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BINDING MOLECULE HAVING NEUTRALIZING ACTIVITY AGAINST CORONAVIRUS SUPERFAMILY

Abstract

The present invention relates to a binding molecule having neutralizing activity against the coronavirus superfamily. More specifically, the binding molecule of the present invention has excellent binding affinity and excellent neutralizing efficacy against various coronavirus species that may infect humans, including not only wild-type SARS-coronavirus-2 (SARS-CoV-2) and mutant viruses that may occur in the future, but also SARS-coronavirus-1 (SARS-CoV-1), Middle East respiratory syndrome coronavirus (MERS-CoV), etc., which infect humans, causing fatal diseases. Thus, the binding molecule is very useful for the diagnosis, prevention or treatment of diseases caused by coronaviruses.

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Background/Summary

TECHNICAL FIELD

[0001] The present invention relates to a binding molecule having neutralizing activity against the coronavirus superfamily, and more specifically, to a binding molecule having excellent binding affinity and neutralizing efficacy against various coronavirus species that may infect humans, including not only wild type SARS-coronavirus-2 (SARS-CoV-2) and mutant viruses that may occur in the future, but also SARS-coronavirus-1 (SARS-CoV-1), Middle East respiratory syndrome coronavirus (MERS-CoV), etc., which infect humans, causing fatal diseases.

BACKGROUND ART

[0002] Coronaviruses refer to viruses belonging to the family Coronaviridae and are generally found not only in birds but also in various mammals including humans. It is known that there are various coronavirus species, and coronaviruses cause both respiratory and digestive infectious diseases depending on the characteristics of the virus and on the host. Coronaviruses are viruses that cause respiratory illnesses of varying severity from the common cold to fatal pneumonia. Viruses belonging to the family Coronaviridae generally have a single-stranded, infectious, positive sense RNA genome with a length of 27 to 32 kb, and contain a cap at the 5′ end of the genome and a poly A tail at the 3′ end. Coronaviruses have an envelope, and contain major outer membrane proteins such as spike (S) protein and envelope (E) protein. The spike protein is involved in viral infection and pathogenicity, such as neutralizing antibody induction, receptor binding, and membrane fusion, and the envelope (E) protein is involved in morphogenesis of viral particles and extracellular release of the virus after infection.

[0003] Seven types of coronavirus are known to cause disease in humans, and infection with three types among them may cause even more severe or fatal pneumonia in humans. The three types that are fatal to humans include SARS-coronavirus-1 (SARS-CoV-1), which was identified as the cause of the 2003 severe acute respiratory syndrome outbreak which was a worldwide problem, MERS-coronavirus (MERS-CoV), which was identified as the cause of the 2012 Middle East respiratory syndrome outbreak, and the new coronavirus severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), which was first found in Wuhan, China in late 2019 and identified as the cause of coronavirus infection 2019 (COVID-19).

[0004] Severe acute respiratory syndrome (SARS) coronavirus 1 (SARS-CoV-1) is surrounded by a spherical envelope, like other coronaviruses, and has crown-like spikes (spike protein, S protein) on its surface. Severe acute respiratory syndrome caused by SARS coronavirus was first identified in China, and resulted in more than 8,000 cases and more than 800 deaths worldwide by mid-2003. So far, there is no antiviral agent that can treat human SARS coronavirus infection. However, ribavirin is used in the early stage of the infection, and high-concentration steroids may be used to suppress immune-mediated damage to infected tissues.

[0005] Middle East respiratory syndrome (MERS) coronavirus (MERS-CoV) has a single positive-stranded RNA genome, and the genes thereof are arranged in the order of RNA polymerase gene, structural protein genes, envelope protein, membrane protein, and nucleocapsid protein. The virus that causes Middle East respiratory syndrome (MERS) is a coronavirus similar to the virus that causes severe acute respiratory syndrome (SARS). There is no specific treatment for MERS, and nonsteroidal anti-inflammatory drugs (NSAIDs) such as acetaminophen or ibuprofen are administered to relieve fever and muscle pain.

[0006] Severe acute respiratory syndrome (SARS) coronavirus 2 (SARS-CoV-2) is a positive-sense single-stranded RNA coronavirus when subjected to DNA sequencing. SARS-CoV-2 is contagious to humans and is the cause of coronavirus disease 2019 (COVID-19). The first outbreak of COVID-19 occurred in Wuhan, Hubei Province, China.

[0007] People infected with SARS-CoV-2 may exhibit mild to severe symptoms such as fever, cough, shortness of breath, and diarrhea. People with complications or illnesses and the elderly are more likely to die.

[0008] In particular, early detection and treatment are very important because people with underlying diseases such as heart disease and diabetes are more susceptible to infection and more likely to suffer from complications or organ damage. From Dec. 8, 2019 to Mar. 20, 2020, there were 245,550 patients, among whom 10,049 died, which is a mortality rate of 4.09% (WHO). The virus spread to 177 countries, including Korea, by 2020.

[0009] Currently, there is no therapeutic agent for coronavirus disease 2019 (COVID-19), and therapeutic effects are expected to be exhibited by administering existing therapeutic agents to patients. Ebola therapeutic agents or candidates, for example, antiviral drugs such as favipiravir, remdesivir, and galidesivir, and a hepatitis C drug such as ribavirin, are being used as therapeutic agents for COVID-19. In addition, the antimalarial drug chloroquine has also been shown to be effective against COVID-19, and thus is in open-label clinical trials. However, ribavirin, which is a hepatitis C therapeutic drug, may have severe side effects such as anemia, and interferon, which is an antiviral drug, is also recommended to be used with caution because of the various side effects thereof.

[0010] Although these drugs have been used in the treatment of COVID-19 patients and show therapeutic effects thereon, it has not yet been clearly proven on what mechanism they are effective. In China, it was announced that plasma therapy of injecting the plasma of patients who had recovered from COVID-19 was effective in the treatment of severely ill patients, but the therapeutic effect thereof is unclear and is highly uncertain.

[0011] In Korea, the COVID-19 Central Clinical Trial TF (Task Force) established a treatment principle for COVID-19 on Feb. 13, 2020, and announced that Kaletra, which is an AIDS therapeutic agent, and chloroquine and hydroxychloroquine, which are antimalarial drugs, are recommended as the first-line therapeutic agents, and ribavirin and interferon are not recommended as the first-line therapeutic agents due to side effects thereof. As for mild cases or young patients, and 10 days after the onset of the disease, it was judged that the symptoms would improve without administration of an antiviral drug, and it was agreed to administer antiviral drugs to the elderly, patients with underlying diseases, and severely ill patients.

[0012] The US CDC i) announced that COVID-19 could become endemic like MERS rather than a seasonal pandemic virus and cause infection, and ii) mentioned the need to strengthen surveillance so that data-based conclusions can be drawn although there is no evidence that the coronavirus is lurking in the real community due to the spread of the virus to the community at some point this year or next year (Feb. 13, 2020).

[0013] The Korea Disease Control and Prevention Agency (formerly Korea Centers for Disease Control and Prevention) announced that i) COVID-19 could be a long-term epidemic like influenza and thus it should be included in monitoring programs such as that used for influenza, and ii) coronaviruses (4 types) that are prevalent among people are also prevalent from winter to spring, leaving the possibility that COVID-19 could also become endemic (Feb. 17, 2020).

[0014] Unlike SARS and MERS, there are concerns about the realization of the COVID-19 pandemic, but there is the possibility of a lull after spring (April), so there are many experts who take a careful approach depending on the progress thereof. Due to the lack of information on COVID-19, experts have different opinions on future developments, but few experts predict that it will be resolved in a short time. Although further progress of COVID-19 will be influenced by the accuracy of analysis of prevalence and characteristics of COVID-19 and by how long the crisis from COVID-19 will last, there are concerns about the possibility of endemic disease if it is spread worldwide through asymptomatic infected people. There is an urgent need to prepare countermeasures for the likelihood of recurrence of COVID-19 worldwide.

[0015] In addition, recently, there have been more than 50,000 confirmed cases of COVID-19 per day in the United States alone, and it is the opinion of the academic community that the occurrence of about 200,000 confirmed cases of COVID-19 per day around the world is due to mutation of the virus. Research results that coronaviruses mutate into a contagious form and that mutation occurs in the spike protein are amplifying concerns, and if mutation occurs in a part playing an important role in viral infection, such as the spike protein, it may also influence the development of vaccines and therapeutic agents. As various mutant SARS-CoV-2 viruses have been reported, it is urgent to provide a method capable of acting against not only wild-type viruses but also mutant viruses.

[0016] A rapid diagnostic test (RDT) is also referred to by various names such as “immunochromatographic analysis”, “rapid kit analysis”, and the like. A user can simply detect an analyte from a biological or chemical sample by the rapid diagnostic test. The rapid diagnostic test is a method capable of qualitatively and quantitatively testing analytes within a short time using the properties of biological or chemical materials that specifically adhere to each other.

[0017] The rapid diagnostic test is the most advanced assay kit among the detection methods developed until recently, in view of simplicity and quickness, and is usefully used to diagnose various disease-causing substances such as antibodies or antigens of infectious pathogens, cancer factors, heart disease markers, and the like.

[0018] There is no specific preventive agent, therapeutic agent, or diagnostic kit for coronaviruses including SARS-CoV-2, or SARS-CoV-1 and MERS-CoV which are likely to re-emerge. Accordingly, the present inventors have made efforts to develop a therapeutic antibody capable of acting against mutant viruses and coronaviruses that are likely to occur later.

[0019] Accordingly, the present applicant has conducted extensive studies, and as a result, developed an antibody capable of neutralizing not only wild-type COVID-19 and mutant COVID-19 viruses, but also viruses belonging to the family Coronaviridae, such as SARS or MERS, thereby completing the present invention.

DISCLOSURE

Technical Problem

[0020] In order to solve the above-described problems, the present inventors have developed a binding molecule that is able to bind to various coronavirus species that may infect humans, including not only wild type SARS-coronavirus-2 (SARS-CoV-2) and mutant viruses that may occur in the future, but also SARS-coronavirus-1 (SARS-CoV-1), Middle East respiratory syndrome coronavirus (MERS-CoV), etc., which infect humans, causing fatal diseases, and have found that the binding molecule has excellent binding affinity and/or neutralizing efficacy, thereby completing the present invention.

[0021] An object of the present invention is to provide a neutralizing binding molecule that binds to a spike protein (S protein) on the surface of coronavirus.

[0022] Another object of the present invention is to provide a composition for diagnosing, preventing or treating a disease caused by coronavirus, the composition comprising the binding molecule.

[0023] Still another object of the present invention is to provide a kit for diagnosing, preventing or treating a disease caused by coronavirus, the kit comprising the binding molecule.

[0024] Yet another object of the present invention is to provide a method of diagnosing, preventing or treating a disease caused by coronavirus by administering the composition to a subject having the disease caused by coronavirus.

Technical Solution

[0025] To achieve the above objects, the present invention provides a binding molecule, particularly a neutralizing binding molecule, which binds to a spike protein (S protein) on the surface of coronavirus.

[0026] The present invention also provides an immunoconjugate in which at least one tag is additionally conjugated to the binding molecule.

[0027] The present invention also provides a nucleic acid molecule encoding the binding molecule.
[0028] The present invention also provides an expression vector into which the nucleic acid molecule has been inserted.
[0029] The present invention also provides a cell line transformed with the expression vector.
[0030] The present invention also provides a composition for diagnosing, preventing or treating a disease caused by coronavirus, the composition comprising the binding molecule.
[0031] The present invention also provides a kit for diagnosing, preventing or treating a disease caused by coronavirus, the kit comprising the binding molecule.
[0032] The present invention also provides a method for diagnosing, preventing or treating a disease caused by coronavirus, the method comprising a step of administering a therapeutically effective amount of the composition to a subject having the disease caused by coronavirus.
[0033] The present invention also provides a strip for immunochromatographic analysis, the strip comprising the binding molecule.
[0034] The present invention also provides a diagnostic kit for diagnosing a disease caused by coronavirus, the diagnostic kit comprising the strip for immunochromatographic analysis.
[0035] The present invention also provides a method of detecting a disease caused by coronavirus using the diagnostic kit.
[0036] The present invention also provides a method of diagnosing a disease caused by coronavirus using the diagnostic kit.

Advantageous Effects

[0037] The binding molecule of the present invention has excellent binding affinity and excellent neutralizing efficacy against various coronavirus species that may infect humans, including not only wild type SARS-coronavirus-2 (SARS-CoV-2) and mutant viruses that may occur in the future, but also SARS-coronavirus-1 (SARS-CoV-1), Middle East respiratory syndrome coronavirus (MERS-CoV), etc., which infect humans, causing fatal diseases. Thus, the binding molecule is very useful for the diagnosis, prevention or treatment of a disease caused by coronavirus.

Description

BRIEF DESCRIPTION OF DRAWINGS

[0038] FIG. **1** shows the results of evaluating the mechanism of action of antibody No. 32 according to an embodiment of the present invention by performing biolayer interference (BLI) analysis using Octet.
[0039] FIG. **2***a* shows the results of evaluating the average body weight of each group every day for 6 days before and after infection with SARS-CoV-2 virus during a mouse animal experiment conducted using the binding molecule of the present invention.
[0040] FIG. **2***b* shows the results of measuring the virus titer of mouse lung tissue using Vero cells after inoculation with SARS-CoV-2 virus during a mouse animal experiment conducted using the binding molecule of the present invention.
[0041] FIG. **2***c* shows the results of measuring the virus titer of mouse nasal lavage using Vero cells after inoculation with SARS-CoV-2 virus during a mouse animal experiment conducted using the binding molecule of the present invention.

BEST MODE

[0042] Hereinafter, the present invention will be described in more detail.
[0043] The scope of the present invention is not limited by the following description, and in particular, may include all aspects that may vary depending on the experimental conditions described in the following Examples and the like. Since the scope of the present invention will be defined by the appended claims, terms used herein for further understanding are used only for the purpose of describing embodiments of the present invention in detail, and the scope of the present invention is not limited thereby.
[0044] Unless otherwise defined herein, all technical and scientific terms used in the present specification are to be interpreted as having the same meanings as those commonly understood by those of ordinary skill in the art. All of the references mentioned in the present specification are incorporated herein by reference in their entirety to describe the invention of the present specification.
[0045] The present invention includes a binding molecule having ability to bind to or to neutralize all or part of a spike protein (S protein) on the surface of coronavirus, particularly SARS-coronavirus-2 (SARS-CoV-2), SARS-coronavirus-1 (SARS-CoV-1), and/or Middle East respiratory syndrome coronavirus (MERS-CoV), an immunoconjugate in which at least one tag is additionally conjugated to the binding molecule, a nucleic acid molecule encoding the binding molecule, an expression vector into which the nucleic acid molecule has been inserted, and/or a cell line transformed with the expression vector; a composition for diagnosing, ameliorating, preventing and/or treating a disease caused by coronavirus and a kit for diagnosing, ameliorating, preventing and/or treating a disease caused by coronavirus, which comprise at least one of the foregoing; a method of diagnosing, ameliorating, preventing and/or treating a disease caused by coronavirus using at least one of the foregoing, the use thereof for the diagnosis, amelioration, prevention or treatment of a disease caused by coronavirus, and the use thereof for the preparation of the binding molecule, the immunoconjugate, the nucleic acid molecule, the expression vector, the cell line, the composition or the kit for diagnosing, preventing and/or treating a disease caused by coronavirus, but the scope of the present invention is not limited thereto, and all analogues thereof may be included within the scope intended by the present invention.
[0046] The present invention is directed to a binding molecule and a neutralizing binding molecule, which bind to a spike

protein (S protein) on the surface of coronavirus, particularly at least one selected from the group consisting of a receptor binding domain (RBD), S1 domain and S2 domain in the spike protein. The coronavirus may be at least one selected from the group consisting of SARS-coronavirus-2 (SARS-CoV-2), SARS-coronavirus-1 (SARS-CoV-1), and Middle East respiratory syndrome coronavirus (MERS-CoV).

[0047] The spike protein (S protein) on the surface of SARS-coronavirus-2 (SARS-CoV-2) of the present invention may consist of or comprise the sequence of SEQ ID NO: 1,521, and may include derivatives and/or variants thereof, without being limited thereto.

[0048] The receptor binding domain (RBD) of the spike protein on the surface of SARS-coronavirus-2 of the present invention may consist of or comprise the sequence of SEQ ID NO: 1,522, and may include derivatives and/or variants thereof, without being limited thereto.

[0049] In an embodiment of the present invention, the coronavirus may be: [0050] i) SARS-coronavirus-2 (SARS-CoV-2) and SARS-coronavirus-1 (SARS-CoV-1); [0051] ii) SARS-coronavirus-2 (SARS-CoV-2) and Middle East respiratory syndrome coronavirus (MERS-CoV); or [0052] iii) SARS-coronavirus-2 (SARS-CoV-2), SARS-coronavirus-1 (SARS-CoV-1) and Middle East respiratory syndrome coronavirus (MERS-CoV).

