAMGWFRQAPGKEREFVAAINWS GSSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LTVVSS
4-4	2239	EVQLVESGGGLVQPGGSLRLSCAASGRFTFGDYIMGWFRQAPGKEREMVAAINWI AGYTADADSVRRLFTITADNNKNTAHLMMNLLKPENTAVYYCAEPSNTGWHFD HWGQGT LTVVSS
4-2	2240	EVQLVESGGGLVQPGGSLRLSCAASGRFTGDDTMGWFRQAPGKEREFVAAINWS GGNTPYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LTVVSS
4-94	2241	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDTMGWFRQAPGKEREFVAAINWS GDNTHYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LTVVSS
4-95	2242	EVQLVESGGGLVQPGGSLRLSCAASGRFTFGDYIMGWFRQAPGKEREFVAAINWSA GYTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATAPPLFCWHFDH WGQGT LTVVSS
4-12	2243	EVQLVESGGGLVQPGGSLRLSCAASGRFTFGDYVMGWFRQAPGKEREFVAAINWN AGYTAYADSVRGLFTITADNSKNTAYLQMNSLKPEDTAVYYCAKASPNTGWHFD HWGQGT LTVVSS
4-30	2244	EVQLVESGGGLVQPGGSLRLSCAASGRFTFGDYTMGWFRQAPGKEREFVAAINWT GGYTTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LTVVSS
4-27	2245	EVQLVESGGGLVQPGGSLRLSCAASGRFTFGDYIMGWFRQAPGKEREFVAAINWSA GYTAYADSVKGLFTITADNSKNTAYLQMNILKPEDTAVYYCARATPNTGWHFDH WGQGT LTVVSS
4-22	2246	EVQLVESGGGLVQPGGSLRLSCAASGRFTFGDYIMGWFRQAPGKEREFVAAINWSG DNTHYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT LTVVSS
4-96	2247	EVQLVESGGGLVQPGGSLRLSCAASGRFTFGDYIMGWFRQAPGKEREFVAAINWSA GYTPYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFCCHFDH WGQGT LTVVSS
4-97	2248	EVQLVESGGGLVQPGGSLRLSCAASGRFTFGDYIMGWFRQAPGKERESVAAINWSA GYTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATAPPNTGWHFDH WGQGT LTVVSS
4-98	2249	EVQLVESGGGLVQPGGSLRLSCAASGFTWGDYTMGWFRQAPGKEREFVAAINWS GGNTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADRRGLASTRA ADYDWGQGT LTVVSS
4-99	2250	EVQLVESGGGLVQPGGSLRLSCAASGIPSTLRAMGWFRQAPGKEREFVAAVSSLG PFTRYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAKPGWVARDPSQ YNWGQGT LTVVSS
4-100	2251	EVQLVESGGGLVQPGGSLRLSCAASGFSFDDDYVMGWFRQAPGKEREFVAAINW SGGSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADRRGLASTR AADYDWGQGT LTVVSS
4-101	2252	EVQLVESGGGLVQPGGSLRLSCAASGRFTFSNAAMGWFRQAPGKEREFVARILWT GASRSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATTENPNPRWGQ GTLTVVSS
4-102	2253	EVQLVESGGGLVQPGGSLRLSCAASGGTFGVYHMGWFRQAPGKEREGVAAINMS GDDSAAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAILVGPQVFEFDH WGQGT LTVVSS
4-103	2254	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMGWFRQAPGKEREFVARI-- SGSTFYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAALPFVCPSGSYS

		DYGDEYDWGQGLTVTVSS
4-104	2255	EVQLVESGGGLVQPGGSLRLSCAASGRTFSGDFMGWFRQAPGKEREFVGRINWSG GNTYYADSVRGLFTITADNNKNTAYLMMNLLKPEDTAVYYCPTDPPLFWGLGTL VTWSS
4-105	2256	EVQLVESGGGLVQPGGSLRLSCAASGSTRDYAMGWFRQAPGKERESVAAITWS GGSTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCASLLAGDRYFDY WGQGLTVTVSS
4-106	2257	EVQLVESGGGLVQPGGSLRLSCAASGFTFDDYTMGWFRQAPGKEREFVAAITDNG GSKYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADRRGLASTRAA DYDWGQGLTVTVSS
4-107	2258	EVQLVESGGGLVQPGGSLRLSCAASGGTFSSYGMGWFRQAPGKEREFVAAINWS GASTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARDWRDRTWGN SLDYWGQGLTVTVSS
4-108	2259	EVQLVESGGGLVQPGGSLRLSCAASGFSFDDDYVMGWFRQAPGKEREFVAAISW SEDNTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADRRGLASTR AADYDWGQGLTVTVSS
4-109	2260	EVQLVESGGGLVQPGGSLRLSCAASGFSFDDDYVMGWFRQAPGKEREFVAAVSG SGDDTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADRRGLASTR AADYDWGQGLTVTVSS
4-11	2261	EVQLVESGGGLVQPGGSLRLSCAASGNIAAINVMGWFRQAPGKEREFVAAISASG RRTDYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARRVYYYDSSGPP GVTFDIWGQGLTVTVSS
4-111	2262	EVQLVESGGGLVQPGGSLRLSCAASGIITSRYVMGWFRQAPGKEREFVAAISTGGS TIYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARQDSSSPYFDYWGQG TLTVTVSS
4-112	2263	EVQLVESGGGLVQPGGSLRLSCAASGFSFDDDYVMGWFRQAPGKEREFVAAISNS GLSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADRRGLASTRA ADYDWGQGLTVTVSS
4-113	2264	EVQLVESGGGLVQPGGSLRLSCAASGSISSINVMGWFRQAPGKEREFVATMRWST GSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAQVRVGFGLPLRTT PSWYEWGQGLTVTVSS
4-114	2265	EVQLVESGGGLVQPGGSLRLSCAASGLTFILYRMGWFRQAPGKEREFVAAINNFG TTKYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARTHYDFWSGYTSR TPNYFDYWGQGLTVTVSS
4-115	2266	EVQLVESGGGLVQPGGSLRLSCAASGGTFSVYHMGWFRQAPGKEREPVAAISWS GGSTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAVNTWTSPSFDS WGQGLTVTVSS
4-116	2267	EVQLVESGGGLVQPGGSLRLSCAASGRAFSTYGMGWFRQAPGKEREFVAGINWS GDTPLYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAREVGPPPGYFDL WGQGLTVTVSS
4-117	2268	EVQLVESGGGLVQPGGSLRLSCAASGRTFSDIAMGWFRQAPGKEREFVASINWGG GNTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAKGIWDYLGRRD FGDWGQGLTVTVSS
4-118	2269	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSARMGWFRQAPGKEREFVAAISWSG DNTHYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATTENPNPRWGQG TLTVTVSS
4-119	2270	EVQLVESGGGLVQPGGSLRLSCAASGFAFSSYAMGWFRQAPGKEREFVATINGD DYTTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCVATPGGYGLWGQ GLTVTVSS
4-12	2271	EVQLVESGGGLVQPGGSLRLSCAASGITFRRHDMGWFRQAPGKEREFVAAIRWSS SSTVYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADRGVYGGRWYR TSQYTWGQGLTVTVSS
4-121	2272	EVQLVESGGGLVQPGGSLRLSCAASGTAASFNPMGWFRQAPGKEREFVAAITSGG STNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAIAEEGVYRWDW GQGLTVTVSS