[0053] The binding molecule may bind to a spike protein on the surface of SARS-coronavirus-2 (SARS-CoV-2), particularly the receptor binding domain (RBD), S1 domain and S2 domain; and/or a spike protein on SARS-coronavirus-1 (SARS-CoV-1); and/or a spike protein on MERS-coronavirus (MERS-CoV).

[0054] In one embodiment of the present invention, the neutralizing binding molecule of the present invention may have excellent binding affinity and/or excellent neutralizing activity against the spike protein of coronavirus, in particular, SARS-coronavirus-2 (SARS-CoV-2). The neutralizing binding molecule of the present invention may have excellent binding affinity for the spike protein of SARS-coronavirus-2 (SARS-CoV-2), and/or exhibit excellent neutralizing activity against wild-type SARS-coronavirus-2 (SARS-CoV-2). In addition, the neutralizing binding molecule of the present invention may also exhibit excellent neutralizing activity against a mutant virus having a mutation in the spike protein of SARS-coronavirus-2 (SARS-CoV-2). As an example, the neutralizing binding molecule of the present invention may also exhibit neutralizing activity against a virus having a mutation in S protein domains other than the RBD of the spike protein of SARS-coronavirus-2 (SARS-CoV-2), without being limited thereto.

[0055] In one embodiment of the present invention, the neutralizing binding molecule of the present invention may bind to the spike protein of SARS-coronavirus-2 (SARS-CoV-2), particularly the receptor binding domain (RBD), S1 domain and S2 domain; and/or the spike protein of SARS-coronavirus-1 (SARS-CoV-1); and/or the spike protein of MERS-coronavirus (MERS-CoV), and exhibit neutralizing activity against various coronavirus species, including SARS-coronavirus-2 (SARS-CoV-2), SARS-coronavirus-1 (SARS-CoV-1) and/or MERS-coronavirus (MERS-CoV).

[0056] Coronaviruses are RNA viruses belonging to the subfamily Coronavirinae of the family Coronaviridae, and are divided according to the host into four genera: alpha-, beta-, delta-, and gamma-coronaviruses. Not only human corona viruses but also mammalian coronaviruses found in cats, pigs, cattle, and bats mainly belong to the alpha- and beta-coronavirus genera, and most viruses infecting birds belong to the genus gamma-coronavirus. It is known that there are various coronavirus species, and coronaviruses cause both respiratory and digestive infectious diseases depending on the characteristics of the virus and on the host. Coronaviruses are viruses that cause respiratory illnesses of varying severity from the common cold to fatal pneumonia. Viruses belonging to the family Coronaviridae generally have a single-stranded, infectious, positive sense RNA genome with a length of 27 to 32 kb, and contain a cap at the 5′ end of the genome and a poly A tail at the 3′ end. Coronaviruses have an envelope, and contain major outer membrane proteins such as spike (S) protein and envelope (E) protein. The spike protein is involved in viral infection and pathogenicity, such as neutralizing antibody induction, receptor binding, and membrane fusion, and the envelope (E) protein is involved in morphogenesis of viral particles and extracellular release of the virus after infection.

[0057] Seven types of coronavirus are known to cause disease in humans, and infection with three types among them may cause even more severe or fatal pneumonia in humans. The three types that are fatal to humans include SARS-coronavirus-1 (SARS-CoV-1), which was identified as the cause of the 2002 severe acute respiratory syndrome outbreak which was a worldwide problem, MERS-coronavirus (MERS-CoV), which was identified as the cause of the 2012 Middle East respiratory syndrome outbreak, and the new coronavirus severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), which was first found in Wuhan, China in late 2019 and identified as the cause of coronavirus infection 2019 (COVID-19). Severe acute respiratory syndrome (SARS) coronavirus 2, SARS-CoV-2) is the cause of coronavirus infection 2019 (COVID-19), and is a novel coronavirus first found in Wuhan, China in late 2019.

[0058] SARS-coronavirus-1 (SARS-CoV-1) is a new infectious disease that has spread to countries worldwide, including Hong Kong, Singapore, and Canada, within a few months after its first outbreak in China in the winter of 2002, and the causative agent of SARS is SARS coronavirus-1. SARS-CoV-1 is presumed to have crossed the interspecies barrier from animals to infect humans by coronavirus variants that use animals as hosts. It is known that the main symptoms of SARS-CoV-1 are fever and cough, a sharp decrease in blood oxygen saturation, dyspnea, pneumonia, etc., and most of SARS-CoV-1 patients recover, but SARS-CoV-1 can be the cause of death in the elderly or children. Since there is no vaccine or therapeutic agent for prevention, it has been recommended to prescribe flu drugs, antiviral drugs, and the like.

[0059] MERS-coronavirus (MERS-CoV) was first detected in Jordan and Saudi Arabia in 2012, and most MERS-CoV infections occurred in Saudi Arabia, and occurred in people who traveled to the Middle East from other countries or worked in the Middle East. MERS-coronavirus is spread through close contact with MERS patients or through airborne droplets released by an infected person coughing or sneezing, and most people infected with MERS experience fever,

chills, muscle pain, and cough. So far, there is no MERS vaccine and therapeutic agent in Korea and other countries. For treatment of MERS-CoV, it is generally recommended to use drugs such as the immunomodulator interferon and the antiviral agent ribavirin or lopinavir. However, it has been reported that interferon and ribavirin cause side effects such as bone marrow function deterioration, anemia and viral mutations, and thus there are concerns about the safety thereof. In addition, co-administration of interferon and ribavirin showed a therapeutic effect against MERS in the monkey model, but it did not show a great effect on MERS patients in actual clinical practice, and thus there has been a need to develop a safer and more effective agent for treatment of MERS. In Korea, there has been no additional occurrence after the last occurrence of MERS-coronavirus infection, but MERS-coronavirus infection has continuously occurred in Middle Eastern countries, and thus it is necessary to prepare countermeasures against the re-introduction of MERS-coronavirus.

[0060] The World Health Organization (WHO) classifies SARS-coronavirus-2 (SARS-CoV-2) into six types based on amino acid changes due to differences in the gene sequence. SARS-CoV-2 was first classified into S and L types, and was then further divided into L, V, and G types, and G was subdivided into GH and GR, resulting in a total of six types: S, L, V, G, GH, and GR. At the beginning of the outbreak of COVID-19, S and V types were prevalent in Asian regions including Wuhan, China, and then different types were discovered in each continent, and the SARS-coronavirus-2 of the present invention includes these types. Among these, it has been reported that the GH type is likely to have high transmissibility. In Korea, based on the results of classifying genes collected from patients with coronavirus infection, most of them were found to be GH type, which is a variant of the G type prevalent in Europe and the United States, and this type is known to be highly transmissible. In particular, the G-type virus, in which the amino acid at position 614 of the spike protein, which plays an important role in the intracellular invasion of the virus, changed from aspartic acid (D) to glycine (G), has increased rapidly in Europe and the United States since March, and now appears in almost all regions, and the SARS-coronavirus-2 of the present invention includes the same. A recent report showed that more than 70 coronavirus variants occurred, among which 8 variants (D614G, etc.) having increased transmissibility, 10 variants (A841V, etc.) avoiding neutralizing antibodies, and 17 variants (I472V, etc.) on which plasma treatment effects are low, were identified, and the SARS-coronavirus-2 of the present invention includes these variants.

[0061] In one embodiment, the neutralizing binding molecule of the present invention may exhibit neutralizing activity against strains such as an S type (the amino acid at position 614 of the S protein is D), L type, V type, G type (the amino acid at position 614 of the S protein is G), GH type, or GR type, based on the amino acid mutation in SARS-coronavirus-2 (SARS-CoV-2), without being limited thereto. Examples of the SARS-CoV-2 virus S-type include, but are not limited to, a BetaCoV/Korea/KCDC03/2020 strain. Examples of the SARS-CoV-2 virus G-type include, but are not limited to, hCoV-19/South Korea/KUMC17/2020 strain. In one embodiment, the neutralizing binding molecule of the present invention may also exhibit neutralizing activity against a mutant virus having D614G mutation at amino acid position 614 of the spike protein of SARS-coronavirus-2 (SARS-CoV-2).

[0062] In one embodiment of the present invention, the neutralizing binding molecule of the present invention may have neutralizing activity against any one or more mutant viruses selected from the group consisting of the following mutant viruses 1) to 39), without being limited thereto. [0063] 1) a mutant virus having a mutation at one or more of amino acid positions 69 and 70 of the spike protein of SARS-coronavirus-2; [0064] 2) a mutant virus having a mutation at amino acid position 80 of the spike protein of SARS-coronavirus-2; [0065] 3) a mutant virus having a mutation at amino acid position 222 of the spike protein of SARS-coronavirus-2; [0066] 4) a mutant virus having a mutation at amino acid position 234 of the spike protein of SARS-coronavirus-2; [0067] 5) a mutant virus having a mutation at amino acid position 372 of the spike protein of SARS-coronavirus-2; [0068] 6) a mutant virus having a mutation at amino acid position 384 of the spike protein of SARS-coronavirus-2; [0069] 7) a mutant virus having a mutation at amino acid position 406 of the spike protein of SARS-coronavirus-2; [0070] 8) a mutant virus having a mutation at amino acid position 417 of the spike protein of SARS-coronavirus-2; [0071] 9) a mutant virus having a mutation at amino acid position 420 of the spike protein of SARS-coronavirus-2; [0072] 10) a mutant virus having a mutation at amino acid position 439 of the spike protein of SARS-coronavirus-2; [0073] 11) a mutant virus having a mutation at amino acid position 440 of the spike protein of SARS-coronavirus-2; [0074] 12) a mutant virus having a mutation at amino acid position 444 of the spike protein of SARS-coronavirus-2; [0075] 13) a mutant virus having a mutation at amino acid position 445 of the spike protein of SARS-coronavirus-2; [0076] 14) a mutant virus having a mutation at amino acid position 446 of the spike protein of SARS-coronavirus-2; [0077] 15) a mutant virus having a mutation at amino acid position 449 of the spike protein of SARS-coronavirus-2; [0078] 16) a mutant virus having a mutation at amino acid position 452 of the spike protein of SARS-coronavirus-2; [0079] 17) a mutant virus having a mutation at amino acid position 453 of the spike protein of SARS-coronavirus-2; [0080] 18) a mutant virus having a mutation at amino acid position 455 of the spike protein of SARS-coronavirus-2; [0081] 19) a mutant virus having a mutation at amino acid position 456 of the spike protein of SARS-coronavirus-2; [0082] 20) a mutant virus having a mutation at amino acid position 460 of the spike protein of SARS-coronavirus-2; [0083] 21) a mutant virus having a mutation at amino acid position 473 of the spike protein of SARS-coronavirus-2; [0084] 22) a mutant virus having a mutation at amino acid position 475 of the spike protein of SARS-coronavirus-2; [0085] 23) a mutant virus having a mutation at amino acid position 476 of the spike protein of SARS-coronavirus-2; [0086] 24) a mutant virus having a mutation at amino acid position 477 of the spike protein of SARS-coronavirus-2; [0087] 25) a mutant virus having a mutation at amino acid position 478 of the spike protein of SARS-coronavirus-2; [0088] 26) a mutant virus having a mutation at amino acid position 484 of the spike protein of SARS-coronavirus-2; [0089] 27) a mutant virus having a mutation at amino acid position 486 of the spike protein of SARS-coronavirus-2; [0090] 28) a mutant virus having a mutation at amino acid position 489 of the spike protein of SARS-

coronavirus-2; [0091] 29) a mutant virus having a mutation at amino acid position 490 of the spike protein of SARS-coronavirus-2; [0092] 30) a mutant virus having a mutation at amino acid position 493 of the spike protein of SARS-coronavirus-2; [0093] 31) a mutant virus having a mutation at amino acid position 494 of the spike protein of SARS-coronavirus-2; [0094] 32) a mutant virus having a mutation at amino acid position 498 of the spike protein of SARS-coronavirus-2; [0095] 33) a mutant virus having a mutation at amino acid position 501 of the spike protein of SARS-coronavirus-2; [0096] 34) a mutant virus having a mutation at amino acid position 614 of the spike protein of SARS-coronavirus-2; [0097] 35) a mutant virus having a mutation at amino acid position 677 of the spike protein of SARS-coronavirus-2; [0098] 36) a mutant virus having a mutation at amino acid position 681 of the spike protein of SARS-coronavirus-2; [0099] 37) a mutant virus having a mutation at amino acid position 685 of the spike protein of SARS-coronavirus-2; [0100] 38) a mutant virus having a mutation at amino acid position 701 of the spike protein of SARS-coronavirus-2; and [0101] 39) a mutant virus having a mutation at amino acid position 1,176 of the spike protein of SARS-coronavirus-2.

[0102] In one embodiment of the present invention, the neutralizing binding molecule of the present invention may have neutralizing activity against any one or more mutant viruses selected from the group consisting of the following mutant viruses 1) to 39), without being limited thereto. [0103] 1) a mutant virus having HV69-70del mutation at amino acid positions 69 and 70 of the spike protein of SARS-coronavirus-2; [0104] 2) a mutant virus having D80A mutation at amino acid position 80 of the spike protein of SARS-coronavirus-2; [0105] 3) a mutant virus having A222V mutation at amino acid position 222 of the spike protein of SARS-coronavirus-2; [0106] 4) a mutant virus having N234Q mutation at amino acid position 234 of the spike protein of SARS-coronavirus-2; [0107] 5) a mutant virus having A372V mutation at amino acid position 372 of the spike protein of SARS-coronavirus-2; [0108] 6) a mutant virus having P384L mutation at amino acid position 384 of the spike protein of SARS-coronavirus-2; [0109] 7) a mutant virus having E406Q mutation or E406W mutation at amino acid position 406 of the spike protein of SARS-coronavirus-2; [0110] 8) a mutant virus having K417N mutation, K417T mutation or K417E mutation at amino acid position 417 of the spike protein of SARS-coronavirus-2; [0111] 9) a mutant virus having D420N mutation at amino acid position 420 of the spike protein of SARS-coronavirus-2; [0112] 10) a mutant virus having N439K mutation at amino acid position 439 of the spike protein of SARS-coronavirus-2; [0113] 11) a mutant virus having N440D mutation at amino acid position 440 of the spike protein of SARS-coronavirus-2; [0114] 12) a mutant virus having K444Q mutation at amino acid position 444 of the spike protein of SARS-coronavirus-2; [0115] 13) a mutant virus having V445A mutation at amino acid position 445 of the spike protein of SARS-coronavirus-2; [0116] 14) a mutant virus having G446V mutation or G446S mutation at amino acid position 446 of the spike protein of SARS-coronavirus-2; [0117] 15) a mutant virus having Y449N mutation at amino acid position 449 of the spike protein of SARS-coronavirus-2; [0118] 16) a mutant virus having L452R mutation at amino acid position 452 of the spike protein of SARS-coronavirus-2; [0119] 17) a mutant virus having Y453F mutation at amino acid position 453 of the spike protein of SARS-coronavirus-2; [0120] 18) a mutant virus having L455F mutation at amino acid position 455 of the spike protein of SARS-coronavirus-2; [0121] 19) a mutant virus having F456L mutation at amino acid position 456 of the spike protein of SARS-coronavirus-2; [0122] 20) a mutant virus having N460T mutation at amino acid position 460 of the spike protein of SARS-coronavirus-2; [0123] 21) a mutant virus having Y473F mutation at amino acid position 473 of the spike protein of SARS-coronavirus-2; [0124] 22) a mutant virus having A475V mutation at amino acid position 475 of the spike protein of SARS-coronavirus-2; [0125] 23) a mutant virus having G476S mutation at amino acid position 476 of the spike protein of SARS-coronavirus-2; [0126] 24) a mutant virus having S477N mutation or S477R mutation at amino acid position 477 of the spike protein of SARS-coronavirus-2; [0127] 25) a mutant virus having T478K mutation at amino acid position 478 of the spike protein of SARS-coronavirus-2; [0128] 26) a mutant virus having E484K mutation, E484G mutation or E484Q mutation at amino acid position 484 of the spike protein of SARS-coronavirus-2; [0129] 27) a mutant virus having F486V mutation, F486I mutation, F486S mutation or F486L mutation at amino acid position 486 of the spike protein of SARS-coronavirus-2; [0130] 28) a mutant virus having Y489H mutation at amino acid position 489 of the spike protein of SARS-coronavirus-2; [0131] 29) a mutant virus having F490S mutation at amino acid position 490 of the spike protein of SARS-coronavirus-2; [0132] 30) a mutant virus having Q493K mutation, Q493R mutation, Q493M mutation, Q493Y mutation or Q493A mutation at amino acid position 493 of the spike protein of SARS-coronavirus-2; [0133] 31) a mutant virus having S494P mutation, S494Q mutation or S494L mutation at amino acid position 494 of the spike protein of SARS-coronavirus-2; [0134] 32) a mutant virus having Q498H mutation at amino acid position 498 of the spike protein of SARS-coronavirus-2; [0135] 33) a mutant virus having N501Y mutation, N501T mutation or N501F mutation at amino acid position 501 of the spike protein of SARS-coronavirus-2; [0136] 34) a mutant virus having D614G mutation at amino acid position 614 of the spike protein of SARS-coronavirus-2; [0137] 35) a mutant virus having Q677H mutation at amino acid position 677 of the spike protein of SARS-coronavirus-2; [0138] 36) a mutant virus having P681H mutation or P681R mutation at amino acid position 681 of the spike protein of SARS-coronavirus-2; [0139] 37) a mutant virus having R685H mutation at amino acid position 685 of the spike protein of SARS-coronavirus-2; [0140] 38) a mutant virus having A701V mutation at amino acid position 701 of the spike protein of SARS-coronavirus-2; and [0141] 39) a mutant virus having V1176F mutation at amino acid position 1,176 of the spike protein of SARS-coronavirus-2.