4-122	2273	EVQLVESGGGLVQPGGSLRLSCAASGNINIINMGWFRQAPGKEREGVAAIHWNG DSTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCASGPPYSNYFAYW GQGTLTVSS
4-123	2274	EVQLVESGGGLVQPGGSLRLSCAASGFTFDDYAMGWFRQAPGKERESVAAISGSG GSTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAKIMGSGRPYFDH WGQGLTVTVSS
4-124	2275	EVQLVESGGGLVQPGGSLRLSCAASGNIFTRNVMGWFRQAPGKEREFVAAITSSG STNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARPSSDLQGGVDYW GQGTLTVTVSS
4-125	2276	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSIAMGWFRQAPGKEREFVASINWGG GNTIYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAKGIWDYLGRRD FGDWGQGLTVTVSS
4-126	2277	EVQLVESGGGLVQPGGSLRLSCAASGIPSTLRAMGWFRQAPGKEREFVAAVSSLG PFTRYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAKPGWVARDPSE YNWGQGLTVTVSS
4-127	2278	EVQLVESGGGLVQPGGSLRLSCAASGFTLDDSAMGWFRQAPGKEREWVAAITNG GSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARFARGSPYFDW GQGTLTVTVSS
4-128	2279	EVQLVESGGGLVQPGGSLRLSCAASGSISSFNAMGWFRQAPGKERESVAAIDWDG STAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGGGYYGSGSFEY WGQGLTVTVSS
4-129	2280	EVQLVESGGGLVQPGGSLRLSCAASGNIFSDNIIGWFRQAPGKEREMVAYYTSGGS IDYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGTAVGRPPPGGMD VWGQGLTVTVSS
4-13	2281	EVQLVESGGGLVQPGGSLRLSCAASGSISSIGAMGWFRQAPGKEREGVAAISSSGS STVYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARVPPQAYFDSWG QGTLTVTVSS
4-131	2282	EVQLVESGGGLVQPGGSLRLSCAASGFTFDDYGMGWFRQAPGKERELVATITWS GDSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAKGGSWYYDSSG YYGRWGQGLTVTVSS
4-132	2283	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSNYTMGWFRQAPGKEREWVSAISWS TGSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADRYGPPWYD WGQGLTVTVSS
4-134	2284	EVQLVESGGGLVQPGGSLRLSCAASGGTFSSVGMGWFRQAPGKERELVAVINWS GARTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAVPWMDYNRRD WGQGLTVTVSS
4-135	2285	EVQLVESGGGLVQPGGSLRLSCAASGRIFTNTAMGWFRQAPGKEREGVAAINWS GGSTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARTSGSYSFYDW GQGTLTVTVSS
4-136	2286	EVQLVESGGGLVQPGGSLRLSCAASGEEFSDHWMGWFRQAPGKEREFVGAIHWS GGRYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADRRGLASTRA ADYDWGQGLTVTVSS
4-137	2287	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSIAMGWFRQAPGKEREFVAAINWSG ARTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAKGIWDYLGRRD FGDWGQGLTVTVSS
4-138	2288	EVQLVESGGGLVQPGGSLRLSCAASGSTSSLRTMGWFRQAPGKEREGVAAISSRD GSTIYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARDSSSPYFDYWG QGTLTVTVSS
4-139	2289	EVQLVESGGGLVQPGGSLRLSCAASGGGTFGSYAMGWFRQAPGKEREFVAAISIA SGASGGTTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATTMNP RWGQGLTVTVSS
4-14	2290	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSNAAMGWFRQAPGKEREFVARITWN GGSTFYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATTENPNPRWGQ GTLTVTVSS
4-141	2291	EVQLVESGGGLVQPGGSLRLSCAASGIILSDNAMGWFRQAPGKEREFVAAISWLG

		ESTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADRRGLASTRAA DYDWGQGLTVTVSS
4-142	2292	EVQLVESGGGLVQPGGSLRLSCAASGRFTFGDYIMGWFRQAPGKERESVAAINWN GGYTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATTSPNTGWHYY RWGQGLTVTVSS
4-143	2293	EVQLVESGGGLVQPGGSLRLSCAASGFNFWYPMGWFRQAPGKERESVAAISWT GVSTYTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARWGPGPAGG SPGLVGFYDWGQGLTVTVSS
4-144	2294	EVQLVESGGGLVQPGGSLRLSCAASGSIRSVSMGWFRQAPGKEREAVA AISWSG VGTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAYQRGWGDWQG GTLTVTVSS
4-145	2295	EVQLVESGGGLVQPGGSLRLSCAASGMTFRLYAMGWFRQAPGKEREFVGA INWL SESTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAKPGWVARDPS EYNWGQGLTVTVSS
4-146	2296	EVQLVESGGGLVQPGGSLRLSCAASGRFTSDDAMGWFRQAPGKEREFVAAINWS GGSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATDPPLFWGQGT MVTVSS
4-147	2297	EVQLVESGGGLVQPGGSLRLSCAASGGTFSVYAMGWFRQAPGKEREGVAAISMS GDDAAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAKISKDDGGKPR GAFFDSWGQGLTVTVSS
4-148	2298	EVQLVESGGGLVQPGGSLRLSCAASGFALGYAMGWFRQAPGKERESVAAISSRD GSTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARLATGPQAYFHH WGQGLTVTVSS
4-149	2299	EVQLVESGGGLVQPGGSLRLSCAASGFNLDDYAMGWFRQAPGKERESVAAISWD GGATAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARVGRGTTAFDS WGQGLTVTVSS
4-15	2300	EVQLVESGGGLVQPGGSLRLSCAASGNTFSGGFMGWFRQAPGKEREFVASIRSGA RTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAQVRGFFGPLRTP SWYEWGQGLTVTVSS
4-151	2301	EVQLVESGGGLVQPGGSLRLSCAASGSIRSINIMGWFRQAPGKEREAVA AISWSG STVYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCASLLAGDRYFDYWG QGLTVTVSS

Table 39. SARS-CoV-2 Variant Variable Heavy Chain Sequences

7-1	2302	EVQLVESGGGLVQPGGSLRLSCAASGFTLGDYVMGWFRQAPGKEREFVAAIHSG GSTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAKEYGGTRRYDRA YNWGQGLTVTVSS
7-2	2303	EVQLVESGGGLVQPGGSLRLSCAASGGTFTGSYAMGWFRQAPGKERELVAAISSG GSTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGDWRYGWGQG TLTVTVSS
7-3	2304	EVQLVESGGGLVQPGGSLRLSCAASGRYSISAMGWFRQAPGKEREFVAAISMSG DDSAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAQLGYESGYSLT YDYDWGQGLTVTVSS
7-4	2305	EVQLVESGGGLVQPGGSLRLSCAASGGTFSTYPMGWFRQAPGKEREFVAAITSDG STLYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAATDYNKAYAREGR RYDWGQGLTVTVSS
7-5	2306	EVQLVESGGGLVQPGGSLRLSCAASGSIFRINAMGWFRQAPGKEREFVAAIHWSG SSTRYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAQDRRRGDYYTF DYHWGQGLTVTVSS
7-6	2307	EVQLVESGGGLVQPGGSLRLSCAASGGTFNNYAMGWFRQAPGKERELVAAITSG GSTDYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGDWRYGWGQG TLTVTVSS
7-7	2308	EVQLVESGGGLVQPGGSLRLSCAASGTIVNINVMGWFRQAPGKEREFVAAIHWSG GLKAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAMNRAGIYEWGQ

		GTLVTVSS
7-8	2309	EVQLVESGGGLVQPGGSLRLSCAASGSTFSNYAMGWFRQAPGKERELVAAITSGG STSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGDWRYGWGQGT LTVTVSS
7-9	2310	EVQLVESGGGLVQPGGSLRLSCAASGFSFDDYVMGWFRQAPGKEREFVAAISRSG NLKSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAKEYGGTRYDR AYNWGQGT LTVTVSS
7-10	2311	EVQLVESGGGLVQPGGSLRLSCAASGSAFRSTVMGWFRQAPGKEREFVAAVIGSS GITDYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGDWRYGWGQG TLVTVSS
7-11	2312	EVQLVESGGGLVQPGGSLRLSCAASGRTFSDAGMGWFRQAPGKEREFVAAISRSG NLKAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAVQVNGTWAWGQ GTLVTVSS
7-12	2313	EVQLVESGGGLVQPGGSLRLSCAASGFTLDYYAMGWFRQAPGKERELVAAISWN GGSTSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGDWRYGWGQ GTLVTVSS
7-13	2314	EVQLVESGGGLVQPGGSLRLSCAASGGTFSTYVMGWFRQAPGKEREFVAAISWSG ESTLYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADLMYGVDTRYD WGQGT LTVTVSS
7-14	2315	EVQLVESGGGLVQPGGSLRLSCAASGISSSKRNMGWFRQAPGKEREFVAGISWTG GITYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAIAGRGRWGQGT LTVTVSS
7-15	2316	EVQLVESGGGLVQPGGSLRLSCAASGRRFSAYGMGWFRQAPGKEREFVAVISRSG TLTRYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCASSGPADARNGER WHWGQGT LTVTVSS
7-16	2317	EVQLVESGGGLVQPGGSLRLSCAASGLTFSSVMGWFRQAPGKEREFVAAISSNG GSTRYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAKEYGGTRYDR AYNWGQGT LTVTVSS
7-17	2318	EVQLVESGGGLVQPGGSLRLSCAASGTVFSISAMGWFRQAPGKEREFVAAISMSG DDTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAQLGYESGYSLT YDYDWGQGT LTVTVSS
7-18	2319	EVQLVESGGGLVQPGGSLRLSCAASGSIFSPNVMGWFRQAPGKEREFVAAITNGG STKYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAQRWRGGSYEWG QGTLVTVSS
7-19	2320	EVQLVESGGGLVQPGGSLRLSCAASGIPASIRVMGWFRQAPGKEREFVAAIHWG SSTRYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCALSRAIVPGDSEYD YRWGQGT LTVTVSS
7-20	2321	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSMSAMGWFRQAPGKEREFVSAISWSG GSTLYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAQLGYESGYSLTY DYDWGQGT LTVTVSS
7-21	2322	EVQLVESGGGLVQPGGSLRLSCAASGRTFSNYAMGWFRQAPGKERELVAAITSGG STDYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGDWRYGWGQGT LTVTVSS
7-22	2323	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSYAMGWFRQAPGKERELVAAISTGG STYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGDWRYGWGQGT LTVTVSS
7-23	2324	EVQLVESGGGLVQPGGSLRLSCAASGRSFSSVMGWFRQAPGKEREFVAVISRSG ASTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCASAGPADARNGER WAWGQGT LTVTVSS
7-24	2325	EVQLVESGGGLVQPGGSLRLSCAASGRAFRRYTMGWFRQAPGKERELIAVINWSG DRRYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAATLAKGGGRWG QGTLVTVSS
7-25	2326	EVQLVESGGGLVQPGGSLRLSCAAMAWAGFARRRAKNAKWWRALPRGGPTYA DSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGGMWYGSSLYVRFDLLE DGM DWGQGT LTVTVSS