[0142] In one embodiment thereof, the neutralizing binding molecule of the present invention has binding affinity and/or neutralizing activity against SARS-coronavirus-2 strains isolated to date, for example, the UNKNOWN-LR757996 strain and the SARS-CoV-2/Hu/DP/Kng/19-027 strain, the isolation date and location of which are unknown; Wuhan-Hu-1 strain isolated in China in December 2019; BetaCoV/Wuhan/IPBCAMS-WH-01/2019 strain first isolated in China on Dec. 23, 2019; BetaCoV/Wuhan/IPBCAMS-WH-02/2019 strain, BetaCoV/Wuhan/IPBCAMS-WH-03/2019 strain,

BetaCoV/Wuhan/IPBCAMS-WH-04/2019 strain, WIV02 strain, WIV04 strain, WIV05 strain, WIV06 strain, and WIV07 strain isolated in China on Dec. 30, 2019; 2019-nCoV/Japan/TY/WK-521/2020 strain, 2019-nCoV/Japan/TY/WK-501/2020 strain, 2019-nCoV/Japan/TY/WK-012/2020 strain, and 2019-nCoV/Japan/KY/V-029/2020 strain isolated in Japan in January 2020; SNU01 strain isolated in Korea in January 2020; BetaCoV/Korea/KCDC03/2020 strain isolated in Korea; BetaCoV/Wuhan/IPBCAMS-WH-05/2020 strain isolated in China in Jan. 1, 2020; 2019-nCoV WHU02 strain, and 2019-nCoV WHU01 strain isolated in China on Jan. 2, 2020; SARS-CoV-2/WH-09/human/2020/CHN strain isolated in China in Jan. 8, 2020; 2019-nCoV_HKU-SZ-002a_2020 strain isolated in China on Jan. 10, 2020; 2019-nCoV_HKU-SZ-005b_2020 strain isolated in China on Jan. 11, 2020; SARS-CoV-2/Yunnan-01/human/2020/CHN strain isolated in China on Jan. 17, 2020; 2019-nCoV/USA-WA1/2020 strain isolated in the United States on Jan. 19, 2020; HZ-1 strain isolated in China on Jan. 20, 2020; 2019-nCoV/USA-IL1/2020 strain isolated in the United States on Jan. 21, 2020; 2019-nCoV/USA-CA2/2020 strain, and 2019-nCoV/USA-AZ1/2020 strain isolated in the United States on Jan. 22, 2020; 2019-nCoV/USA-CA1/2020 strain isolated in the United States on Jan. 23, 2020; Australia/VIC01/2020 strain isolated in Australia on Jan. 25, 2020; 2019-nCoV/USA-WA1-F6/2020 strain, and 2019-nCoV/USA-WA1-A12/2020 strain isolated in the United States on Jan. 25, 2020; 2019-nCoV/USA-CA6/2020 strain isolated in the United States on Jan. 27, 2020; 2019-nCoV/USA-IL2/2020 strain isolated in the United States on Jan. 28, 2020; 2019-nCoV/USA-MA1/2020 strain, 2019-nCoV/USA-CA5/2020 strain, 2019-nCoV/USA-CA4/2020 strain, and 2019-nCoV/USA-CA3/2020 strain isolated in the United States on Jan. 29, 2020; nCoV-FIN-29 Jan. 2020 strain isolated in Finland on Jan. 29, 2020; SARS-CoV-2/IQTC02/human/2020/CHN strain isolated in China on Jan. 29, 2020; 2019-nCoV/USA-WI1/2020 strain isolated in the United States on Jan. 31, 2020; SARS-CoV-2/NTU01/2020/TWN strain isolated in Taiwan on Jan. 31, 2020; SARS-CoV-2/NTU02/2020/TWN strain isolated in Taiwan on Feb. 5, 2020; 2019-nCoV/USA-CA7/2020 strain isolated in the United States on Feb. 6, 2020; SARS-CoV-2/01/human/2020/SWE strain isolated in Sweden on Feb. 7, 2020; 2019-nCoV/USA-CA8/2020 strain isolated in the United States on Feb. 10, 2020; 2019-nCoV/USA-TX1/2020 strain isolated in the United States on Feb. 11, 2020; 2019-nCoV/USA-CA9/2020 strain isolated in the United States on Feb. 23, 2020; SARS-CoV-2/SP02/human/2020/BRA strain isolated in Brazil on Feb. 28, 2020; UNKNOWN-LR757995, UNKNOWN-LR757997, UNKNOWN-LR757998, and SARS-CoV-2/Hu/DP/Kng/19-020, the isolation date and location of which are unknown; 2019-nCoV/Japan/AI/I-004/2020 isolated in Japan in January 2020; SARS0CoV-2/61-TW/human/2020/NPL isolated in Nepal on Jan. 13, 2020; SARS-CoV-2/IQTC01/human/2020/CHN strain isolated in China on Feb. 5, 2020; hCoV-19/South Korea/KUMC17/2020 strain isolated in Korea, and SARS-coronavirus-2 strain to be isolated in the future, without being limited thereto.

[0143] In one embodiment, the neutralizing binding molecule of the present invention has binding affinity and/or neutralizing activity against SARS-coronavirus-1 (SARS-CoV-1) strains, for example, SIN2500, SIN2677, SIN2679, SIN2748 and SIN2744 strains isolated in Singapore; icSARS-CoV (SARS-CoV Urbani strain) strain isolated in Hanoi; Urbani v2163 strain; TW-1 strain; TOR-2 strain isolated in Canada; CUHK-W1 and HKU-39849 strains isolated in Hong Kong; and GZ01 strain isolated in Guangzhou; and BJ01, BJ02, BJ03 and BJ04 strains isolated in Beijing, without being limited thereto.

[0144] In one embodiment, the neutralizing binding molecule of the present invention has binding affinity and/or neutralizing activity against Middle East respiratory syndrome coronavirus (MERS-CoV) strains, for example, EMC/2012 strain isolated in Saudi Arabia; MERS-HCoV/Jordan/01 strain isolated in Jordan; 2c England-Qatar/2012 strain isolated in England; MERS-CoV/Korea/KNIH/002_05_2015 and KOREA/Seoul/168-2-2015 strains isolated in Korea; Jeddah_C9313/KSA/2014 strain; Florida/USA-2_Saudi Arabia 2014 strain isolated in Saudi Arabia; and icMERS-CoV-T1015N strain, without being limited thereto.

[0145] Coronaviruses can cause not only the common cold in humans, but also direct viral bronchitis or secondary bacterial bronchitis. Seven types of human coronavirus have been reported, such as human coronavirus 299E (HCoV-229E), human coronavirus OC43 (HCoV-OC43), human coronavirus NL63 (HCoV-NL63), human coronavirus HKU1 (HCoV-HKU1), Middle East respiratory syndrome coronavirus (MERS-CoV), severe acute respiratory syndrome coronavirus 1 (SARS-CoV-1), and SARS-coronavirus-2 (SARS-CoV-2). Infection with four types (HCoV-229E, HCoV-OC43, HCoV-NL63, and HCoV-HKU1) results in mild upper respiratory tract disease causing symptoms of the common cold, but three types (SARS-CoV-1, MERS-CoV, and SARS-CoV-2) can cause severe and fatal pneumonia. The human coronavirus that first occurred in China in the winter of 2002 is severe acute respiratory syndrome coronavirus 1 (SARS-CoV-1), which causes severe acute respiratory syndrome, and the main symptoms thereof are fever, malaise, muscle pain, headache, chills, etc., and cough and shortness of breath may appear. SARS-CoV-1 causes upper and lower respiratory tract infections. Currently, there is no fundamental treatment method for SARS-CoV-1, and an antibacterial agent against the causative agent of common pneumonia is administered. The main clinical symptoms of Middle East respiratory syndrome coronavirus (MERS-CoV) found in 2012 are fever, cough, and shortness of breath. Most MERS-CoV patients have severe acute respiratory tract disease (pneumonia), but some patients have mild acute upper respiratory tract disease or are asymptomatic. In particular, MERS-Cov has a high infection rate and poor prognosis in people with underlying diseases (diabetes, renal failure, chronic lung disease, or immunodeficiency disease). As of 2020, MERS-CoV outbreaks have been reported in about 27 countries. Currently, a vaccine for preventing MERS-CoV infection has not been developed worldwide, and a therapeutic agent for MERS-CoV has not been developed due to limited information on the disease.

[0146] In one embodiment of the present invention, the present invention is directed to binding molecules that are able to bind to and neutralize the coronavirus superfamily against which a preventive or therapeutic agent has not yet been developed, and the binding molecules of the present invention may also have binding affinity and/or neutralizing activity

against coronaviruses, including wild-type and mutant SARS-CoV-2, and/or SARS-CoV-1, and/or MERS-CoV.
[0147] In one embodiment of the present invention, the binding molecule comprises any one binding molecule among binding molecule Nos. 1 to 190 shown in Table 1 below, or comprises a binding molecule derived therefrom. For example, for each of binding molecule Nos. 1 to 190 shown in Table 1 below, the scope of the present invention includes a binding molecule that comprises all of three light-chain CDR regions (LC CDR1, LC CDR2, and LC CDR3) and three heavy-chain CDR regions (HC CDR1, HC CDR2, and HC CDR3), or comprises a light-chain CDR region comprising at least one CDR region among the three light-chain CDR regions (LC CDR1, LC CDR2, and LC CDR3) and/or a heavy-chain CDR region comprising at least one CDR region among the three heavy-chain CDR regions (HC CDR1, HC CDR2, and HC CDR3), as long as this binding molecule achieves the purposes and effects of the present invention. In Table 1 below, No. represents each binding molecule number.
[0148] The "binding molecule that achieves the purposes and effects of the present invention" may be one satisfying the following: the minimum concentration value of the binding molecule that neutralizes 100 TCID50 of virus for SARS-coronavirus-2 (SARS-CoV-2) is preferably 2 μg/ml or less, more preferably 1 μg/ml or less, even more preferably 0.5 μg/ml or less, even more preferably 0.25 μg/ml or less, even more preferably 0.125 μg/ml or less; and/or [0149] the binding molecule is able to bind to a receptor-binding domain (RBD) of the spike protein of SARS-coronavirus-2 (SARS-CoV-2) with an equilibrium dissociation constant (K.sub.D) of preferably 1.0×10.sup.−8M or less, more preferably 1.0×10.sup.−9M or less, even more preferably 1.0×10.sup.−10 M or less; and/or [0150] the binding molecule has an IC.sub.50 value of preferably 200 ng/ml or less, more preferably 100 ng/ml or less, even more preferably 50 ng/ml or less, even more preferably 25 ng/ml or less, even more preferably 10 ng/ml or less, as evaluated according to a plaque reduction neutralization test (PRNT) method for SARS-coronavirus-2 (SARS-CoV-2), without being limited thereto. Here, IC.sub.50 value is the antibody concentration at which the antibody exhibits 50% of neutralizing activity against the virus.
[0151] In another embodiment of the present invention, the binding molecule comprises any one binding molecule selected from the group consisting of binding molecule Nos. 2, 3, 12, 15, 16, 18, 19, 20, 22, 23, 24, 26, 31, 32, 33, 34, 37, 43, 45, 48, 50, 51, 53, 54, 55, 56, 59, 60, 61, 66, 69, 74, 75, 76, 81, 82, 83, 85, 86, 87, 93, 94, 95, 96, 98, 102, 103, 104 and 108 among the binding molecules shown in Table 1 below, or a binding molecule derived therefrom. That is, for each of the above binding molecule numbers, the scope of the present invention includes a binding molecule that comprises all of three light-chain CDR regions (LC CDR1, LC CDR2, and LC CDR3) and three heavy-chain CDR regions (HC CDR1, HC CDR2, and HC CDR3), or comprises a light-chain CDR region comprising at least one CDR region among the three light-chain CDR regions (LC CDR1, LC CDR2, and LC CDR3) and/or a heavy-chain CDR region comprising at least one CDR region among the three heavy-chain CDR regions (HC CDR1, HC CDR2, and HC CDR3), as long as this binding molecule achieves the purposes and effects of the present invention.
[0152] In another embodiment, the binding molecule comprises any one binding molecule selected from the group consisting of binding molecule Nos. 2, 32, 59, 95, 102 and 103 among the binding molecules shown in Table 1 below, or a binding molecule derived therefrom. That is, for each of the above binding molecule numbers, the scope of the present invention includes a binding molecule that comprises all of three light-chain CDR regions (LC CDR1, LC CDR2, and LC CDR3) and three heavy-chain CDR regions (HC CDR1, HC CDR2, and HC CDR3), or comprises a light-chain CDR region comprising at least one CDR region among the three light-chain CDR regions (LC CDR1, LC CDR2, and LC CDR3) and/or a heavy-chain CDR region comprising at least one CDR region among the three heavy-chain CDR regions (HC CDR1, HC CDR2, and HC CDR3), as long as this binding molecule achieves the purposes and effects of the present invention.
[0153] In another embodiment, the binding molecule comprises any one binding molecule selected from the group consisting of binding molecule Nos. 32, 33, 34, 37, 45, 48, 53, 54, 59, 61 and 81 among the binding molecules shown in Table 1 below, or a binding molecule derived therefrom. That is, for each of the above binding molecule numbers, the scope of the present invention includes a binding molecule that comprises all of three light-chain CDR regions (LC CDR1, LC CDR2, and LC CDR3) and three heavy-chain CDR regions (HC CDR1, HC CDR2, and HC CDR3), or comprises a light-chain CDR region comprising at least one CDR region among the three light-chain CDR regions (LC CDR1, LC CDR2, and LC CDR3) and/or a heavy-chain CDR region comprising at least one CDR region among the three heavy-chain CDR regions (HC CDR1, HC CDR2, and HC CDR3), as long as this binding molecule achieves the purposes and effects of the present invention.
[0154] In another embodiment, the binding molecule comprises any one binding molecule selected from the group consisting of binding molecule Nos. 32, 34, 37, 45 and 54 among the binding molecules shown in Table 1 below, or a binding molecule derived therefrom. That is, for each of the above binding molecule numbers, the scope of the present invention includes a binding molecule that comprises all of three light-chain CDR regions (LC CDR1, LC CDR2, and LC CDR3) and three heavy-chain CDR regions (HC CDR1, HC CDR2, and HC CDR3), or comprises a light-chain CDR region comprising at least one CDR region among the three light-chain CDR regions (LC CDR1, LC CDR2, and LC CDR3) and/or a heavy-chain CDR region comprising at least one CDR region among the three heavy-chain CDR regions (HC CDR1, HC CDR2, and HC CDR3), as long as this binding molecule achieves the purposes and effects of the present invention.
[0155] In another embodiment, the binding molecule comprises any one binding molecule selected from the group consisting of binding molecule Nos. 32 and 54 among the binding molecules shown in Table 1 below, or a binding molecule derived therefrom. That is, for each of the above binding molecule numbers, the scope of the present invention includes a binding molecule that comprises all of three light-chain CDR regions (LC CDR1, LC CDR2, and LC CDR3)

and three heavy-chain CDR regions (HC CDR1, HC CDR2, and HC CDR3), or comprises a light-chain CDR region comprising at least one CDR region among the three light-chain CDR regions (LC CDR1, LC CDR2, and LC CDR3) and/or a heavy-chain CDR region comprising at least one CDR region among the three heavy-chain CDR regions (HC CDR1, HC CDR2, and HC CDR3), as long as this binding molecule achieves the purposes and effects of the present invention.