7-26	2327	EVQLVESGGGLVQPGGSLRLSCAASGSISSINGMGWFRQAPGKERELVALISRSGG TTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCASAGPADARNGERW AWGQGLTVTVSS
7-27	2328	EVQLVESGGGLVQPGGSLRLSCAASGRFTSNNVMGWFRQAPGKERELVAAISG GSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGDWRYGWGQG TLTVTVSS
7-28	2329	EVQLVESGGGLVQPGGSLRLSCAASGRFTSISAMGWFRQAPGKEREFVAAISRSGT TMYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAQLGYESGYSLTID YDWGQGLTVTVSS
7-29	2330	EVQLVESGGGLVQPGGSLRLSCAASGGTFSYYDLAAMGWFRQAPGKEREFVAAIS WSQYNTKYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAARVVVRTA HGFEDNWGQGLTVTVSS
7-30	2331	EVQLVESGGGLVQPGGSLRLSCAASGRFTFNNGMGWFRQAPGKEREFVAVISRSG SLKAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCASDPTYGSGRWTTW GQGLTVTVSS
7-31	2332	EVQLVESGGGLVQPGGSLRLNCAASGFTLDDYVMGWFRQTPGKEREFVAAISSG ALTSYADSVKGRFTISADNSKNTAYLQMNSLKPEDAAVYYCAAKEYGGTRRYDR AYNWGQGLTVTVSS
7-32	2333	EVQLVESGGGLVQPGGSLRLSCAASGRFTFNAMGWFRQAPGKEREFVAAIRWSGD MSVYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAQDRRRGDYYTFD YHWGQGLTVTVSS
7-33	2334	EVQLVESGGGLVQPGGSLRLSCAASGLTFSTYAMGWFRQAPGKEREFVAAITSGG STDYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGDWRYGWGQGT LTVTVSS
7-34	2335	EVQLVESGGGLVQPGGSLRLSCAASGSIFTINAMGWFRQAPGKEREFVAAIGSDGS TSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAVVRWGADWGQGLT VTVSS
7-35	2336	EVQLVESGGGLVQPGGSLRLSCAASGLTFSSYAMGWFRQAPGKERELVAAITSSS GSTPAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGDWRYGWGQ GTLTVTVSS
7-36	2337	EVQLVESGGGLVQPGGSLRLSCAASGIPFSTRTMGWFRQAPGKEREFVAAISWSQ YNTKYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAARHWGMFSRSEN DYNWGQGLTVTVSS
7-37	2338	EVQLVESGGGLVQPGGSLRLSCAASGRSRFSTYVMGWFRQAPGKEREFVAAISWS QYNTKYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRNYGH SRARYDWGQGLTVTVSS
7-38	2339	EVQLVESGGGLVQPGGSLRLSCAASGLTLSSYMGWFRQAPGKEREFVAVISRSG SLKAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATRADAEGWWDW GQGLTVTVSS
7-39	2340	EVQLVESGGGLVQPGGSLRLSCAASGSIFRVNVMGWFRQAPGKEREFVAAINNFG TTKYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADLPSRWGQGLTV TVSS
7-40	2341	EVQLVESGGGLVQPGGSLRLSCAASGRFTFRNYAMGWFRQAPGKERELVAAISSG STDYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGDWRYGWGQGT LTVTVSS
7-41	2342	EVQLVESGGGLVQPGGSLRLSCAASGRFTSSFAMGWFRQAPGKERELVAAISSG STNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGDWRYGWGQGT LTVTVSS
7-42	2343	EVQLVESGGGLVQPGGSLRLSCAASGTFRINAMGWFRQAPGKEREFVAAAMNWS GGSTKYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAQDRRRGDYYT FDYHWGQGLTVTVSS
7-43	2344	EVQLVESGGGLVQPGGSLRLSCAASGFTLGDYVMGWFRQAPGKEREFVAAIHSG GSTLYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAKEYGGTRRYDR TYNWGQGLTVTVSS
7-44	2345	EVQLVESGGGLVQPGGSLRLSCAASGFTFSRSAMGWFRQAPGKERELVAGILSSG

		ATVYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAKAPRDWGQGTTLVT VSS
7-45	2346	EVQLVESGGGLVQPGGSLRLSCAASGRTFNMYAMGWFRQAPGKERELVAAITSG GSTDYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGDWRYGWGQG TLVTVSS
7-46	2347	EVQLVESGGGLVQPGGSLRLSCAASGFTFRSYPMGWFRQAPGKEREFVAAINNFG TTKYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAGKIGVYGWGQG TLVTVSS
7-47	2348	EVQLVESGGGLVQPGGSLRLSCAASGNIFTRNVMGWFRQAPGKEREFVAAIHW GDSTKYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGSNIGGSRRW YDWGQGTTLVTVSS
7-48	2349	EVQLVESGGGLVQPGGSLRLSCAASGRTISRYTMGWFRQAPGKERELVAAIKWSG ASTVYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAGIWDYLGRD FGDWGQGTTLVTVSS
7-49	2350	EVQLVESGGGLVQPGGSLRLSCAASGFRFSSYGMGWFRQAPGKEREFVAAITSGGL TVYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAARKTFYFGTSSYPND YAWGQGTTLVTVSS
7-50	2351	EVQLVESGGGLVQPGGSLRLSCAASGRTFDNHAMGWFRQAPGKEREGVAAIGSD GSTSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAVVRWGVWDWGQG TLVTVSS
7-51	2352	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSHAMGWFRQAPGKEREFVAGISWSG ESTLTRYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCADVNGDWGQGT LTVTVSS
7-52	2353	EVQLVESGGGLVQPGGSLRLSCAASGMTFRLYAMGWFRQAPGKEREFVAAISWS QYNTKYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAQLGYESGYSL TYDYDWGQGTTLVTVSS
7-53	2354	EVQLVESGGGLVQPGGSLRLSCAASGGTFRKLAMGWFRQAPGKEREFVAVISWT GGSSYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARLTSFATWGQG TLVTVSS
7-54	2355	EVQLVESGGGLVQPGGSLRLSCAASGRTFSANGMGWFRQAPGKEREFVAAISASG TLRAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAARSPMSPTWDWG QGTTLVTVSS
7-55	2356	EVQLVESGGGLVQPGGSLRLSCAASGSFAFRSTVMGWFRQAPGKEREFVAAISWTG ESTLYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATGPYRSYFARSYL WGQGTTLVTVSS
7-56	2357	EVQLVESGGGLVQPGGSLRLSCAASGGTFDYSGMGWFRQAPGKEREFVAVVSQS GRTTYADSVKGLFTITADNSKNTAYLQMNLKPEDTAVYYCPTATRPGEWDGG QGTTLVTVSR
7-57	2358	EVQLVESGGGLVQPGGSLRLSCAASGVFGPIRAMGWFRQAPGKERELVALMGND GSTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAIGWRWGQGTTLVT VSS
7-58	2359	EVQLVESGGGLVQPGGSLRLSCAASGFNFNWYPMGWFRQAPGKEREFVAAIRWS GGITYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATGPYRSYFARSY LWGQGTTLVTVSS
7-59	2360	EVQLVESGGGLVQPGGSLRLSCAASGMTFHRYVMGWFRQAPGKERELVASITTG GTPNYADSVKGRFTIITDNNKNTAYLLMINLQPEDTAVYYCCKVPYIWGQGTLTG VGT
7-60	2361	EVQLVESGGGLVQPGGSLRLSCAASGISTMGWFRQAPGKEREFVAAINNFGTTKY ADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAASQSGSGYDWGQGTTLV TVSS
7-61	2362	EVQLVESGGGLVQPGGSLRLSCAASGRAFNTRAMGWFRQAPGKERELVALMGN DGSTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAIGWRWGQGTTLV TVSS
7-62	2363	EVQLVESGGGLVQPGGSLRLSCAASGLTDRRYTMGWFRQAPGKEREFVAAINS GSTLYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHRS

		ARYEWGQGLTVTVSS
7-63	2364	EVQLVESGGGLVQPGGSLRLSCAASGRFTNVMGWFRQAPGKERELVALMGNDGSTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAA VRWGV DWGQGLTVTVSS
7-64	2365	EVQLVESGGGLVQPGGSLRLSCAASGRAFNTRAMGWFRQAPGKERELVALMGNDGSTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAIGWRWGQGLTVTVSS
7-65	2366	EVQVVESGGGVVHPGGSVRMCAASGVTVDYSGMGWFGQAPGKEREFVAVVSQSARTTYADSVKGRFTISADNSKNTAYLQMNSMKPEDTAVYYCATATRPGEWDWGQGLTVTVSS
7-66	2367	EVQLVESGGGLVQPGGSLRLSCAASGRTPRLGAMGWFRQAPGKEREFVAAISRSGGLTSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAQLVGSNIGGSRWRYDWGQGLTVTVSS
7-67	2368	EVQLVESGGGLVQPGGSLRLSCAASGLTFRNYAMGWFRQAPGKEREFVAAITSGGSTLYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGDWRYGWGHGTLVTESS
8-1	2369	EVQLVESGGGLVQPGGSLRLSCAASGGRTFSDLAMGWFRQAPGKEREFVALITRSGGTTFYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAIGRGSWGQGLTVTVSS
8-2	2370	EVQLVESGGGLVQPGGSLRLSCAASGFTFGEYAMGWFRQAPGKEREFVAAVSSLGPFTRYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAVLDGYSGSWGQGLTVTVSS
8-3	2371	EVQLVESGGGLVQPGGSLRLSCAASGFAFSSYGMGWFRQAPGKEREFVAAISWSGVRSGVSAIYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCTDLTGDLWYFDLWGQGLTVTVSS
8-4	2372	EVQLVESGGGLVQPGGSLRLSCAASGLTAGTYAMCWFRQAPGKEREGVACASSTDGSTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAVRTYGSATYDWGQGLTVTVSS
8-5	2373	EVQLVESGGGLVQPGGSLRLSCAASGFTLDDYVMGWFRQAPGKERELVAAVSSLGPFTRYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAKEYGGTRRYDRAYNWGQGLTVTVSS
8-6	2374	EVQLVESGGGLVQPGGSLRLSCAASGPTLGSYVMGWFRQAPGKEREFVAAISWSQYNTKYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAQRWRGGSYEWGQGLTVTVSS
8-7	2375	EVQLVESGGGLVQPGGSLRLSCAASGPTFSSYVMGWFRQAPGKEREFVAAISWSQYNTKYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAASRSGSGYDWGQGLTVTVSS
8-8	2376	EVQLVESGGGLVQPGGSLRLSCAASGYLYSKDCMGWFRQAPGKEREGVATICTGDGSTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAVIAYEEGVYRW DWGQGLTVTVSS
8-9	2377	EVQLVESGGGLVQPGGSLRLSCAASGFTIDDYAMGWFRQAPGKEREGVAAISGSGDDTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAKLPYVSGDYWQGQGLTVTVSS
8-10	2378	EVQLVESGGGLVQPGGSLRLSCAASGGRFSDYGMGWFRQAPGKERELVALISRSGNLKSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAKTGTSFVWGQGLTVTVSS
8-11	2379	EVQLVESGGGLVQPGGSLRLSCAASGLSFSNYAMGWFRQAPGKERELVAAITSGGSTDYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGDWRYGWGQGLTVTVSS
8-12	2380	EVQLVESGGGLVQPGGSLRLSCAASGIPSTLRAMGWFRQAPGKEREFVALINRSGGSQFYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAIGRGSWGQGLTVTVSS

Table 40. Membrane Protein CDR Sequences

Variant	SEQ ID NO	CDRH1	SEQ ID NO	CDRH2	SEQ ID NO	CDRH3
9-1	2381	RTFSRLAMG	2453	AAISRSGRSTSYA	2525	CAARRSQILFTRTDYEW
9-2	2382	SFSIAAMG	2454	ATINYSGGGTYYA	2526	CAAVNTFDESAYAAFACYDVW
9-3	2383	RTFSRYAMG	2455	AAISRSKGSTYYA	2527	CAASSVFSDLRYRKNPKW
9-4	2384	RTFSKYAMG	2456	ALITPSSRTTYYA	2528	CAIAGRGRW
9-5	2385	RTFRRYAMG	2457	ASINWGGGNTYYA	2529	CAKTKRTGIFTTARMVDW
9-6	2386	RTFSRFAMG	2458	AAIRWSGGRTVYA	2530	CAIEPGTIRNWRNRVPFARGNFGW
9-7	2387	LGIAPSRRTAMG	2459	AAISWRGGNTYYA	2531	CAARRWIPPGPIW
9-8	2388	RTFRRYPMG	2460	AAISRSGGSTYYA	2532	CAAKRLRSFASGGSYDW
9-9	2389	GTLRGYGMG	2461	ASISRSGGSTYYA	2533	CAARRRVTLFTSRADYDW
9-10	2390	RMFSSRSMG	2462	ALINRSGGSQFYA	2534	CAARRWIPPGPIW
9-11	2391	RTFGRRAMG	2463	AGISRGGGTNYA	2535	CAAKGIWDYLGRRDGFDW
10-1	2392	LSSPPFDDFPMG	2464	SSIYSDDGDSMYA	2536	CARQTFDFWSASLGGNFWYFDLW
10-2	2393	GTFSSYSMG	2465	SAISWIIGSGGTTNYA	2537	CTAGAGDSW
10-3	2394	SIFSTRTMG	2466	ASITKFGSTNYA	2538	CTRGGGRFFDWLYLRW
10-4	2395	RTLWRSNMG	2467	ASISSFGSTKYA	2539	CARGHGRYFDWLLFARPPDYW
10-5	2396	RSLGIYRMG	2468	AAITSGGRKNYA	2540	CAKRTIFGVGRWLDPW
10-6	2397	TTLTFRIMG	2469	PAISSTGLASYT	2541	CSKDRAPNCFACCPNGFDVW
10-7	2398	SRFSGRFNILNMG	2470	ARIGYSGQSISYA	2542	CARGRFLGGTEW
10-8	2399	TLFKINAMG	2471	AQINRHGVTTYA	2543	CARGRTIFFGGGRYFDYW
10-9	2400	IPFRSRTMG	2472	AGITGSGRSQYYA	2544	CARGARIFGSVAPWRGGNYYGMDVW
10-10	2401	FTFSSFRMG	2473	AGISRGGSTNYA	2545	CARASGLWFRRPHVW
10-11	2402	RNFRRNSMG	2474	AGISWSGARTHYA	2546	CARVSRPRSPPGYYYGMDVW
10-12	2403	RNLRMYRMG	2475	ATIRWSDGSTYYA	2547	CTRARLRYFDWLFPTNFDYW
10-13	2404	GLTFSSNTMG	2476	ASISSSGRTSYA	2548	CARRVRRLWFRSYFDLW
10-14	2405	FTLAYYAMG	2477	AAISWSGRNINYA	2549	CARERARWFGKFSVSW
10-15	2406	RTFSSFPMG	2478	AAISWSGSTSYA	2550	SACGRLGFGAW
10-16	2407	ISSSKRNMG	2479	ATWTSRGITTYA	2551	CARGGPRLWGSYRRKYFDYW
10-17	2408	RTFSIYAMG	2480	ARITRGGITKYA	2552	CARGLGWLLGYYW