[0156] In another embodiment, the binding molecule may be the binding molecule of binding molecule No. 32 among the binding molecules shown in Table 1 below, or a binding molecule derived therefrom. That is, for binding molecule No. 32, the scope of the present invention includes a binding molecule that comprises all of three light-chain CDR regions (LC CDR1, LC CDR2, and LC CDR3) and three heavy-chain CDR regions (HC CDR1, HC CDR2, and HC CDR3), or comprises a light-chain CDR region comprising at least one CDR region among the three light-chain CDR regions (LC CDR1, LC CDR2, and LC CDR3) and/or a heavy-chain CDR region comprising at least one CDR region among the three heavy-chain CDR regions (HC CDR1, HC CDR2, and HC CDR3), as long as this binding molecule achieves the purposes and effects of the present invention.

TABLE-US-00001 TABLE 1 No. SEQID LC CDR1 SEQID LC CDR2 SEQID LC CDR3 SEQID HC CDR1 SEQID HC CDR2 SEQID HC CDR3 1 text missing or illegible when filed text missing or illegible when filed text missing or illegible when filed text missing or illegible when filed text missing or illegible when filed text missing or illegible when filed text missing or illegible when filed text missing or illegible when filed text missing or illegible when filed text missing or illegible when filed text missing or illegible when filed text missing or illegible when filed text missing or illegible when filed text missing or illegible when filed text missing or illegible when filed 2 text missing or illegible when filed text missing or illegible when filed text missing or illegible when filed text missing or illegible when filed text missing or illegible when filed text missing or illegible when filed text missing or illegible when filed text missing or illegible when filed text missing or illegible when 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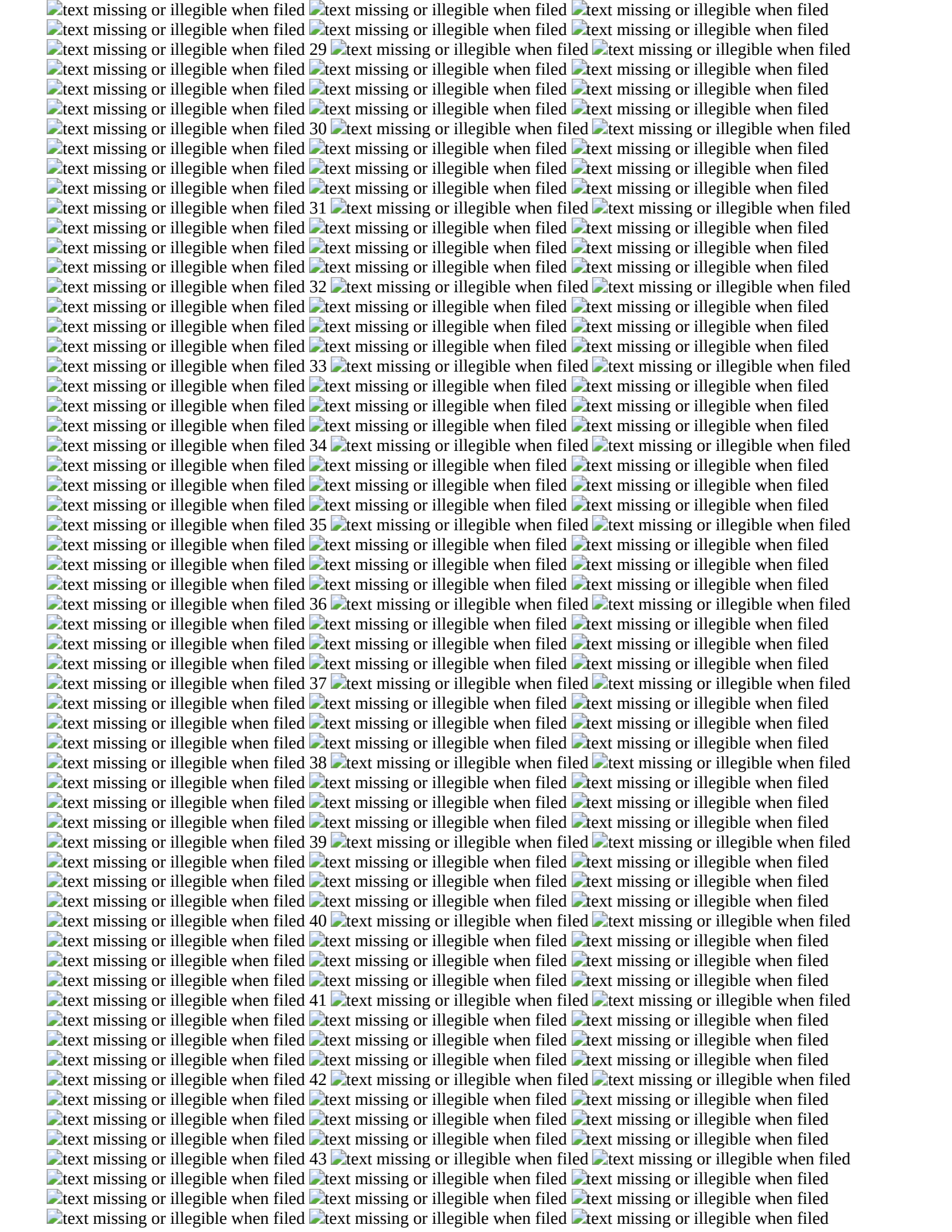
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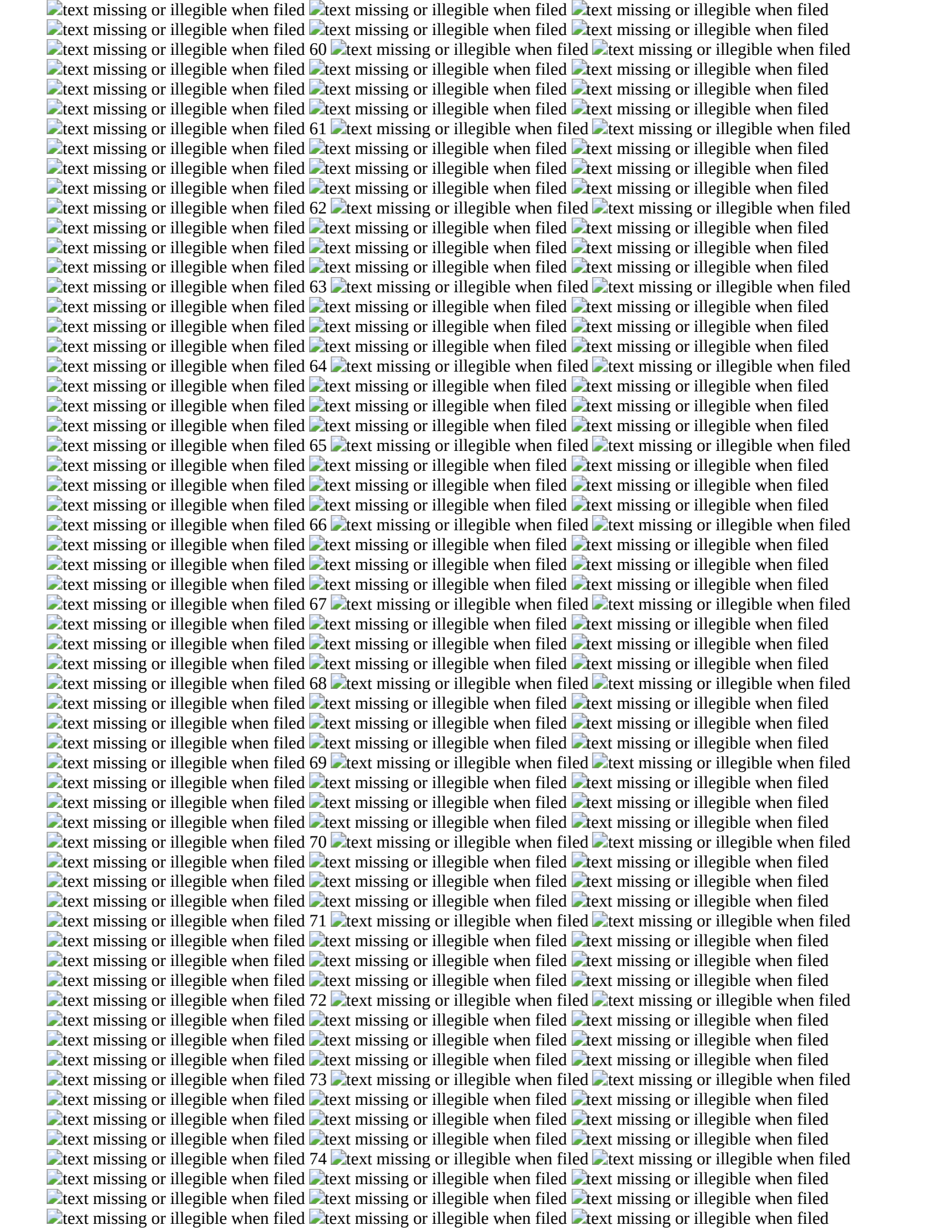
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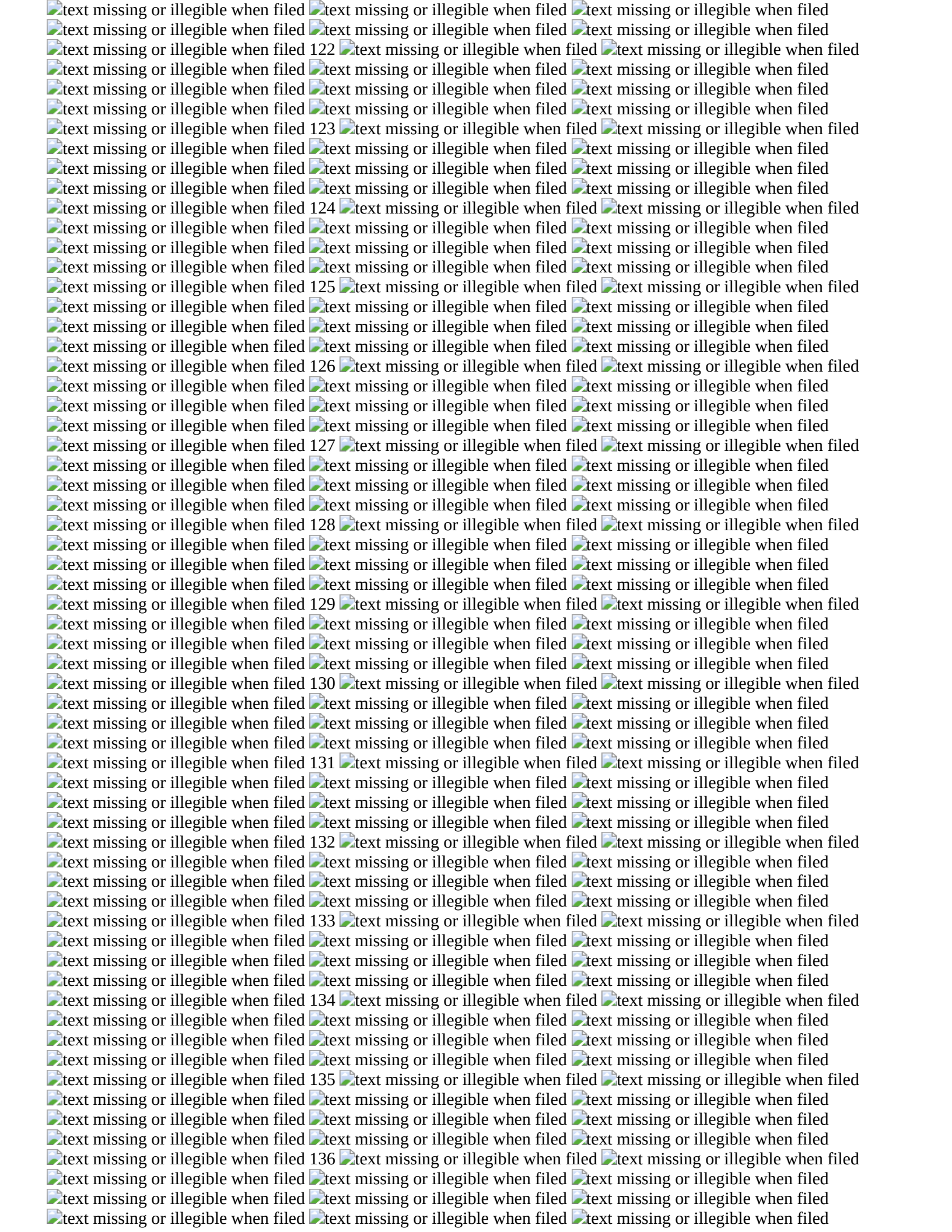
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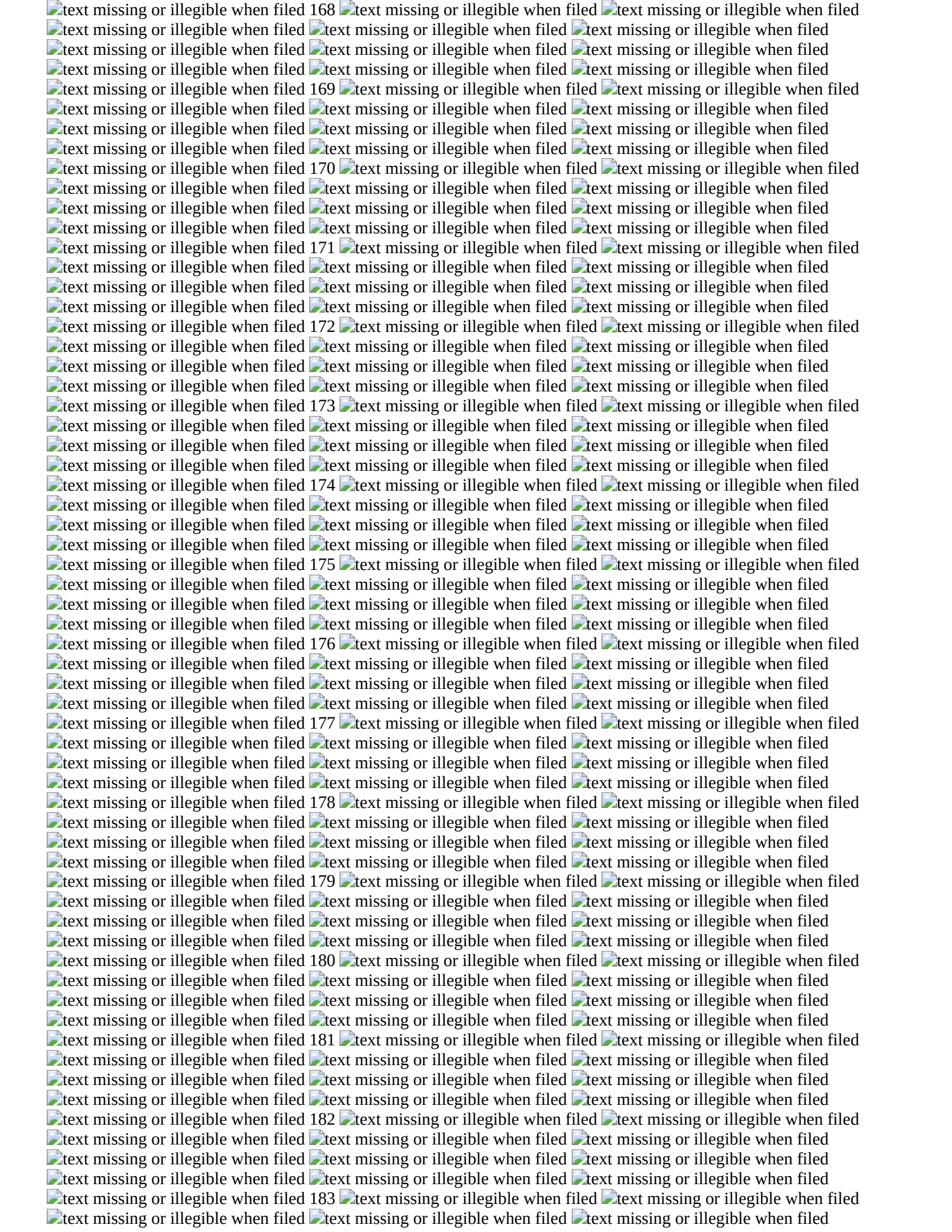

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[0157] In the present invention, CDRs of variable regions were determined through a conventional method using a system devised by Kabat et al. (see Kabat et al., Sequences of Proteins of Immunological Interest (5.sup.th), National Institutes of Health, Bethesda, MD. (1991)). The CDR numbering used in the present invention is determined using the Kabat method, but the present invention also encompasses binding molecules comprising CDRs determined through other methods such as an IMGT method, Chothia method, AbM method, or the like. For example, as shown in Table 2 below, as binding molecules comprising three light-chain CDR regions (LC CDR1, LC CDR2, and LC CDR3) contained in the light-chain (LC) variable region and three heavy-chain CDR regions (HC CDR1, HC CDR2, and HC CDR3) contained in the heavy-chain (HC) variable region, binding molecules comprising CDRs determined through a Kabat method, an IMGT method, a Chothia method and/or an AbM method are included within the scope of the present invention.

[0158] In one embodiment of the present invention, the binding molecule comprises any one binding molecule selected from the group consisting of binding molecules Nos. 1 to 190 shown in Table 2 below, or comprises a binding molecule derived therefrom. In Table 2 below, No. represents each binding molecule number.

[0159] In another embodiment of the present invention, the binding molecule may be any one selected from the group consisting of binding molecule Nos. 2, 3, 12, 15, 16, 18, 19, 20, 22, 23, 24, 26, 31, 32, 33, 34, 37, 43, 45, 48, 50, 51, 53, 54, 55, 56, 59, 60, 61, 66, 69, 74, 75, 76, 81, 82, 83, 85, 86, 87, 93, 94, 95, 96, 98, 102, 103, 104 and 108 among the binding molecules shown in Table 2 below, or may be a binding molecule comprising a sequence derived therefrom.

[0160] In another embodiment of the present invention, the binding molecule may be any one selected from the group consisting of binding molecule Nos. 2, 32, 59, 95, 102 and 103 among the binding molecules shown in Table 2 below, or may be a binding molecule comprising a sequence derived therefrom.

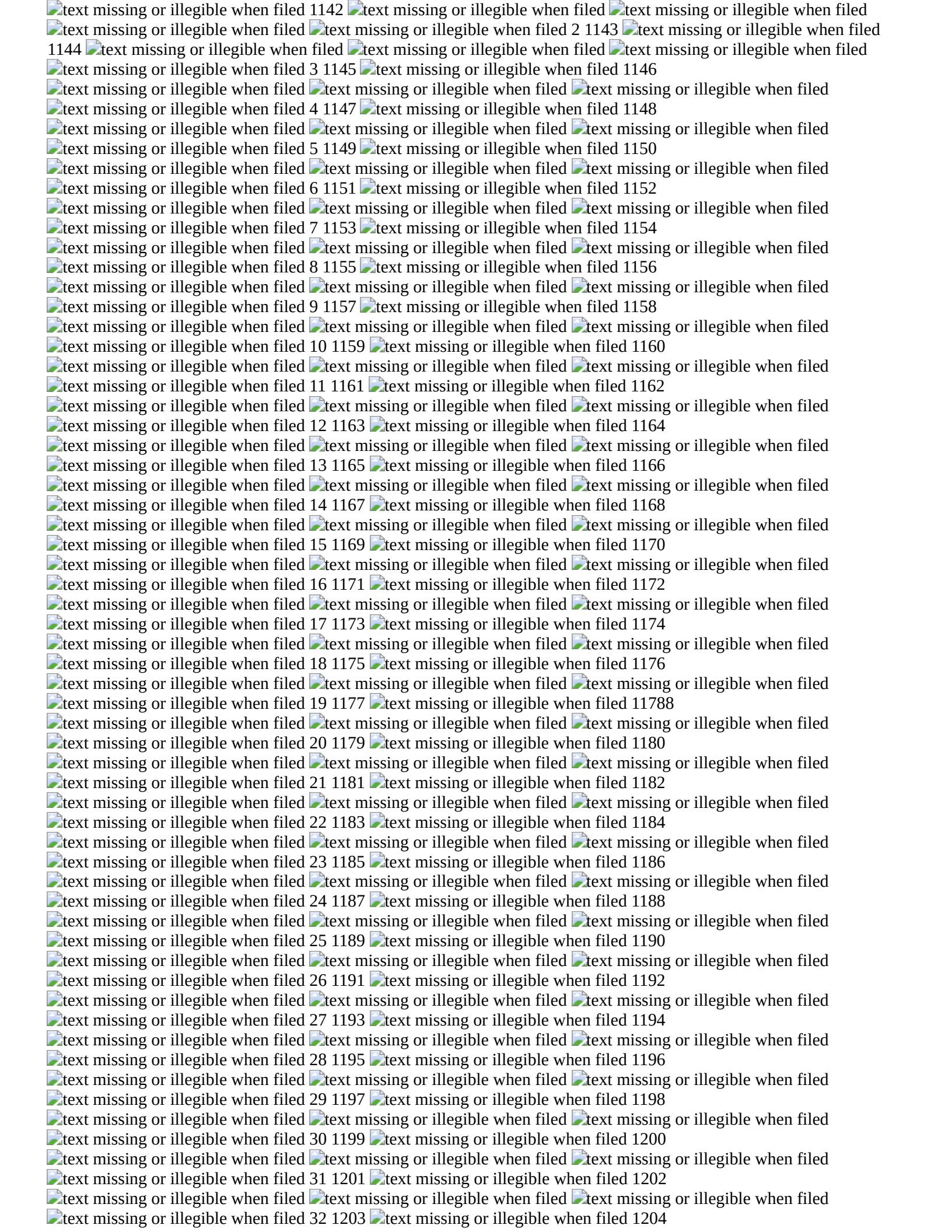
[0161] In another embodiment of the present invention, the binding molecule may be any one selected from the group consisting of binding molecule Nos. 32, 33, 34, 37, 45, 48, 53, 54, 59, 61 and 81 among the binding molecules shown in Table 2 below, or may be a binding molecule comprising a sequence derived therefrom.

[0162] In another embodiment of the present invention, the binding molecule may be any one selected from the group consisting of binding molecule Nos. 32, 34, 37, 45 and 54 among the binding molecules shown in Table 2 below, or may be a binding molecule comprising a sequence derived therefrom.

[0163] In another embodiment of the present invention, the binding molecule may be any one selected from the group consisting of binding molecule Nos. 32 and 54 among the binding molecules shown in Table 2 below, or may be a binding molecule comprising the same.

[0164] In another embodiment of the present invention, the binding molecule may be the binding molecule of binding molecule No. 32 among the binding molecules shown in Table 2 below.

TABLE-US-00002 TABLE 2 No. SEQID LC variable region SEQID HC variable region 1 1141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[0165] In another embodiment of the present invention, the binding molecule comprises a binding molecule having a sequence identity of 80% to 99%, preferably 85 to 99%, more preferably 90 to 99% to any one binding molecule selected from the group consisting of binding molecule Nos. 1 to 190 shown in Table 2 above, and this binding molecule is included within the scope of the present invention as long as it achieves the purposes and effects of the present invention.

[0166] In another embodiment of the present invention, the binding molecule comprises a binding molecule having a sequence identity of 80% to 99%, preferably 85 to 99%, more preferably 90 to 99% to any one binding molecule selected from the group consisting of binding molecule Nos. 2, 3, 12, 15, 16, 18, 19, 20, 22, 23, 24, 26, 31, 32, 33, 34, 37, 43, 45, 48, 50, 51, 53, 54, 55, 56, 59, 60, 61, 66, 69, 74, 75, 76, 81, 82, 83, 85, 86, 87, 93, 94, 95, 96, 98, 102, 103, 104 and 108 shown in Table 2 above, and this binding molecule is included within the scope of the present invention as long as it achieves the purposes and effects of the present invention.

[0167] In another embodiment of the present invention, the binding molecule comprises a binding molecule having a sequence identity of 80% to 99%, preferably 85 to 99%, more preferably 90 to 99% to any one binding molecule selected from the group consisting of binding molecule Nos. 2, 32, 59, 95, 102 and 103 shown in Table 2 above, and this binding molecule is included within the scope of the present invention as long as it achieves the purposes and effects of the present invention.

[0168] In another embodiment of the present invention, the binding molecule comprises a binding molecule having a sequence identity of 80% to 99%, preferably 85 to 99%, more preferably 90 to 99% to any one binding molecule selected from the group consisting of binding molecule Nos. 32, 33, 34, 37, 45, 48, 53, 54, 59, 61 and 81 shown in Table 2 above, and this binding molecule is included within the scope of the present invention as long as it achieves the purposes and effects of the present invention.

[0169] In another embodiment of the present invention, the binding molecule comprises a binding molecule having a sequence identity of 80% to 99%, preferably 85 to 99%, more preferably 90 to 99% to any one binding molecule selected from the group consisting of binding molecule Nos. 32, 34, 37, 45 and 54 shown in Table 2 above, and this binding molecule is included within the scope of the present invention as long as it achieves the purposes and effects of the present invention.

[0170] In another embodiment of the present invention, the binding molecule comprises a binding molecule having a sequence identity of 80% to 99%, preferably 85 to 99%, more preferably 90 to 99% to any one binding molecule selected from the group consisting of binding molecule Nos. 32 and 54 shown in Table 2 above, and this binding molecule is included within the scope of the present invention as long as it achieves the purposes and effects of the present invention.

[0171] In another embodiment of the present invention, the binding molecule comprises a binding molecule having a sequence identity of 80% to 99%, preferably 85 to 99%, more preferably 90 to 99% to the binding molecule of binding molecule No. 32 shown in Table 2 above, and this binding molecule is included within the scope of the present invention as long as it achieves the purposes and effects of the present invention.

[0172] In one embodiment of the present invention, the binding molecule may be a binding molecule comprising three light-chain CDR regions (LC CDR1, LC CDR2, and LC CDR3) contained in a light-chain (LC) variable region set forth in any one selected from the group consisting of SEQ ID NOS: 1141, 1143, 1145, 1147, 1149, 1151, 1153, 1155, 1157, 1159, 1161, 1163, 1165, 1167, 1169, 1171, 1173, 1175, 1177, 1179, 1181, 1183, 1185, 1187, 1189, 1191, 1193, 1195, 1197, 1199, 1201, 1203, 1205, 1207, 1209, 1211, 1213, 1215, 1217, 1219, 1221, 1223, 1225, 1227, 1229, 1231, 1233, 1235, 1237, 1239, 1241, 1243, 1245, 1247, 1249, 1251, 1253, 1255, 1257, 1259, 1261, 1263, 1265, 1267, 1269, 1271, 1273, 1275, 1277, 1279, 1281, 1283, 1285, 1287, 1289, 1291, 1293, 1295, 1297, 1299, 1301, 1303, 1305, 1307, 1309, 1311, 1313, 1315, 1317, 1319, 1321, 1323, 1325, 1327, 1329, 1331, 1333, 1335, 1337, 1339, 1341, 1343, 1345, 1347, 1349, 1351, 1353, 1355, 1357, 1359, 1361, 1363, 1365, 1367, 1369, 1371, 1373, 1375, 1377, 1379, 1381, 1383, 1385, 1387, 1389, 1391, 1393, 1395, 1397, 1399, 1401, 1403, 1405, 1407, 1409, 1411, 1413, 1415, 1417, 1419, 1421, 1423, 1425, 1427, 1429, 1431, 1433, 1435, 1437, 1439, 1441, 1443, 1445, 1447, 1449, 1451, 1453, 1455, 1457, 1459, 1461, 1463, 1465, 1467, 1469, 1471, 1473, 1475, 1477, 1479, 1481, 1483, 1485, 1487, 1489, 1491, 1493, 1495, 1497, 1499, 1501, 1503, 1505, 1507, 1509, 1511, 1513, 1515, 1517, and 1519, and three heavy-chain CDR regions (HC CDR1, HC CDR2, and HC CDR3) contained in a heavy-chain (HC) variable region set forth in any one selected from the group consisting of SEQ ID NOS: 1142, 1144, 1146, 1148, 1150, 1152, 1154, 1156, 1158, 1160, 1162, 1164, 1166, 1168, 1170, 1172, 1174, 1176, 1178, 1180, 1182, 1184, 1186, 1188, 1190, 1192, 1194, 1196, 1198, 1200, 1202, 1204, 1206, 1208, 1210, 1212, 1214, 1216, 1218, 1220, 1222, 1224, 1226, 1228, 1230, 1232, 1234, 1236, 1238, 1240, 1242, 1244, 1246, 1248, 1250, 1252, 1254, 1256, 1258, 1260, 1262, 1264, 1266, 1268, 1270, 1272, 1274, 1276, 1278, 1280, 1282, 1284, 1286, 1288, 1290, 1292, 1294, 1296, 1298, 1300, 1302, 1304, 1306, 1308, 1310, 1312, 1314, 1316, 1318, 1320, 1322, 1324, 1326, 1328, 1330, 1332, 1334, 1336, 1338, 1340, 1342, 1344, 1346, 1348, 1350, 1352, 1354, 1356, 1358, 1360, 1362, 1364, 1366, 1368, 1370, 1372, 1374, 1376, 1378, 1380, 1382, 1384, 1386, 1388, 1390, 1392, 1394, 1396, 1398, 1400, 1402, 1404, 1406, 1408,

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[0173] In another embodiment of the present invention, the binding molecule may be a binding molecule comprising three light-chain CDR regions (LC CDR1, LC CDR2, and LC CDR3) contained in a light-chain (LC) variable region set forth in any one selected from the group consisting of SEQ ID NOS: 1143, 1145, 1163, 1169, 1171, 1175, 1177, 1179, 1183, 1185, 1187, 1191, 1201, 1203, 1205, 1207, 1213, 1225, 1229, 1235, 1239, 1241, 1245, 1247, 1249, 1251, 1257, 1259, 1261, 1271, 1277, 1287, 1289, 1291, 1301, 1303, 1305, 1309, 1311, 1313, 1325, 1327, 1329, 1331, 1335, 1343, 1345, 1347 and 1355, and three heavy-chain CDR regions (HC CDR1, HC CDR2, and HC CDR3) contained in a heavy-chain (HC) variable region set forth in any one selected from the group consisting of SEQ ID NOS: 1144, 1146, 1164, 1170, 1172, 1176, 1178, 1180, 1184, 1186, 1188, 1192, 1202, 1204, 1206, 1208, 1214, 1226, 1230, 1236, 1240, 1242, 1246, 1248, 1250, 1252, 1258, 1260, 1262, 1272, 1278, 1288, 1290, 1292, 1302, 1304, 1306, 1310, 1312, 1314, 1326, 1328, 1330, 1332, 1336, 1344, 1346, 1348 and 1356.

[0174] In another embodiment of the present invention, the binding molecule may be a binding molecule comprising three light-chain CDR regions (LC CDR1, LC CDR2, and LC CDR3) contained in a light-chain (LC) variable region set forth in any one selected from the group consisting of SEQ ID NOS: 1143, 1203, 1257, 1329, 1343 and 1345, and three heavy-chain CDR regions (HC CDR1, HC CDR2, and HC CDR3) contained in a heavy-chain (HC) variable region set forth in any one selected from the group consisting of SEQ ID NOS: 1144, 1204, 1258, 1330, 1344 and 1346.

[0175] In another embodiment of the present invention, the binding molecule may be a binding molecule comprising three light-chain CDR regions (LC CDR1, LC CDR2, and LC CDR3) contained in a light-chain (LC) variable region set forth in any one selected from the group consisting of SEQ ID NOS: 1203, 1205, 1207, 1213, 1229, 1235, 1245, 1247, 1257, 1261 and 1301, and three heavy-chain CDR regions (HC CDR1, HC CDR2, and HC CDR3) contained in a heavy-chain (HC) variable region set forth in any one selected from the group consisting of SEQ ID NOS: 1204, 1206, 1208, 1214, 1230, 1236, 1246, 1248, 1258, 1262 and 1302.

[0176] In another embodiment of the present invention, the binding molecule may be a binding molecule comprising three light-chain CDR regions (LC CDR1, LC CDR2, and LC CDR3) contained in a light-chain (LC) variable region set forth in any one selected from the group consisting of SEQ ID NOS: 1203, 1207, 1213, 1229 and 1247, and three heavy-chain CDR regions (HC CDR1, HC CDR2, and HC CDR3) contained in a heavy-chain (HC) variable region set forth in any one selected from the group consisting of SEQ ID NOS: 1204, 1208, 1214, 1230 and 1248.

[0177] In another embodiment of the present invention, the binding molecule may be a binding molecule comprising three light-chain CDR regions (LC CDR1, LC CDR2, and LC CDR3) contained in a light-chain (LC) variable region set forth in any one selected from the group consisting of SEQ ID NOS: 1203 and 1247, and three heavy-chain CDR regions (HC CDR1, HC CDR2, and HC CDR3) contained in a heavy-chain (HC) variable region set forth in any one selected from the group consisting of SEQ ID NOS: 1204 and 1248.

[0178] In another embodiment of the present invention, the binding molecule may be a binding molecule comprising three light-chain CDR regions (LC CDR1, LC CDR2, and LC CDR3) contained in a light-chain (LC) variable region set forth in SEQ ID NO: 1203, and three heavy-chain CDR regions (HC CDR1, HC CDR2, and HC CDR3) contained in a heavy-chain (HC) variable region set forth in SEQ ID NO: 1204.