10-18	2409	RMYNYSYMG	2481	ARISPGGTFYA	2553	CTTSARSGWFWRYFDSW
10-19	2410	RTFRSYGMG	2482	ASISRSGTTMYA	2554	CARRGLLQWFGAPNSWFDW
10-20	2411	RTIRTMG	2483	ATINSRGITNYA	2555	CTTERDGLLWFRELFPSW
10-21	2412	RSFSFNAMG	2484	ARISRFGRNTYA	2556	CAKVHSYVWGGHSDYW
10-22	2413	RTYYAMG	2485	GAIDWSGRRITYA	2557	CARVRFSLGGVIGRPIDSW
10-23	2414	RAFRRYTMG	2486	ASITKFGSTNYA	2558	CAKDRGVLWFELWYW
10-24	2415	RTFSNYRMG	2487	ASINRGGSTKYA	2559	CASGKGGSATIFHLSRRPLYFDYW
10-25	2416	ITFSPYAMG	2488	ATINWSGGYTVYA	2560	CAKRKNRGPLWFGGGGWYW
10-26	2417	RTFSGFTMSS TWMG	2489	AGIITNGSTNYA	2561	CARRVAYSSFWGLRKHMD VW
10-27	2418	RTFRRYSMG	2490	ASITPGGNTNYA	2562	CASRRRWLTPYIFW
10-28	2419	SIFSIMG	2491	ARIWWRSGATY YA	2563	CAAISIFGRLKW
10-29	2420	RTFTSYRMG	2492	AEISSSGGYTY A	2564	CARVGPLRFLAQRPLRPDY W
10-30	2421	RTFSSFRFRA MG	2493	ALIFSGGSTYYA	2565	CAREWGRWLQRGSYW
10-31	2422	RTFGSYGMG	2494	ATISIGGRTYYA	2566	CARGSGSGFMWYHGNNNYD RWRYW
10-32	2423	RTFRSYPMG	2495	ASINRGGSTNYA	2567	CARGRYDFWSGYRWFDPW
10-33	2424	RTFSRSDMG	2496	AAISWSGGSTSY A	2568	CATVPPRRFLEWLPRRLTYI W
10-34	2425	RTFRRYTMG	2497	ASMRGSRSYA	2569	CARMSGFPFLDYW
10-35	2426	SIFRLSTMG	2498	ASISSFGSTYYA	2570	CARTRGIFLWFGESFDYW
10-36	2427	IAFRIRTMG	2499	ASITSGGSTNYA	2571	CARGGPRFGGFRGYFDPW
10-37	2428	FTFTSYRMG	2500	AGISRFFGTAYY A	2572	CARVTRWFGLDVGW
10-38	2429	RTFSRYVMG	2501	ASISRFGRNTYA	2573	CARHHGLGILWWGTMDVW
10-39	2430	RTFSMG	2502	ASISRFGRNTYA	2574	CAKRSTWLPQHFDW
10-40	2431	RTFSTYTMG	2503	ARIWRS GGNTY YA	2575	CARGVRGVFRAYFDHW
10-41	2432	RNLRMYRMG	2504	ALISRVGVTSYA	2576	CARGTSFFNFWSGSLGRVGF DSW
10-42	2433	ITIRTHAMG	2505	ATISRSGGNTYY A	2577	CTTAGVRLRYFDWFRPPYW
10-43	2434	RTFRRYHMG	2506	AAITSGGRTNYA	2578	CTTDGLRYFDWFPWASAFDI W
10-44	2435	RTFRRYTMG	2507	AVISWSGGSTKY A	2579	CARKGRWSGMNVW
10-45	2436	RTFSWYPMG	2508	ASISWGGARTYY A	2580	CARSTGPRGSGRYRAHWFD SW
10-46	2437	RTFTSYRMG	2509	AAITWNSGRTRY A	2581	CSPSSWPFYFGAW
10-47	2438	RPLRRYVMG	2510	AAITNGGSTKYA	2582	CARGTPWRLLWFGTLGPPPA FDYW

10-48	2439	RTFRRYAMG	2511	AAINRSGSTEYA	2583	CARQHQDFWTGYTVW
10-49	2440	RTFRRYTMG	2512	ASISRSGTTYA	2584	CAKEGWRWLQLRGGFDYW
10-50	2441	RTLSTYNMG	2513	ASISRFGRNTYA	2585	CARRGKLSAAMHWFDPW
10-51	2442	RFFSTRVMG	2514	ARIWPGGSTYYA	2586	CARDRGIFGVSRW
10-52	2443	RFFSICSMG	2515	AGINWRSGGSTY YA	2587	CARGSGWWEYW
10-53	2444	RMFSSRSNMG	2516	ASISSGGTTAYA	2588	CARGFGRRFLEWLPRFDYW
10-54	2445	RTFSSARMG	2517	AGINMISSTKYA	2589	CAHFRRFLPRGYVDYW
10-55	2446	RTFRRYTMG	2518	ARIAGGSTYYA	2590	CARQQYYDFWSGYFRSGYFD LW
10-56	2447	HTFRNYGMG	2519	AAITSSGSTNTYA	2591	CATVPPRRFLEWLPRRLTYT W
10-57	2448	RTFSRYAMG	2520	ASITKFGSTNTYA	2592	CAKERESRFLKWRKTDW
10-58	2449	RNLRMYRMG	2521	ASISRFGRNTYA	2593	CARHDSIGLFRHGMDVW
10-59	2450	RTFRRYAMG	2522	ARISSGGSTSYA	2594	CARDRGFGFWSGLRGYFDL W
10-60	2451	IPASMYLG	2523	AAITSGGRTSYA	2595	CAKRKKRGPLWFGGGGWGY W
10-61	2452	IPFRSRTFSAY AMG	2524	AQITRGGSTNTYA	2596	CARRHWFGFDYW

Table 41. Membrane Protein VH Sequences

Variant	SEQ ID NO	VH
9-1	2597	EVQLVESGGGLVQPGGSLRLSCAASGRFTSRLAMGWFRQAPGKEREFVAAISRSG RSTSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAARRSQILFTSRTDY EWGQGTLTVSS
9-2	2598	EVQLVESGGGLVQPGGSLRLSCAASGSFSIAAMGWFRQAPGKEREFVATINYSGG GTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAVNTFDESAYAAF ACYDVVWGQGTLTVSS
9-3	2599	EVQLVESGGGLVQPGGSLRLSCAASGRFTSRYAMGWFRQAPGKEREFVAAISRSG KSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAASSVFSDLRYRKN PKWGQGTLTVSS
9-4	2600	EVQLVESGGGLVQPGGSLRLSCAASGRFTFSKYAMGWFRQAPGKEREFVSHISRDG GRTFSSSTMGWFRQAPGKERELVALITPSSRTTYADSVKGRFTISADNSKNTAYL QMNSLKPEDTAVYYCAIAGRGRWGQGTLTVSS
9-5	2601	EVQLVESGGGLVQPGGSLRLSCAASGRFTFRRYAMGWFRQAPGKEREFVASINWG GGNTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAKTKRTGIFTAR MVDWGQGTLTVSS
9-6	2602	EVQLVESGGGLVQPGGSLRLSCAASGRFTSRFAMGWFRQAPGKEREFVAAIRWSG GRTVYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAIEPGTIRNWRNRV PFARGNFGWGQGTLTVSS
9-7	2603	EVQLVESGGGLVQPGGSLRLSCAASGLGIAFSRRTAMGWFRQAPGKEREFVAAIS WRGGNTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAARRWIPPGPI WGQGTLTVSS
9-8	2604	EVQLVESGGGLVQPGGSLRLSCAASGRFTFRYPMGWFRQAPGKEREFVAAISRSG GSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAKRLRSFASGGSY DWGQGTLTVSS

9-9	2605	EVQLVESGGGLVQPGGSLRLSCAASGGTLRGYGMGWFRQAPGKEREFVASISRSRGSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAARRRVTLFTSRADYDWGQGTLTVSS
9-10	2606	EVQLVESGGGLVQPGGSLRLSCAASGRMFSSRSMGWFRQAPGKEREFVALINRSGGSQFYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAARRWIPPGPIWGQGTLTVSS
9-11	2607	EVQLVESGGGLVQPGGSLRLSCAASGRTFGRRAMGWFRQAPGKEREFVAGISRGGGTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAKGIWDYLGRRDFGDWGQGTLTVSS
10-1	2608	EVQLVESGGGLVQPGGSLRLSCAASGLSPFFDDFPMGWFRQAPGKEREFVSSIYSDDGDSMYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARQTFDFWSASLGGNFWYFDLWGQGTLTVSS
10-2	2609	EVQLVESGGGLVQPGGSLRLSCAASGGTFSSYSMGWFRQAPGKEREFVSAISWIIGSGGTTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCTAGAGDSWGQGTTLTVSS
10-3	2610	EVQLVESGGGLVQPGGSLRLSCAASGSIFSTRTMGWFRQAPGKEREFVASITKFGSTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCTRGGGRFFDWLYLRWQGTLTVSS
10-4	2611	EVQLVESGGGLVQPGGSLRLSCAASGRTLWRSNMGWFRQAPGKEREFVASISSFGSTKYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGHGRYFDWLLFARPPDYWGQGTLTVSS
10-5	2612	EVQLVESGGGLVQPGGSLRLSCAASGRSLGIYRMGWFRQAPGKEREFVAAITSGGRKNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAKRTIFGVGRWLDPWGQGTLTVSS
10-6	2613	EVQLVESGGGLVQPGGSLRLSCAASGTTLTFRIMGWFRQAPGKEREFVPAISSTGLASYTDSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCSKDRAPNCFACCPNGFDVWGQGTLTVSS
10-7	2614	EVQLVESGGGLVQPGGSLRLSCAASGRFSRSGRFNINMGWFRQAPGKEREFVARI GYSGQSISYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGRFLGGTEWGQGTLTVSS
10-8	2615	EVQLVESGGGLVQPGGSLRLSCAASGTLFKINAMGWFRQAPGKEREFVAQINRHGVITYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGRTIFFGGGRYFDYWGQGTLTVSS
10-9	2616	EVQLVESGGGLVQPGGSLRLSCAASGIPFRSRTMGWFRQAPGKEREFVAGITGSGRSQYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGARIFGSVAPWRGGNYYGMDVWGQGTLTVSS
10-10	2617	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSFRMGWFRQAPGKEREFVAGISRGGSTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARASGLWFRRPHVWQGTLTVSS
10-11	2618	EVQLVESGGGLVQPGGSLRLSCAASGRNFRNRSMGWFRQAPGKEREFVAGISWSGARTHYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARVSRPRSPPGYYGMDVWGQGTLTVSS
10-12	2619	EVQLVESGGGLVQPGGSLRLSCAASGRNLRMYRMGWFRQAPGKEREFVATIRWSDGSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCTRARLRYFDWLFPTNFDYWGQGTLTVSS
10-13	2620	EVQLVESGGGLVQPGGSLRLSCAASGGLTFSSNTMGWFRQAPGKEREFVASISSGRTSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARRVRRLWFRSYFDLWGQGTLTVSS
10-14	2621	EVQLVESGGGLVQPGGSLRLSCAASGFTLAYYAMGWFRQAPGKEREFVAAISWSGRNINYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARERARWFGKFSVSWGQGTLTVSS
10-15	2622	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSFPMGWFRQAPGKEREFVAAISWSGSTSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAGRLGFGAWGQGTTLTVSS
10-16	2623	EVQLVESGGGLVQPGGSLRLSCAASGISSSKRNMGWFRQAPGKEREFVATWTSRG

		ITTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGGPPRLWGSYRRK YFDYWGGTLTVSS
10-17	2624	EVQLVESGGGLVQPGGSLRLSCAASGRFTFSIYAMGWFRQAPGKEREFVARITRGGI TKYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGLGWLLGYYWGQ GTLTVSS
10-18	2625	EVQLVESGGGLVQPGGSLRLSCAASGRMYNSYSMGWFRQAPGKEREFVARISPG GTFYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCTTSARSGWFWRYFD SWGQGTTLTVSS
10-19	2626	EVQLVESGGGLVQPGGSLRLSCAASGRFTFSYGMGWFRQAPGKEREFVASISRSG TTMYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARRLLQWFGAPNS WFDPWGQGTTLTVSS
10-20	2627	EVQLVESGGGLVQPGGSLRLSCAASGRFTIRTMGWFRQAPGKEREFVATINSRGITN YADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCTTERDGLLWFRELFRPSW GQGTTLTVSS
10-21	2628	EVQLVESGGGLVQPGGSLRLSCAASGRSFSFNAMGWFRQAPGKEREFVARISRFG RTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAKVHSYVWGGHSD YWGGQGTTLTVSS
10-22	2629	EVQLVESGGGLVQPGGSLRLSCAASGRTTYAMGWFRQAPGKEREFVGAIDWSGR RITYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARVRSRLGGVIGRPI DSWGQGTTLTVSS
10-23	2630	EVQLVESGGGLVQPGGSLRLSCAASGRAFRRYTMGWFRQAPGKEREFVASITKFG STNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAKDRGVLWFGELWY WGQGTTLTVSS
10-24	2631	EVQLVESGGGLVQPGGSLRLSCAASGRFTFSNYRMGWFRQAPGKEREFVASINRGG STKYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCASGKGGSATIFHLSR RPLYFDYWGGQGTTLTVSS
10-25	2632	EVQLVESGGGLVQPGGSLRLSCAASGITFSPIYAMGWFRQAPGKEREFVATINWSG GYTVYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAKRKNRGLPLWFGG GGWGYWGQGTTLTVSS
10-26	2633	EVQLVESGGGLVQPGGSLRLSCAASGRFTFSGFTMSSTWMGWFRQAPGKEREFVA GIITNGSTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARRVAYSSF WSGLRKHMDVWGQGTTLTVSS
10-27	2634	EVQLVESGGGLVQPGGSLRLSCAASGRTFRRYSMGWFRQAPGKEREFVASITPGG NTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCASRRRWLTPYIFWG QGTTLTVSS
10-28	2635	EVQLVESGGGLVQPGGSLRLSCAASGSIFSIGMGWFRQAPGKEREFVARIWWRSG ATYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAISIFGRLLKWGGQT LTVSS
10-29	2636	EVQLVESGGGLVQPGGSLRLSCAASGRFTFSYRMGWFRQAPGKEREFVAEISSSG GYTTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARVGPLRFLAQR RLRPDYWGQGTTLTVSS
10-30	2637	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSFRFRAMGWFRQAPGKEREFVALIFS GGSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAREWGRWLQRGS YWGGQGTTLTVSS
10-31	2638	EVQLVESGGGLVQPGGSLRLSCAASGRTFGSYGMGWFRQAPGKEREFVATISIGG RTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGSGSGFMWYHG NNNYDRWRYWGQGTTLTVSS
10-32	2639	EVQLVESGGGLVQPGGSLRLSCAASGRFTFSYPMGWFRQAPGKEREFVASINRGG STNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGRYDFWSGYR WFDPWGQGTTLTVSS
10-33	2640	EVQLVESGGGLVQPGGSLRLSCAASGRFTFSRSDMGWFRQAPGKEREFVAAISWSG GSTSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATVPPPRRFLWLP RRLTYIWGGQGTTLTVSS
10-34	2641	EVQLVESGGGLVQPGGSLRLSCAASGRTFRRYTMGWFRQAPGKEREFVASMGRS RSYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARMSGFPFLDYWGQ

		GTLVTVSS
10-35	2642	EVQLVESGGGLVQPGGSLRLSCAASGSIFRLSTMGWFRQAPGKEREFVASISSFGST YYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARTRGIFLWFGESFDY WGQGLTVTVSS
10-36	2643	EVQLVESGGGLVQPGGSLRLSCAASGIAFRIRTMGWFRQAPGKEREFVASITSGGS TNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGGPRFGGFRGYFDP WGQGLTVTVSS
10-37	2644	EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYRMGWFRQAPGKEREFVAGISRFF GTAYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARVTRWFGLDV WGQGLTVTVSS
10-38	2645	EVQLVESGGGLVQPGGSLRLSCAASGRTFSTRYVMGWFRQAPGKEREFVASISRFG RTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARHHGLGILWWGT MDVWGQGLTVTVSS
10-39	2646	EVQLVESGGGLVQPGGSLRLSCAASGRTFSMGWFRQAPGKEREFVASISRFGRTN YADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAKRSTWLPQHFDWSGQG TLVTVSS
10-40	2647	EVQLVESGGGLVQPGGSLRLSCAASGRTFSTYTMGWFRQAPGKEREFVARIWRSG GNTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGVRGVFRAYFD HWGQGLTVTVSS
10-41	2648	EVQLVESGGGLVQPGGSLRLSCAASGRNLRMYRMGWFRQAPGKEREFVALISRV GVTSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGTSFFNFWSGSL GRVGFDSWGQGLTVTVSS
10-42	2649	EVQLVESGGGLVQPGGSLRLSCAASGITIRTHAMGWFRQAPGKEREFVATISRSGG NTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCTTAGVLRVFDWFRR PYWGQGLTVTVSS
10-43	2650	EVQLVESGGGLVQPGGSLRLSCAASGRTFRRYHMGWFRQAPGKEREFVAAITSGG RTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCTTDGLRYFDWFPWA SAFDIWGQGLTVTVSS
10-44	2651	EVQLVESGGGLVQPGGSLRLSCAASGRTFRRYTMGWFRQAPGKEREFVAVISWSG GSTKYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARKGRWSGMNVW GQGLTVTVSS
10-45	2652	EVQLVESGGGLVQPGGSLRLSCAASGRTFSWYPMGWFRQAPGKEREFVASISWG GARTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARSTGPRGSGRY RAHWFDWSWGQGLTVTVSS
10-46	2653	EVQLVESGGGLVQPGGSLRLSCAASGRTFSTRYMGWFRQAPGKEREFVAAITWNS GRTRYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCSPSSWPFFYFGAWG QGTLTVTVSS
10-47	2654	EVQLVESGGGLVQPGGSLRLSCAASGRPLRRYVMGWFRQAPGKEREFVAAITNG GSTKYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGTPWRLLWFGT LGPPPAFDYWGQGLTVTVSS
10-48	2655	EVQLVESGGGLVQPGGSLRLSCAASGRTFRRYAMGWFRQAPGKEREFVAAINRSG STEYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARQHQDFWTGYTIV WGQGLTVTVSS
10-49	2656	EVQLVESGGGLVQPGGSLRLSCAASGRTFRRYTMGWFRQAPGKEREFVASISRSG TTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAKEGWRWLQLRGGF DYWGQGLTVTVSS
10-50	2657	EVQLVESGGGLVQPGGSLRLSCAASGRTLSTYNMGWFRQAPGKEREFVASISRFG RTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARRGKLSAAMHWF DPWGQGLTVTVSS
10-51	2658	EVQLVESGGGLVQPGGSLRLSCAASGRFFSTRVMGWFRQAPGKEREFVARIWPGG STYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARDRGIFGVSRWGQ GTLTVTVSS
10-52	2659	EVQLVESGGGLVQPGGSLRLSCAASGRFFSICSMGWFRQAPGKEREFVAGINWRS GGSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGSGWWEYWG QGTLTVTVSS