[0179] In one embodiment, the LC CDR1 may comprises any one selected from the group consisting of SEQ ID NOS: 1, 7, 13, 19, 25, 31, 37, 43, 49, 55, 61, 67, 73, 79, 85, 91, 97, 103, 109, 115, 121, 127, 133, 139, 145, 151, 157, 163, 169, 175, 181, 187, 193, 199, 205, 211, 217, 223, 229, 235, 241, 247, 253, 259, 265, 271, 277, 283, 289, 295, 301, 307, 313, 319, 325, 331, 337, 343, 349, 355, 361, 367, 373, 379, 385, 391, 397, 403, 409, 415, 421, 427, 433, 439, 445, 451, 457, 463, 469, 475, 481, 487, 493, 499, 505, 511, 517, 523, 529, 535, 541, 547, 553, 559, 565, 571, 577, 583, 589, 595, 601, 607, 613, 619, 625, 631, 637, 643, 649, 655, 661, 667, 673, 679, 685, 691, 697, 703, 709, 715, 721, 727, 733, 739, 745, 751, 757, 763, 769, 775, 781, 787, 793, 799, 805, 811, 817, 823, 829, 835, 841, 847, 853, 859, 865, 871, 877, 883, 889, 895, 901, 907, 913, 919, 925, 931, 937, 943, 949, 955, 961, 967, 973, 979, 985, 991, 997, 1003, 1009, 1015, 1021, 1027, 1033, 1039, 1045, 1051, 1057, 1063, 1069, 1075, 1081, 1087, 1093, 1099, 1105, 1111, 1117, 1123, 1129 and 1135, or a sequence derived therefrom, or [0180] comprise any one selected from the group consisting of SEQ ID NOS: 7, 13, 67, 85, 91, 103, 109, 115, 127, 133, 139, 151, 181, 187, 193, 199, 217, 253, 265, 283, 295, 301, 313, 319, 325, 331, 349, 355, 361, 391, 409, 439, 445, 451, 481, 487, 493, 505, 511, 517, 553, 559, 565, 571, 583, 607, 613, 619 and 643, or a sequence derived therefrom, or [0181] comprise any one selected from the group consisting of SEQ ID NOS: 7, 187, 349, 565, 607 and 613, or a sequence derived therefrom, or [0182] comprise any one selected from the group consisting of SEQ ID NOS: 187, 193, 199, 217, 265, 283, 313, 319, 349, 361 and 481, or a sequence derived therefrom, or [0183] comprise any one selected from the group consisting of SEQ ID NOS: 187, 199, 217, 265 and 319, or a sequence derived therefrom, or [0184] comprise any one selected from the group consisting of SEQ ID NOS: 187 and 319, or a sequence derived therefrom.

[0185] The LC CDR2 may comprise any one selected from the group consisting of SEQ ID NOS: 2, 8, 14, 20, 26, 32, 38, 44, 50, 56, 62, 68, 74, 80, 86, 92, 98, 104, 110, 116, 122, 128, 134, 140, 146, 152, 158, 164, 170, 176, 182, 188, 194, 200, 206, 212, 218, 224, 230, 236, 242, 248, 254, 260, 266, 272, 278, 284, 290, 296, 302, 308, 314, 320, 326, 332, 338, 344, 350, 356, 362, 368, 374, 380, 386, 392, 398, 404, 410, 416, 422, 428, 434, 440, 446, 452, 458, 464, 470, 476, 482, 488, 494, 500, 506, 512, 518, 524, 530, 536, 542, 548, 554, 560, 566, 572, 578, 584, 590, 596, 602, 608, 614, 620, 626, 632, 638, 644, 650, 656, 662, 668, 674, 680, 686, 692, 698, 704, 710, 716, 722, 728, 734, 740, 746, 752, 758, 764, 770, 776, 782, 788, 794, 800, 806, 812, 818, 824, 830, 836, 842, 848, 854, 860, 866, 872, 878, 884, 890, 896, 902, 908, 914, 920,

926, 932, 938, 944, 950, 956, 962, 968, 974, 980, 986, 992, 998, 1004, 1010, 1016, 1022, 1028, 1034, 1040, 1046, 1052, 1058, 1064, 1070, 1076, 1082, 1088, 1094, 1100, 1106, 1112, 1118, 1124, 1130 and 1136, or a sequence derived therefrom, or [0186] comprise any one selected from the group consisting of SEQ ID NOS: 8, 14, 68, 86, 92, 104, 110, 116, 128, 134, 140, 152, 182, 188, 194, 200, 218, 254, 266, 284, 296, 302, 314, 320, 326, 332, 350, 356, 362, 392, 410, 440, 446, 452, 482, 488, 494, 506, 512, 518, 554, 560, 566, 572, 584, 608, 614, 620 and 644, or a sequence derived therefrom, or [0187] comprise any one selected from the group consisting of SEQ ID NOS: 8, 188, 350, 566, 608 and 614, or a sequence derived therefrom, or [0188] comprise any one selected from the group consisting of SEQ ID NOS: 188, 194, 200, 218, 266, 284, 314, 320, 350, 362 and 482, or a sequence derived therefrom, or [0189] comprise any one selected from the group consisting of SEQ ID NOS: 188, 200, 218, 266 and 320, or a sequence derived therefrom, or [0190] comprise any one selected from the group consisting of SEQ ID NOS: 188 and 320, or a sequence derived therefrom.

[0191] The LC CDR3 may comprise any one selected from the group consisting of SEQ ID NOS: 3, 9, 15, 21, 27, 33, 39, 45, 51, 57, 63, 69, 75, 81, 87, 93, 99, 105, 111, 117, 123, 129, 135, 141, 147, 153, 159, 165, 171, 177, 183, 189, 195, 201, 207, 213, 219, 225, 231, 237, 243, 249, 255, 261, 267, 273, 279, 285, 291, 297, 303, 309, 315, 321, 327, 333, 339, 345, 351, 357, 363, 369, 375, 381, 387, 393, 399, 405, 411, 417, 423, 429, 435, 441, 447, 453, 459, 465, 471, 477, 483, 489, 495, 501, 507, 513, 519, 525, 531, 537, 543, 549, 555, 561, 567, 573, 579, 585, 591, 597, 603, 609, 615, 621, 627, 633, 639, 645, 651, 657, 663, 669, 675, 681, 687, 693, 699, 705, 711, 717, 723, 729, 735, 741, 747, 753, 759, 765, 771, 777, 783, 789, 795, 801, 807, 813, 819, 825, 831, 837, 843, 849, 855, 861, 867, 873, 879, 885, 891, 897, 903, 909, 915, 921, 927, 933, 939, 945, 951, 957, 963, 969, 975, 981, 987, 993, 999, 1005, 1011, 1017, 1023, 1029, 1035, 1041, 1047, 1053, 1059, 1065, 1071, 1077, 1083, 1089, 1095, 1101, 1107, 1113, 1119, 1125, 1131 and 1137, or a sequence derived therefrom, or [0192] comprise any one selected from the group consisting of SEQ ID NOS: 9, 15, 69, 87, 93, 105, 111, 117, 129, 135, 141, 153, 183, 189, 195, 201, 219, 255, 267, 285, 297, 303, 315, 321, 327, 333, 351, 357, 363, 393, 411, 441, 447, 453, 483, 489, 495, 507, 513, 519, 555, 561, 567, 573, 585, 609, 615, 621 and 645, or a sequence derived therefrom, or [0193] comprise any one selected from the group consisting of SEQ ID NOS: 9, 189, 351, 567, 609 and 615, or a sequence derived therefrom, or [0194] comprise any one selected from the group consisting of SEQ ID NOS: 189, 195, 201, 219, 267, 285, 315, 321, 351, 363 and 483, or a sequence derived therefrom, or [0195] comprise any one selected from the group consisting of SEQ ID NOS: 189, 201, 219, 267 and 321, or a sequence derived therefrom, or [0196] comprise any one selected from the group consisting of SEQ ID NOS: 189 and 321, or a sequence derived therefrom.

[0197] The HC CDR1 may comprise any one selected from the group consisting of SEQ ID NOS: 4, 10, 16, 22, 28, 34, 40, 46, 52, 58, 64, 70, 76, 82, 88, 94, 100, 106, 112, 118, 124, 130, 136, 142, 148, 154, 160, 166, 172, 178, 184, 190, 196, 202, 208, 214, 220, 226, 232, 238, 244, 250, 256, 262, 268, 274, 280, 286, 292, 298, 304, 310, 316, 322, 328, 334, 340, 346, 352, 358, 364, 370, 376, 382, 388, 394, 400, 406, 412, 418, 424, 430, 436, 442, 448, 454, 460, 466, 472, 478, 484, 490, 496, 502, 508, 514, 520, 526, 532, 538, 544, 550, 556, 562, 568, 574, 580, 586, 592, 598, 604, 610, 616, 622, 628, 634, 640, 646, 652, 658, 664, 670, 676, 682, 688, 694, 700, 706, 712, 718, 724, 730, 736, 742, 748, 754, 760, 766, 772, 778, 784, 790, 796, 802, 808, 814, 820, 826, 832, 838, 844, 850, 856, 862, 868, 874, 880, 886, 892, 898, 904, 910, 916, 922, 928, 934, 940, 946, 952, 958, 964, 970, 976, 982, 988, 994, 1000, 1006, 1012, 1018, 1024, 1030, 1036, 1042, 1048, 1054, 1060, 1066, 1072, 1078, 1084, 1090, 1096, 1102, 1108, 1114, 1120, 1126, 1132 and 1138, or a sequence derived therefrom, or [0198] comprise any one selected from the group consisting of SEQ ID NOS: 10, 16, 70, 88, 94, 106, 112, 118, 130, 136, 142, 154, 184, 190, 196, 202, 220, 256, 268, 286, 298, 304, 316, 322, 328, 334, 352, 358, 364, 394, 412, 442, 448, 454, 484, 490, 496, 508, 514, 520, 556, 562, 568, 574, 586, 610, 616, 622 and 646, or a sequence derived therefrom, or [0199] comprise any one selected from the group consisting of SEQ ID NOS: 10, 190, 352, 568, 610 and 616, or a sequence derived therefrom, or [0200] comprise any one selected from the group consisting of SEQ ID NOS: 190, 196, 202, 220, 268, 286, 316, 322, 352, 364 and 484, or a sequence derived therefrom, or [0201] comprise any one selected from the group consisting of SEQ ID NOS: 190, 202, 220, 268 and 322, or a sequence derived therefrom, or [0202] comprise any one selected from the group consisting of SEQ ID NOS: 190 and 322, or a sequence derived therefrom.

[0203] The HC CDR2 may any one selected from the group consisting of SEQ ID NOS: 5, 11, 17, 23, 29, 35, 41, 47, 53, 59, 65, 71, 77, 83, 89, 95, 101, 107, 113, 119, 125, 131, 137, 143, 149, 155, 161, 167, 173, 179, 185, 191, 197, 203, 209, 215, 221, 227, 233, 239, 245, 251, 257, 263, 269, 275, 281, 287, 293, 299, 305, 311, 317, 323, 329, 335, 341, 347, 353, 359, 365, 371, 377, 383, 389, 395, 401, 407, 413, 419, 425, 431, 437, 443, 449, 455, 461, 467, 473, 479, 485, 491, 497, 503, 509, 515, 521, 527, 533, 539, 545, 551, 557, 563, 569, 575, 581, 587, 593, 599, 605, 611, 617, 623, 629, 635, 641, 647, 653, 659, 665, 671, 677, 683, 689, 695, 701, 707, 713, 719, 725, 731, 737, 743, 749, 755, 761, 767, 773, 779, 785, 791, 797, 803, 809, 815, 821, 827, 833, 839, 845, 851, 857, 863, 869, 875, 881, 887, 893, 899, 905, 911, 917, 923, 929, 935, 941, 947, 953, 959, 965, 971, 977, 983, 989, 995, 1001, 1007, 1013, 1019, 1025, 1031, 1037, 1043, 1049, 1055, 1061, 1067, 1073, 1079, 1085, 1091, 1097, 1103, 1109, 1115, 1121, 1127, 1133 and 1139, or a sequence derived therefrom, or [0204] comprise any one selected from the group consisting of SEQ ID NOS: 11, 17, 71, 89, 95, 107, 113, 119, 131, 137, 143, 155, 185, 191, 197, 203, 221, 257, 269, 287, 299, 305, 317, 323, 329, 335, 353, 359, 365, 395, 413, 443, 449, 455, 485, 491, 497, 509, 515, 521, 557, 563, 569, 575, 587, 611, 617, 623 and 647, or a sequence derived therefrom, or [0205] comprise any one selected from the group consisting of SEQ ID NOS: 11, 191, 353, 569, 611 and 617, or a sequence derived therefrom, or [0206] comprise any one selected from the group consisting of SEQ ID NOS: 191, 197, 203, 221, 269, 287, 317, 323, 353, 365 and 485, or a sequence derived therefrom, or [0207] comprise any one selected from the group consisting of SEQ ID NOS: 191, 203, 221, 269 and 323, or a sequence derived therefrom, or [0208] comprise any one selected from the group consisting of SEQ ID NOS: 191 and 323, or a sequence derived therefrom.

[0209] The HC CDR3 may comprise any one selected from the group consisting of SEQ ID NOS: 6, 12, 18, 24, 30, 36, 42,

48, 54, 60, 66, 72, 78, 84, 90, 96, 102, 108, 114, 120, 126, 132, 138, 144, 150, 156, 162, 168, 174, 180, 186, 192, 198, 204, 210, 216, 222, 228, 234, 240, 246, 252, 258, 264, 270, 276, 282, 288, 294, 300, 306, 312, 318, 324, 330, 336, 342, 348, 354, 360, 366, 372, 378, 384, 390, 396, 402, 408, 414, 420, 426, 432, 438, 444, 450, 456, 462, 468, 474, 480, 486, 492, 498, 504, 510, 516, 522, 528, 534, 540, 546, 552, 558, 564, 570, 576, 582, 588, 594, 600, 606, 612, 618, 624, 630, 636, 642, 648, 654, 660, 666, 672, 678, 684, 690, 696, 702, 708, 714, 720, 726, 732, 738, 744, 750, 756, 762, 768, 774, 780, 786, 792, 798, 804, 810, 816, 822, 828, 834, 840, 846, 852, 858, 864, 870, 876, 882, 888, 894, 900, 906, 912, 918, 924, 930, 936, 942, 948, 954, 960, 966, 972, 978, 984, 990, 996, 1002, 1008, 1014, 1020, 1026, 1032, 1038, 1044, 1050, 1056, 1062, 1068, 1074, 1080, 1086, 1092, 1098, 1104, 1110, 1116, 1122, 1128, 1134 and 1140, or a sequence derived therefrom, or [0210] comprise any one selected from the group consisting of SEQ ID NOS: 12, 18, 72, 90, 96, 108, 114, 120, 132, 138, 144, 156, 186, 192, 198, 204, 222, 258, 270, 288, 300, 306, 318, 324, 330, 336, 354, 360, 366, 396, 414, 444, 450, 456, 486, 492, 498, 510, 516, 522, 558, 564, 570, 576, 588, 612, 618, 624 and 648, or a sequence derived therefrom, or [0211] comprise any one selected from the group consisting of SEQ ID NOS: 12, 192, 354, 570, 612 and 618, or a sequence derived therefrom, or [0212] comprise any one selected from the group consisting of SEQ ID NOS: 192, 198, 204, 222, 270, 288, 318, 324, 354, 366 and 486, or a sequence derived therefrom, or [0213] comprise any one selected from the group consisting of SEQ ID NOS: 192, 204, 222, 270 and 324, or a sequence derived therefrom, or [0214] comprise any one selected from the group consisting of SEQ ID NOS: 192 and 324, or a sequence derived therefrom.