10-53	2660	EVQLVESGGGLVQPGGSLRLSCAASGRMFSSRSNMGWFRQAPGKEREFVASISSG GTTAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGFGRRFLEWLP RFDYWGQGLTVTVSS
10-54	2661	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSARMGWFRQAPGKEREFVAGINMIS STKYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAHFRRFLPRGYVDY WGQGLTVTVSS
10-55	2662	EVQLVESGGGLVQPGGSLRLSCAASGRTFRRYTMGWFRQAPGKEREFVARIAGGS TYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARQQYYDFWSGYFRS GYFDLWGQGLTVTVSS
10-56	2663	EVQLVESGGGLVQPGGSLRLSCAASGHTFRNYGMGWFRQAPGKEREFVAAITSSG STNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCATVPPRRFLEWLPR RLTYTWGQGLTVTVSS
10-57	2664	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSRYAMGWFRQAPGKEREFVASITKFG STNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAKERESRFLKWRKT DWGQGLTVTVSS
10-58	2665	EVQLVESGGGLVQPGGSLRLSCAASGRNLRMYRMGWFRQAPGKEREFVASISRFG RTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARHDSIGLFRHGMD VWGQGLTVTVSS
10-59	2666	EVQLVESGGGLVQPGGSLRLSCAASGRTFRRYAMGWFRQAPGKEREFVARISSGG STSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARDRGFGFWSGLRG YFDLWGQGLTVTVSS
10-60	2667	EVQLVESGGGLVQPGGSLRLSCAASGIPASMYLGWFRQAPGKEREFVAAITSGGR TSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAKRKKRGPLWFGGGG WGYWGQGLTVTVSS
10-61	2668	EVQLVESGGGLVQPGGSLRLSCAASGIPFRSRTFSAYAMGWFRQAPGKEREFVAQI TRGGSTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARRHWFGFDY WGQGLTVTVSS

[00334] While preferred embodiments of the present disclosure have been shown and described herein, it will be obvious to those skilled in the art that such embodiments are provided by way of example only. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from the disclosure. It should be understood that various alternatives to the embodiments of the disclosure described herein may be employed in practicing the disclosure. It is intended that the following claims define the scope of the disclosure and that methods and structures within the scope of these claims and their equivalents be covered thereby.

CLAIMS

WHAT IS CLAIMED IS:

1. An antibody or antibody fragment comprising a variable domain, heavy chain region (VH) and a variable domain, light chain region (VL), wherein VH comprises complementarity determining regions CDRH1, CDRH2, and CDRH3, wherein VL comprises complementarity determining regions CDRL1, CDRL2, and CDRL3, and wherein (a) an amino acid sequence of CDRH1 is as set forth in any one of SEQ ID NOs: 151-165, 241-255, 331-357, and 547-575; (b) an amino acid sequence of CDRH2 is as set forth in any one of SEQ ID NOs: 166-180, 256-270, 358-384, and 576-604; (c) an amino acid sequence of CDRH3 is as set forth in any one of SEQ ID NOs: 181-195, 271-285, 385-411, and 605-633; (d) an amino acid sequence of CDRL1 is as set forth in any one of SEQ ID NOs: 196-210, 286-300, 412-438, and 634-662; (e) an amino acid sequence of CDRL2 is as set forth in any one of SEQ ID NOs: 211-225, 301-315, 439-465, and 663-691; and (f) an amino acid sequence of CDRL3 is as set forth in any one of SEQ ID NOs: 226-240, 316-330, 466-492, and 692-720.
2. The antibody or antibody fragment of claim 1, wherein (a) an amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 155; (b) an amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 170; (c) an amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 185; (d) an amino acid sequence of CDRL1 is as set forth in SEQ ID NO: 200; (e) an amino acid sequence of CDRL2 is as set forth in SEQ ID NO: 215; and (f) an amino acid sequence of CDRL3 is as set forth in SEQ ID NO: 230.
3. The antibody or antibody fragment of claim 1, wherein (a) an amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 152; (b) an amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 167; (c) an amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 182; (d) an amino acid sequence of CDRL1 is as set forth in SEQ ID NO: 197; (e) an amino acid sequence of CDRL2 is as set forth in SEQ ID NO: 212; and (f) an amino acid sequence of CDRL3 is as set forth in SEQ ID NO: 227.
4. The antibody or antibody fragment of claim 1, wherein (a) an amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 335; (b) an amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 362; (c) an amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 389; (d) an amino acid sequence of CDRL1 is as set forth in SEQ ID NO: 199; (e) an amino acid sequence of CDRL2 is as set forth in SEQ ID NO: 214; and (f) an amino acid sequence of CDRL3 is as set forth in SEQ ID NO: 229.
5. The antibody or antibody fragment of claim 1, wherein (a) an amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 336; (b) an amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 363; (c) an amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 390; (d) an amino acid sequence of CDRL1 is as set forth in SEQ ID NO: 201; (e) an amino acid sequence of CDRL2 is as set forth in SEQ ID NO: 216; and (f) an amino acid sequence of CDRL3 is as set forth in SEQ ID NO: 231.
6. The antibody or antibody fragment of claim 1, wherein (a) an amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 158; (b) an amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 173; (c) an amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 188; (d) an amino acid sequence of

CDRL1 is as set forth in SEQ ID NO: 203; (e) an amino acid sequence of CDRL2 is as set forth in SEQ ID NO: 218; and (f) an amino acid sequence of CDRL3 is as set forth in SEQ ID NO: 233.

7. The antibody or antibody fragment of claim 1, wherein (a) an amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 551; (b) an amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 580; (c) an amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 609; (d) an amino acid sequence of CDRL1 is as set forth in SEQ ID NO: 290; (e) an amino acid sequence of CDRL2 is as set forth in SEQ ID NO: 305; and (f) an amino acid sequence of CDRL3 is as set forth in SEQ ID NO: 320.

8. The antibody or antibody fragment of claim 1, wherein (a) an amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 549; (b) an amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 578; (c) an amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 607; (d) an amino acid sequence of CDRL1 is as set forth in SEQ ID NO: 292; (e) an amino acid sequence of CDRL2 is as set forth in SEQ ID NO: 307; and (f) an amino acid sequence of CDRL3 is as set forth in SEQ ID NO: 322.

9. The antibody or antibody fragment of claim 1, wherein (a) an amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 552; (b) an amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 581; (c) an amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 610; (d) an amino acid sequence of CDRL1 is as set forth in SEQ ID NO: 291; (e) an amino acid sequence of CDRL2 is as set forth in SEQ ID NO: 306; and (f) an amino acid sequence of CDRL3 is as set forth in SEQ ID NO: 321.

10. The antibody or antibody fragment of claim 1, wherein (a) an amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 554; (b) an amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 583; (c) an amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 612; (d) an amino acid sequence of CDRL1 is as set forth in SEQ ID NO: 288; (e) an amino acid sequence of CDRL2 is as set forth in SEQ ID NO: 303; and (f) an amino acid sequence of CDRL3 is as set forth in SEQ ID NO: 318.

11. The antibody or antibody fragment of claim 1, wherein the antibody or antibody fragment binds to a spike glycoprotein.

12. The antibody or antibody fragment of claim 1, wherein the antibody or antibody fragment binds to a receptor binding domain of the spike glycoprotein.

13. The antibody or antibody fragment of claim 1, wherein the antibody or antibody fragment comprises a K_D of less than 50 nM.

14. The antibody or antibody fragment of claim 1, wherein the antibody or antibody fragment comprises a K_D of less than 25 nM.

15. The antibody or antibody fragment of claim 1, wherein the antibody or antibody fragment comprises a K_D of less than 10 nM.

16. The antibody or antibody fragment of claim 1, wherein the antibody or antibody fragment comprises a K_D of less than 5 nM.

17. An antibody or antibody fragment comprising a variable domain, heavy chain region (VH) wherein VH comprises complementarity determining regions CDRH1, CDRH2, and CDRH3, wherein (a) an amino acid sequence of CDRH1 is as set forth in any one of SEQ ID NOs: 1-50, 779-919, 1344-1523, and 2381-

2452; (b) an amino acid sequence of CDRH2 is as set forth in any one of SEQ ID NOs: 51-100, 920-1061, 1524-1703, and 2453-2524; and (c) an amino acid sequence of CDRH3 is as set forth in any one of SEQ ID NOs: 101-150, 1062-1202, 1704-1883, and 2525-2596.

18. The antibody or antibody fragment of claim 17, wherein (a) the amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 1414; (b) the amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 1594; and (c) the amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 1774.

19. The antibody or antibody fragment of claim 17, wherein (a) the amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 1447; (b) the amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 1627; and (c) the amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 1807.

20. The antibody or antibody fragment of claim 17, wherein (a) the amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 1474; (b) the amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 1654; and (c) the amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 1834.

21. The antibody or antibody fragment of claim 17, wherein (a) the amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 1344; (b) the amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 1524; and (c) the amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 1704.

22. The antibody or antibody fragment of claim 17, wherein (a) the amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 1363; (b) the amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 1543; and (c) the amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 1723.

23. The antibody or antibody fragment of claim 17, wherein (a) the amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 1487; (b) the amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 1667; and (c) the amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 1847.

24. The antibody or antibody fragment of claim 17, wherein (a) the amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 780; (b) the amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 921; and (c) the amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 1063.

25. The antibody or antibody fragment of claim 17, wherein (a) the amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 782; (b) the amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 923; and (c) the amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 1065.

26. The antibody or antibody fragment of claim 17, wherein (a) the amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 39; (b) the amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 89; and (c) the amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 139.

27. The antibody or antibody fragment of claim 17, wherein (a) the amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 832; (b) the amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 973; and (c) the amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 1115.

28. The antibody or antibody fragment of claim 17, wherein (a) the amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 869; (b) the amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 1010; and (c) the amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 1152.

29. The antibody or antibody fragment of claim 17, wherein (a) the amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 889; (b) the amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 1030; and (c) the amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 1172.
30. The antibody or antibody fragment of claim 17, wherein (a) the amino acid sequence of CDRH1 is as set forth in SEQ ID NO: 908; (b) the amino acid sequence of CDRH2 is as set forth in SEQ ID NO: 1049; and (c) the amino acid sequence of CDRH3 is as set forth in SEQ ID NO: 1191.
31. An antibody or antibody fragment comprising a variable domain, heavy chain region (VH) and a variable domain, light chain region (VL), wherein the VH comprises an amino acid sequence at least about 90% identical to a sequence as set forth in any one of SEQ ID NOs: 493-519 and 721-749, and wherein the VL comprises an amino acid sequence at least about 90% identical to a sequence as set forth in any one of SEQ ID NOs: 520-546 and 750-778.
32. An antibody or antibody fragment comprising a variable domain, heavy chain region (VH) comprising an amino acid sequence at least about 90% identical to a sequence as set forth in any one of SEQ ID NOs: 1884-2063, 2302-2380, and 2597-2668.
33. The antibody or antibody fragment of claim 32, wherein the VH comprises an amino acid sequence at least about 90% identical to SEQ ID NO: 1954.
34. The antibody or antibody fragment of claim 32, wherein the VH comprises an amino acid sequence at least about 90% identical to SEQ ID NO: 1987.
35. The antibody or antibody fragment of claim 32, wherein the VH comprises an amino acid sequence at least about 90% identical to SEQ ID NO: 2014.
36. An antibody, wherein the antibody comprises a sequence comprising at least 90% sequence identity to any one of SEQ ID NOs: 1-2668; and wherein the antibody is a monoclonal antibody, a polyclonal antibody, a bi-specific antibody, a multispecific antibody, a grafted antibody, a human antibody, a humanized antibody, a synthetic antibody, a chimeric antibody, a camelized antibody, a single-chain Fvs (scFv), a single chain antibody, a Fab fragment, a F(ab')₂ fragment, a Fd fragment, a Fv fragment, a single-domain antibody, an isolated complementarity determining region (CDR), a diabody, a fragment comprised of only a single monomeric variable domain, disulfide-linked Fvs (sdFv), an intrabody, an anti-idiotypic (anti-Id) antibody, or ab antigen-binding fragments thereof.
37. A nucleic acid composition comprising: a) a first nucleic acid encoding a variable domain, heavy chain region (VH) comprising an amino acid sequence at least about 90% identical to a sequence as set forth in any one of SEQ ID NOs: 493-519 and 721-749; b) a second nucleic acid encoding a variable domain, light chain region (VL) comprising at least about 90% identical to a sequence as set forth in any one of SEQ ID NOs: 520-546 and 750-778; and an excipient.
38. A nucleic acid composition comprising: a) a first nucleic acid encoding a variable domain, heavy chain region (VH) comprising an amino acid sequence at least about 90% identical to a sequence as set forth in any one of SEQ ID NOs: 1884-2063, 2302-2380, and 2597-2668; and b) an excipient.

39. The nucleic acid composition of claim 38, wherein the VH comprises an amino acid sequence at least about 90% identical to SEQ ID NO: 1954.
40. The nucleic acid composition of claim 38, wherein the VH comprises an amino acid sequence at least about 90% identical to SEQ ID NO: 1987.
41. The nucleic acid composition of claim 38, wherein the VH comprises an amino acid sequence at least about 90% identical to SEQ ID NO: 2014.
42. A method of treating a SARS-CoV-2 infection, comprising administering the antibody or antibody fragment of any one of claims 1-36.
43. The method of claim 37, wherein the antibody is administered prior to exposure to SARS-CoV-2.
44. The method of claim 43, wherein the antibody is administered at least about 1 week prior to exposure to SARS-CoV-2.
45. The method of claim 43, wherein the antibody is administered at least about 1 month prior to exposure to SARS-CoV-2.
46. The method of claim 43, wherein the antibody is administered at least about 5 months prior to exposure to SARS-CoV-2.
47. The method of claim 37, wherein the antibody is administered after exposure to SARS-CoV-2.
48. The method of claim 47, wherein the antibody is administered at most about 24 hours after exposure to SARS-CoV-2.
49. The method of claim 47, wherein the antibody is administered at most about 1 week after exposure to SARS-CoV-2.
50. The method of claim 47, wherein the antibody is administered at most about 1 month after exposure to SARS-CoV-2.
51. A method of treating an individual with a SARS-CoV-2 infection with the antibody or antibody fragment of any one of claims 1-36 comprising:
- (a) obtaining or having obtained a sample from the individual;
 - (b) performing or having performed an expression level assay on the sample to determine expression levels of SARS-CoV-2 antibodies; and
 - (c) if the sample has an expression level of the SARS-CoV-2 antibodies then administering to the individual the antibody or antibody fragment of any one of claims 1-36, thereby treating the SARS-CoV-2 infection.
52. A method for optimizing an antibody comprising:
- (a) providing a plurality of polynucleotide sequences encoding for an antibody or antibody fragment, wherein the antibody or antibody fragment is derived from a subject having SARS-CoV-2;
 - (b) generating a nucleic acid library comprising the plurality of sequences that when translated encode for antibodies or antibody fragments that bind SARS-CoV-2 or ACE2 protein, wherein each of the sequences comprises a predetermined number of variants within a CDR

relative to an input sequence that encodes an antibody; wherein the library comprises at least 50,000 variant sequences; and

(c) synthesizing the at least 50,000 variant sequences.

53. The method of claim 52, wherein the antibody library comprises at least 100,000 sequences.
54. The method of claim 52, wherein the method further comprises enriching a subset of the variant sequences.
55. The method of claim 52, wherein the method further comprises expressing the antibody or antibody fragments corresponding to the variant sequences.
56. The method of claim 52, wherein the polynucleotide sequence is a murine, human, or chimeric antibody sequence.
57. The method of claim 52, wherein each sequence of the plurality of variant sequences comprises at least one variant in each CDR of a heavy chain or light chain, relative to the input sequence.
58. The method of claim 52, wherein each sequence of the plurality of variant sequences comprises at least two variants in each CDR of a heavy chain or light chain relative to the input sequence.
59. The method of claim 52, wherein at least one sequence when translated encodes for an antibody or antibody fragment having at least 5X higher binding affinity than a binding affinity of the input sequence.
60. The method of claim 52, wherein at least one sequence when translated encodes for an antibody or antibody fragment having at least 25X higher binding affinity than a binding affinity of the input sequence.
61. The method of claim 52, wherein at least one sequence when translated encodes for an antibody or antibody fragment having at least 50X higher binding affinity than a binding affinity of the input sequence.
62. The method of claim 52, wherein each sequence comprises at least one variant in each CDR of a heavy chain or light chain relative to a germline sequence of the input sequence.
63. The method of claim 52, wherein the nucleic acid library has a theoretical diversity of at least 10^{10} sequences.
64. The method of claim 52, wherein the nucleic acid library has a theoretical diversity of at least 10^{12} sequences.