[0215] In one embodiment of the present invention, the binding molecule is a binding molecule that binds to a spike protein (S protein) on the surface of SARS-coronavirus-2 (SARS-CoV-2), and comprises a binding molecule that competes with any one binding molecule selected from the group consisting of the following binding molecules 1) to 190), and this binding molecule is included within the scope of the present invention as long as it achieves the purposes and effects of the present invention: [0216] 1) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 1, a CDR2 region of SEQ ID NO: 2, and a CDR3 region of SEQ ID NO: 3, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 4, a CDR2 region of SEQ ID NO: 5, and a CDR3 region of SEQ ID NO: 6; [0217] 2) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 7, a CDR2 region of SEQ ID NO: 8, and a CDR3 region of SEQ ID NO: 9, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 10, a CDR2 region of SEQ ID NO: 11, and a CDR3 region of SEQ ID NO: 12; [0218] 3) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 13, a CDR2 region of SEQ ID NO: 14, and a CDR3 region of SEQ ID NO: 15, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 16, a CDR2 region of SEQ ID NO: 17, and a CDR3 region of SEQ ID NO: 18; [0219] 4) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 19, a CDR2 region of SEQ ID NO: 20, and a CDR3 region of SEQ ID NO: 21, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 22, a CDR2 region of SEQ ID NO: 23, and a CDR3 region of SEQ ID NO: 24; [0220] 5) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 25, a CDR2 region of SEQ ID NO: 26, and a CDR3 region of SEQ ID NO: 27, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 28, a CDR2 region of SEQ ID NO: 29, and a CDR3 region of SEQ ID NO: 30; [0221] 6) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 31, a CDR2 region of SEQ ID NO: 32, and a CDR3 region of SEQ ID NO: 33, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 34, a CDR2 region of SEQ ID NO: 35, and a CDR3 region of SEQ ID NO: 36; [0222] 7) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 37, a CDR2 region of SEQ ID NO: 38, and a CDR3 region of SEQ ID NO: 39, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 40, a CDR2 region of SEQ ID NO: 41, and a CDR3 region of SEQ ID NO: 42; [0223] 8) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 43, a CDR2 region of SEQ ID NO: 44, and a CDR3 region of SEQ ID NO: 45, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 46, a CDR2 region of SEQ ID NO: 47, and a CDR3 region of SEQ ID NO: 48; [0224] 9) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 49, a CDR2 region of SEQ ID NO: 50, and a CDR3 region of SEQ ID NO: 51, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 52, a CDR2 region of SEQ ID NO: 53, and a CDR3 region of SEQ ID NO: 54; [0225] 10) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 55, a CDR2 region of SEQ ID NO: 56, and a CDR3 region of SEQ ID NO: 57, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 58, a CDR2 region of SEQ ID NO: 59, and a CDR3 region of SEQ ID NO: 60; [0226] 11) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 61, a CDR2 region of SEQ ID NO: 62, and a CDR3 region of SEQ ID NO: 63, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 64, a CDR2 region of SEQ ID NO: 65, and a CDR3 region of SEQ ID NO: 66; [0227] 12) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 67, a CDR2 region of SEQ ID NO: 68, and a CDR3 region of SEQ ID NO: 69, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 70, a CDR2 region of SEQ ID NO: 71, and a CDR3 region of SEQ ID NO: 72; [0228] 13) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 73, a CDR2 region of SEQ ID NO: 74, and a CDR3 region of SEQ ID NO: 75, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 76, a CDR2 region of SEQ ID NO: 77, and a CDR3 region of SEQ ID NO: 78; [0229] 14) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 79, a CDR2 region of SEQ ID NO: 80, and a CDR3 region of SEQ ID NO: 81, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 82, a CDR2 region of SEQ ID NO: 83, and a CDR3 region of SEQ ID NO: 84; [0230] 15) a

binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 85, a CDR2 region of SEQ ID NO: 86, and a CDR3 region of SEQ ID NO: 87, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 88, a CDR2 region of SEQ ID NO: 89, and a CDR3 region of SEQ ID NO: 90; [0231] 16) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 91, a CDR2 region of SEQ ID NO: 92, and a CDR3 region of SEQ ID NO: 93, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 94, a CDR2 region of SEQ ID NO: 95, and a CDR3 region of SEQ ID NO: 96; [0232] 17) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 97, a CDR2 region of SEQ ID NO: 98, and a CDR3 region of SEQ ID NO: 99, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 100, a CDR2 region of SEQ ID NO: 101, and a CDR3 region of SEQ ID NO: 102; [0233] 18) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 103, a CDR2 region of SEQ ID NO: 104, and a CDR3 region of SEQ ID NO: 105, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 106, a CDR2 region of SEQ ID NO: 107, and a CDR3 region of SEQ ID NO: 108; [0234] 19) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 109, CDR2 region of SEQ ID NO: 110, and CDR3 region of SEQ ID NO: 111, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 112, a CDR2 region of SEQ ID NO: 113, and a CDR3 region of SEQ ID NO: 114; [0235] 20) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 115, a CDR2 region of SEQ ID NO: 116, and a CDR3 region of SEQ ID NO: 117, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 118, a CDR2 region of SEQ ID NO: 119, and a CDR3 region of SEQ ID NO: 120; [0236] 21) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 121, a CDR2 region of SEQ ID NO: 122, and a CDR3 region of SEQ ID NO: 123, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 124, a CDR2 region of SEQ ID NO: 125, and a CDR3 region of SEQ ID NO: 126; [0237] 22) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 127, a CDR2 region of SEQ ID NO: 128, and a CDR3 region of SEQ ID NO: 129, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 130, a CDR2 region of SEQ ID NO: 131, and a CDR3 region of SEQ ID NO: 132; [0238] 23) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 133, a CDR2 region of SEQ ID NO: 134, and a CDR3 region of SEQ ID NO: 135, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 136, a CDR2 region of SEQ ID NO: 137, and a CDR3 region of SEQ ID NO: 138; [0239] 24) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 139, a CDR2 region of SEQ ID NO: 140, and a CDR3 region of SEQ ID NO: 141, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 142, a CDR2 region of SEQ ID NO: 143, and a CDR3 region of SEQ ID NO: 144; [0240] 25) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 145, a CDR2 region of SEQ ID NO: 146, and a CDR3 region of SEQ ID NO: 147, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 148, a CDR2 region of SEQ ID NO: 149, and a CDR3 region of SEQ ID NO: 150; [0241] 26) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 151, a CDR2 region of SEQ ID NO: 152, and a CDR3 region of SEQ ID NO: 153, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 154, a CDR2 region of SEQ ID NO: 155, and a CDR3 region of SEQ ID NO: 156; [0242] 27) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 157, a CDR2 region of SEQ ID NO: 158, and a CDR3 region of SEQ ID NO: 159, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 160, a CDR2 region of SEQ ID NO: 161, and a CDR3 region of SEQ ID NO: 162; [0243] 28) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 163, a CDR2 region of SEQ ID NO: 164, and a CDR3 region of SEQ ID NO: 165, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 166, a CDR2 region of SEQ ID NO: 167, and a CDR3 region of SEQ ID NO: 168; [0244] 29) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 169, a CDR2 region of SEQ ID NO: 170, and a CDR3 region of SEQ ID NO: 171, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 172, a CDR2 region of SEQ ID NO: 173, and a CDR3 region of SEQ ID NO: 174; [0245] 30) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 175, a CDR2 region of SEQ ID NO: 176, and a CDR3 region of SEQ ID NO: 177, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 178, a CDR2 region of SEQ ID NO: 179, and a CDR3 region of SEQ ID NO: 180; [0246] 31) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 181, a CDR2 region of SEQ ID NO: 182, and a CDR3 region of SEQ ID NO: 183, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 184, a CDR2 region of SEQ ID NO: 185, and a CDR3 region of SEQ ID NO: 186; [0247] 32) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 187, a CDR2 region of SEQ ID NO: 188, and a CDR3 region of SEQ ID NO: 189, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 190, a CDR2 region of SEQ ID NO: 191, and a CDR3 region of SEQ ID NO: 192; [0248] 33) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 193, a CDR2 region of SEQ ID NO: 194, and a CDR3 region of SEQ ID NO: 195, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 196, a CDR2 region of SEQ ID NO: 197, and a CDR3 region of SEQ ID NO: 198; [0249] 34) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 199, a CDR2 region of SEQ ID NO: 200, and a CDR3 region of SEQ ID NO: 201, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 202, a CDR2 region of SEQ ID NO: 203, and a CDR3 region of SEQ ID NO: 204; [0250] 35) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 205, a CDR2 region of SEQ ID NO: 206, and a CDR3 region of SEQ ID NO: 207, and b) a heavy-chain variable region

comprising a CDR1 region of SEQ ID NO: 208, a CDR2 region of SEQ ID NO: 209, and a CDR3 region of SEQ ID NO: 210; [0251] 36) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 211, a CDR2 region of SEQ ID NO: 212, and a CDR3 region of SEQ ID NO: 213, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 214, a CDR2 region of SEQ ID NO: 215, and a CDR3 region of SEQ ID NO: 216; [0252] 37) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 217, a CDR2 region of SEQ ID NO: 218, and a CDR3 region of SEQ ID NO: 219, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 220, a CDR2 region of SEQ ID NO: 221, and a CDR3 region of SEQ ID NO: 222; [0253] 38) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 223, a CDR2 region of SEQ ID NO: 224, and a CDR3 region of SEQ ID NO: 225, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 226, a CDR2 region of SEQ ID NO: 227, and a CDR3 region of SEQ ID NO: 228; [0254] 39) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 229, a CDR2 region of SEQ ID NO: 230, and a CDR3 region of SEQ ID NO: 231, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 232, a CDR2 region of SEQ ID NO: 233, and a CDR3 region of SEQ ID NO: 234; [0255] 40) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 235, a CDR2 region of SEQ ID NO: 236, and a CDR3 region of SEQ ID NO: 237, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 238, a CDR2 region of SEQ ID NO: 239, and a CDR3 region of SEQ ID NO: 240; [0256] 41) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 241, a CDR2 region of SEQ ID NO: 242, and a CDR3 region of SEQ ID NO: 243, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 244, a CDR2 region of SEQ ID NO: 245, and a CDR3 region of SEQ ID NO: 246; [0257] 42) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 247, a CDR2 region of SEQ ID NO: 248, and a CDR3 region of SEQ ID NO: 249, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 250, a CDR2 region of SEQ ID NO: 251, and a CDR3 region of SEQ ID NO: 252; [0258] 43) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 253, a CDR2 region of SEQ ID NO: 254, and a CDR3 region of SEQ ID NO: 255, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 256, a CDR2 region of SEQ ID NO: 257, and a CDR3 region of SEQ ID NO: 258; [0259] 44) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 259, a CDR2 region of SEQ ID NO: 260, and a CDR3 region of SEQ ID NO: 261, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 262, a CDR2 region of SEQ ID NO: 263, and a CDR3 region of SEQ ID NO: 264; [0260] 45) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 265, a CDR2 region of SEQ ID NO: 266, and a CDR3 region of SEQ ID NO: 267, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 268, a CDR2 region of SEQ ID NO: 269, and a CDR3 region of SEQ ID NO: 270; [0261] 46) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 271, a CDR2 region of SEQ ID NO: 272, and a CDR3 region of SEQ ID NO: 273, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 274, a CDR2 region of SEQ ID NO: 275, and a CDR3 region of SEQ ID NO: 276; [0262] 47) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 277, a CDR2 region of SEQ ID NO: 278, and a CDR3 region of SEQ ID NO: 279, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 280, a CDR2 region of SEQ ID NO: 281, and a CDR3 region of SEQ ID NO: 282; [0263] 48) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 283, a CDR2 region of SEQ ID NO: 284, and a CDR3 region of SEQ ID NO: 285, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 286, a CDR2 region of SEQ ID NO: 287, and a CDR3 region of SEQ ID NO: 288; [0264] 49) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 289, a CDR2 region of SEQ ID NO: 290, and a CDR3 region of SEQ ID NO: 291, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 292, a CDR2 region of SEQ ID NO: 293, and a CDR3 region of SEQ ID NO: 294; [0265] 50) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 295, a CDR2 region of SEQ ID NO: 296, and a CDR3 region of SEQ ID NO: 297, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 298, a CDR2 region of SEQ ID NO: 299, and a CDR3 region of SEQ ID NO: 300; [0266] 51) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 301, a CDR2 region of SEQ ID NO: 302, and a CDR3 region of SEQ ID NO: 303, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 304, a CDR2 region of SEQ ID NO: 305, and a CDR3 region of SEQ ID NO: 306; [0267] 52) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 307, a CDR2 region of SEQ ID NO: 308, and a CDR3 region of SEQ ID NO: 309, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 310, a CDR2 region of SEQ ID NO: 311, and a CDR3 region of SEQ ID NO: 312; [0268] 53) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 313, a CDR2 region of SEQ ID NO: 314, and a CDR3 region of SEQ ID NO: 315, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 316, a CDR2 region of SEQ ID NO: 317, and a CDR3 region of SEQ ID NO: 318; [0269] 54) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 319, a CDR2 region of SEQ ID NO: 320, and a CDR3 region of SEQ ID NO: 321, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 322, a CDR2 region of SEQ ID NO: 323, and a CDR3 region of SEQ ID NO: 324; [0270] 55) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 325, a CDR2 region of SEQ ID NO: 326, and a CDR3 region of SEQ ID NO: 327, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 328, a CDR2 region of SEQ ID NO: 329, and a CDR3 region of SEQ ID NO: 330; [0271] 56) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO:

331, a CDR2 region of SEQ ID NO: 332, and a CDR3 region of SEQ ID NO: 333, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 334, a CDR2 region of SEQ ID NO: 335, and a CDR3 region of SEQ ID NO: 336; [0272] 57) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 337, a CDR2 region of SEQ ID NO: 338, and a CDR3 region of SEQ ID NO: 339, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 340, a CDR2 region of SEQ ID NO: 341, and a CDR3 region of SEQ ID NO: 342; [0273] 58) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 343, a CDR2 region of SEQ ID NO: 344, and a CDR3 region of SEQ ID NO: 345, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 346, a CDR2 region of SEQ ID NO: 347, and a CDR3 region of SEQ ID NO: 348; [0274] 59) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 349, a CDR2 region of SEQ ID NO: 350, and a CDR3 region of SEQ ID NO: 351, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 352, a CDR2 region of SEQ ID NO: 353, and a CDR3 region of SEQ ID NO: 354; [0275] 60) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 355, a CDR2 region of SEQ ID NO: 356, and a CDR3 region of SEQ ID NO: 357, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 358, a CDR2 region of SEQ ID NO: 359, and a CDR3 region of SEQ ID NO: 360; [0276] 61) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 361, a CDR2 region of SEQ ID NO: 362, and a CDR3 region of SEQ ID NO: 363, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 364, a CDR2 region of SEQ ID NO: 365, and a CDR3 region of SEQ ID NO: 366; [0277] 62) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 367, a CDR2 region of SEQ ID NO: 368, and a CDR3 region of SEQ ID NO: 369, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 370, a CDR2 region of SEQ ID NO: 371, and a CDR3 region of SEQ ID NO: 372; [0278] 63) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 373, a CDR2 region of SEQ ID NO: 374, and a CDR3 region of SEQ ID NO: 375, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 376, a CDR2 region of SEQ ID NO: 377, and a CDR3 region of SEQ ID NO: 378; [0279] 64) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 379, a CDR2 region of SEQ ID NO: 380, and a CDR3 region of SEQ ID NO: 381, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 382, a CDR2 region of SEQ ID NO: 383, and a CDR3 region of SEQ ID NO: 384; [0280] 65) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 385, a CDR2 region of SEQ ID NO: 386, and a CDR3 region of SEQ ID NO: 387, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 388, a CDR2 region of SEQ ID NO: 389, and a CDR3 region of SEQ ID NO: 390; [0281] 66) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 391, a CDR2 region of SEQ ID NO: 392, and a CDR3 region of SEQ ID NO: 393, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 394, a CDR2 region of SEQ ID NO: 395, and a CDR3 region of SEQ ID NO: 396; [0282] 67) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 397, a CDR2 region of SEQ ID NO: 398, and a CDR3 region of SEQ ID NO: 399, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 400, a CDR2 region of SEQ ID NO: 401, and a CDR3 region of SEQ ID NO: 402; [0283] 68) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 403, a CDR2 region of SEQ ID NO: 404, and a CDR3 region of SEQ ID NO: 405, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 406, a CDR2 region of SEQ ID NO: 407, and a CDR3 region of SEQ ID NO: 408; [0284] 69) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 409, a CDR2 region of SEQ ID NO: 410, and a CDR3 region of SEQ ID NO: 411, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 412, a CDR2 region of SEQ ID NO: 413, and a CDR3 region of SEQ ID NO: 414; [0285] 70) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 415, a CDR2 region of SEQ ID NO: 416, and a CDR3 region of SEQ ID NO: 417, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 418, a CDR2 region of SEQ ID NO: 419, and a CDR3 region of SEQ ID NO: 420; [0286] 71) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 421, a CDR2 region of SEQ ID NO: 422, and a CDR3 region of SEQ ID NO: 423, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 424, a CDR2 region of SEQ ID NO: 425, and a CDR3 region of SEQ ID NO: 426; [0287] 72) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 427, a CDR2 region of SEQ ID NO: 428, and a CDR3 region of SEQ ID NO: 429, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 430, a CDR2 region of SEQ ID NO: 431, and a CDR3 region of SEQ ID NO: 432; [0288] 73) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 433, a CDR2 region of SEQ ID NO: 434, and a CDR3 region of SEQ ID NO: 435, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 436, a CDR2 region of SEQ ID NO: 437, and a CDR3 region of SEQ ID NO: 438; [0289] 74) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 439, a CDR2 region of SEQ ID NO: 440, and a CDR3 region of SEQ ID NO: 441, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 442, a CDR2 region of SEQ ID NO: 443, and a CDR3 region of SEQ ID NO: 444; [0290] 75) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 445, a CDR2 region of SEQ ID NO: 446, and a CDR3 region of SEQ ID NO: 447, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 448, a CDR2 region of SEQ ID NO: 449, and a CDR3 region of SEQ ID NO: 450; [0291] 76) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 451, a CDR2 region of SEQ ID NO: 452, and a CDR3 region of SEQ ID NO: 453, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 454, a CDR2 region of SEQ ID NO: 455, and a CDR3 region of SEQ ID NO:

456; [0292] 77) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 457, a CDR2 region of SEQ ID NO: 458, and a CDR3 region of SEQ ID NO: 459, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 460, a CDR2 region of SEQ ID NO: 461, and a CDR3 region of SEQ ID NO: 462; [0293] 78) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 463, a CDR2 region of SEQ ID NO: 464, and a CDR3 region of SEQ ID NO: 465, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 466, a CDR2 region of SEQ ID NO: 467, and a CDR3 region of SEQ ID NO: 468; [0294] 79) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 469, a CDR2 region of SEQ ID NO: 470, and a CDR3 region of SEQ ID NO: 471, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 472, a CDR2 region of SEQ ID NO: 473, and a CDR3 region of SEQ ID NO: 474; [0295] 80) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 475, a CDR2 region of SEQ ID NO: 476, and a CDR3 region of SEQ ID NO: 477, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 478, a CDR2 region of SEQ ID NO: 479, and a CDR3 region of SEQ ID NO: 480; [0296] 81) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 481, a CDR2 region of SEQ ID NO: 482, and a CDR3 region of SEQ ID NO: 483, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 484, a CDR2 region of SEQ ID NO: 485, and a CDR3 region of SEQ ID NO: 486; [0297] 82) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 487, a CDR2 region of SEQ ID NO: 488, and a CDR3 region of SEQ ID NO: 489, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 490, a CDR2 region of SEQ ID NO: 491, and a CDR3 region of SEQ ID NO: 492; [0298] 83) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 493, a CDR2 region of SEQ ID NO: 494, and a CDR3 region of SEQ ID NO: 495, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 496, a CDR2 region of SEQ ID NO: 497, and a CDR3 region of SEQ ID NO: 498; [0299] 84) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 499, a CDR2 region of SEQ ID NO: 500, and a CDR3 region of SEQ ID NO: 501, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 502, a CDR2 region of SEQ ID NO: 503, and a CDR3 region of SEQ ID NO: 504; [0300] 85) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 505, a CDR2 region of SEQ ID NO: 506, and a CDR3 region of SEQ ID NO: 507, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 508, a CDR2 region of SEQ ID NO: 509, and a CDR3 region of SEQ ID NO: 510; [0301] 86) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 511, a CDR2 region of SEQ ID NO: 512, and a CDR3 region of SEQ ID NO: 513, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 514, a CDR2 region of SEQ ID NO: 515, and a CDR3 region of SEQ ID NO: 516; [0302] 87) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 517, a CDR2 region of SEQ ID NO: 518, and a CDR3 region of SEQ ID NO: 519, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 520, a CDR2 region of SEQ ID NO: 521, and a CDR3 region of SEQ ID NO: 522; [0303] 88) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 523, a CDR2 region of SEQ ID NO: 524, and a CDR3 region of SEQ ID NO: 525, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 526, a CDR2 region of SEQ ID NO: 527, and a CDR3 region of SEQ ID NO: 528; [0304] 89) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 529, a CDR2 region of SEQ ID NO: 530, and a CDR3 region of SEQ ID NO: 531, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 532, a CDR2 region of SEQ ID NO: 533, and a CDR3 region of SEQ ID NO: 534; [0305] 90) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 535, a CDR2 region of SEQ ID NO: 536, and a CDR3 region of SEQ ID NO: 537, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 538, a CDR2 region of SEQ ID NO: 539, and a CDR3 region of SEQ ID NO: 540; [0306] 91) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 541, a CDR2 region of SEQ ID NO: 542, and a CDR3 region of SEQ ID NO: 543, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 544, a CDR2 region of SEQ ID NO: 545, and a CDR3 region of SEQ ID NO: 546; [0307] 92) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 547, a CDR2 region of SEQ ID NO: 548, and a CDR3 region of SEQ ID NO: 549, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 550, a CDR2 region of SEQ ID NO: 551, and a CDR3 region of SEQ ID NO: 552; [0308] 93) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 553, a CDR2 region of SEQ ID NO: 554, and a CDR3 region of SEQ ID NO: 555, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 556, a CDR2 region of SEQ ID NO: 557, and a CDR3 region of SEQ ID NO: 558; [0309] 94) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 559, a CDR2 region of SEQ ID NO: 560, and a CDR3 region of SEQ ID NO: 561, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 562, a CDR2 region of SEQ ID NO: 563, and a CDR3 region of SEQ ID NO: 564; [0310] 95) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 565, a CDR2 region of SEQ ID NO: 566, and a CDR3 region of SEQ ID NO: 567, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 568, a CDR2 region of SEQ ID NO: 569, and a CDR3 region of SEQ ID NO: 570; [0311] 96) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 571, a CDR2 region of SEQ ID NO: 572, and a CDR3 region of SEQ ID NO: 573, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 574, a CDR2 region of SEQ ID NO: 575, and a CDR3 region of SEQ ID NO: 576; [0312] 97) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 577, a CDR2 region of SEQ ID NO: 578, and a CDR3 region of SEQ ID NO: 579, and b) a heavy-chain variable region

comprising a CDR1 region of SEQ ID NO: 580, a CDR2 region of SEQ ID NO: 581, and a CDR3 region of SEQ ID NO: 582; [0313] 98) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 583, a CDR2 region of SEQ ID NO: 584, and a CDR3 region of SEQ ID NO: 585, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 586, a CDR2 region of SEQ ID NO: 587, and a CDR3 region of SEQ ID NO: 588; [0314] 99) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 589, a CDR2 region of SEQ ID NO: 590, and a CDR3 region of SEQ ID NO: 591, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 592, a CDR2 region of SEQ ID NO: 593, and a CDR3 region of SEQ ID NO: 594; [0315] 100) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 595, a CDR2 region of SEQ ID NO: 596, and a CDR3 region of SEQ ID NO: 597, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 598, a CDR2 region of SEQ ID NO: 599, and a CDR3 region of SEQ ID NO: 600; [0316] 101) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 601, a CDR2 region of SEQ ID NO: 602, and a CDR3 region of SEQ ID NO: 603, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 604, a CDR2 region of SEQ ID NO: 605, and a CDR3 region of SEQ ID NO: 606; [0317] 102) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 607, a CDR2 region of SEQ ID NO: 608, and a CDR3 region of SEQ ID NO: 609, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 610, a CDR2 region of SEQ ID NO: 611, and a CDR3 region of SEQ ID NO: 612; [0318] 103) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 613, a CDR2 region of SEQ ID NO: 614, and a CDR3 region of SEQ ID NO: 615, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 616, a CDR2 region of SEQ ID NO: 617, and a CDR3 region of SEQ ID NO: 618; [0319] 104) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 619, a CDR2 region of SEQ ID NO: 620, and a CDR3 region of SEQ ID NO: 621, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 622, a CDR2 region of SEQ ID NO: 623, and a CDR3 region of SEQ ID NO: 624; [0320] 105) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 625, a CDR2 region of SEQ ID NO: 626, and a CDR3 region of SEQ ID NO: 627, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 628, a CDR2 region of SEQ ID NO: 629, and a CDR3 region of SEQ ID NO: 630; [0321] 106) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 631, a CDR2 region of SEQ ID NO: 632, and a CDR3 region of SEQ ID NO: 633, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 634, a CDR2 region of SEQ ID NO: 635, and a CDR3 region of SEQ ID NO: 636; [0322] 107) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 637, a CDR2 region of SEQ ID NO: 638, and a CDR3 region of SEQ ID NO: 639, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 640, a CDR2 region of SEQ ID NO: 641, and a CDR3 region of SEQ ID NO: 642; [0323] 108) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 643, a CDR2 region of SEQ ID NO: 644, and a CDR3 region of SEQ ID NO: 645, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 646, a CDR2 region of SEQ ID NO: 647, and a CDR3 region of SEQ ID NO: 648; [0324] 109) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 649, a CDR2 region of SEQ ID NO: 650, and a CDR3 region of SEQ ID NO: 651, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 652, a CDR2 region of SEQ ID NO: 653, and a CDR3 region of SEQ ID NO: 654; [0325] 110) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 655, a CDR2 region of SEQ ID NO: 656, and a CDR3 region of SEQ ID NO: 657, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 658, a CDR2 region of SEQ ID NO: 659, and a CDR3 region of SEQ ID NO: 660; [0326] 111) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 661, a CDR2 region of SEQ ID NO: 662, and a CDR3 region of SEQ ID NO: 663, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 664, a CDR2 region of SEQ ID NO: 665, and a CDR3 region of SEQ ID NO: 666; [0327] 112) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 667, a CDR2 region of SEQ ID NO: 668, and a CDR3 region of SEQ ID NO: 669, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 670, a CDR2 region of SEQ ID NO: 671, and a CDR3 region of SEQ ID NO: 672; [0328] 113) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 673, a CDR2 region of SEQ ID NO: 674, and a CDR3 region of SEQ ID NO: 675, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 676, a CDR2 region of SEQ ID NO: 677, and a CDR3 region of SEQ ID NO: 678; [0329] 114) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 679, a CDR2 region of SEQ ID NO: 680, and a CDR3 region of SEQ ID NO: 681, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 682, a CDR2 region of SEQ ID NO: 683, and a CDR3 region of SEQ ID NO: 684; [0330] 115) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 685, a CDR2 region of SEQ ID NO: 686, and a CDR3 region of SEQ ID NO: 687, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 688, a CDR2 region of SEQ ID NO: 689, and a CDR3 region of SEQ ID NO: 690; [0331] 116) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 691, a CDR2 region of SEQ ID NO: 692, and a CDR3 region of SEQ ID NO: 693, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 694, a CDR2 region of SEQ ID NO: 695, and a CDR3 region of SEQ ID NO: 696; [0332] 117) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 697, a CDR2 region of SEQ ID NO: 698, and a CDR3 region of SEQ ID NO: 699, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 700, a CDR2 region of SEQ ID NO: 701, and a CDR3 region of SEQ ID NO: 702; [0333] 118) a binding molecule comprising a) a light-chain variable region comprising

a CDR1 region of SEQ ID NO: 703, a CDR2 region of SEQ ID NO: 704, and a CDR3 region of SEQ ID NO: 705, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 706, a CDR2 region of SEQ ID NO: 707, and a CDR3 region of SEQ ID NO: 708; [0334] 119) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 709, a CDR2 region of SEQ ID NO: 710, and a CDR3 region of SEQ ID NO: 711, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 712, a CDR2 region of SEQ ID NO: 713, and a CDR3 region of SEQ ID NO: 714; [0335] 120) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 715, a CDR2 region of SEQ ID NO: 716, and a CDR3 region of SEQ ID NO: 717, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 718, a CDR2 region of SEQ ID NO: 719, and a CDR3 region of SEQ ID NO: 720; [0336] 121) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 721, a CDR2 region of SEQ ID NO: 722, and a CDR3 region of SEQ ID NO: 723, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 724, a CDR2 region of SEQ ID NO: 725, and a CDR3 region of SEQ ID NO: 726; [0337] 122) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 727, a CDR2 region of SEQ ID NO: 728, and a CDR3 region of SEQ ID NO: 729, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 730, a CDR2 region of SEQ ID NO: 731, and a CDR3 region of SEQ ID NO: 732; [0338] 123) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 733, a CDR2 region of SEQ ID NO: 734, and a CDR3 region of SEQ ID NO: 735, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 736, a CDR2 region of SEQ ID NO: 737, and a CDR3 region of SEQ ID NO: 738; [0339] 124) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 739, a CDR2 region of SEQ ID NO: 740, and a CDR3 region of SEQ ID NO: 741, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 742, a CDR2 region of SEQ ID NO: 743, and a CDR3 region of SEQ ID NO: 744; [0340] 125) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 745, a CDR2 region of SEQ ID NO: 746, and a CDR3 region of SEQ ID NO: 747, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 748, a CDR2 region of SEQ ID NO: 749, and a CDR3 region of SEQ ID NO: 750; [0341] 126) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 751, a CDR2 region of SEQ ID NO: 752, and a CDR3 region of SEQ ID NO: 753, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 754, a CDR2 region of SEQ ID NO: 755, and a CDR3 region of SEQ ID NO: 756; [0342] 127) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 757, a CDR2 region of SEQ ID NO: 758, and a CDR3 region of SEQ ID NO: 759, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 760, a CDR2 region of SEQ ID NO: 761, and a CDR3 region of SEQ ID NO: 762; [0343] 128) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 763, a CDR2 region of SEQ ID NO: 764, and a CDR3 region of SEQ ID NO: 765, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 766, a CDR2 region of SEQ ID NO: 767, and a CDR3 region of SEQ ID NO: 768; [0344] 129) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 769, a CDR2 region of SEQ ID NO: 770, and a CDR3 region of SEQ ID NO: 771, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 772, a CDR2 region of SEQ ID NO: 773, and a CDR3 region of SEQ ID NO: 774; [0345] 130) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 775, a CDR2 region of SEQ ID NO: 776, and a CDR3 region of SEQ ID NO: 777, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 778, a CDR2 region of SEQ ID NO: 779, and a CDR3 region of SEQ ID NO: 780; [0346] 131) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 781, a CDR2 region of SEQ ID NO: 782, and a CDR3 region of SEQ ID NO: 783, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 784, a CDR2 region of SEQ ID NO: 785, and a CDR3 region of SEQ ID NO: 786; [0347] 132) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 787, a CDR2 region of SEQ ID NO: 788, and a CDR3 region of SEQ ID NO: 789, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 790, a CDR2 region of SEQ ID NO: 791, and a CDR3 region of SEQ ID NO: 792; [0348] 133) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 793, a CDR2 region of SEQ ID NO: 794, and a CDR3 region of SEQ ID NO: 795, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 796, a CDR2 region of SEQ ID NO: 797, and a CDR3 region of SEQ ID NO: 798; [0349] 134) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 799, a CDR2 region of SEQ ID NO: 800, and a CDR3 region of SEQ ID NO: 801, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 802, a CDR2 region of SEQ ID NO: 803, and a CDR3 region of SEQ ID NO: 804; [0350] 135) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 805, a CDR2 region of SEQ ID NO: 806, and a CDR3 region of SEQ ID NO: 807, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 808, a CDR2 region of SEQ ID NO: 809, and a CDR3 region of SEQ ID NO: 810; [0351] 136) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 811, a CDR2 region of SEQ ID NO: 812, and a CDR3 region of SEQ ID NO: 813, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 814, a CDR2 region of SEQ ID NO: 815, and a CDR3 region of SEQ ID NO: 816; [0352] 137) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 817, a CDR2 region of SEQ ID NO: 818, and a CDR3 region of SEQ ID NO: 819, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 820, a CDR2 region of SEQ ID NO: 821, and a CDR3 region of SEQ ID NO: 822; [0353] 138) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 823, a CDR2 region of SEQ ID NO: 824, and a CDR3 region of SEQ ID NO: 825, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 826, a CDR2 region of SEQ ID NO: 827, and a

CDR3 region of SEQ ID NO: 828; [0354] 139) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 829, a CDR2 region of SEQ ID NO: 830, and a CDR3 region of SEQ ID NO: 831, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 832, a CDR2 region of SEQ ID NO: 833, and a CDR3 region of SEQ ID NO: 834; [0355] 140) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 835, a CDR2 region of SEQ ID NO: 836, and a CDR3 region of SEQ ID NO: 837, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 838, a CDR2 region of SEQ ID NO: 839, and a CDR3 region of SEQ ID NO: 840; [0356] 141) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 841, a CDR2 region of SEQ ID NO: 842, and a CDR3 region of SEQ ID NO: 843, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 844, a CDR2 region of SEQ ID NO: 845, and a CDR3 region of SEQ ID NO: 846; [0357] 142) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 847, a CDR2 region of SEQ ID NO: 848, and a CDR3 region of SEQ ID NO: 849, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 850, a CDR2 region of SEQ ID NO: 851, and a CDR3 region of SEQ ID NO: 852; [0358] 143) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 853, a CDR2 region of SEQ ID NO: 854, and a CDR3 region of SEQ ID NO: 855, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 856, a CDR2 region of SEQ ID NO: 857, and a CDR3 region of SEQ ID NO: 858; [0359] 144) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 859, a CDR2 region of SEQ ID NO: 860, and a CDR3 region of SEQ ID NO: 861, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 862, a CDR2 region of SEQ ID NO: 863, and a CDR3 region of SEQ ID NO: 864; [0360] 145) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 865, a CDR2 region of SEQ ID NO: 866, and a CDR3 region of SEQ ID NO: 867, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 868, a CDR2 region of SEQ ID NO: 869, and a CDR3 region of SEQ ID NO: 870; [0361] 146) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 871, a CDR2 region of SEQ ID NO: 872, and a CDR3 region of SEQ ID NO: 873, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 874, a CDR2 region of SEQ ID NO: 875, and a CDR3 region of SEQ ID NO: 876; [0362] 147) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 877, a CDR2 region of SEQ ID NO: 878, and a CDR3 region of SEQ ID NO: 879, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 880, a CDR2 region of SEQ ID NO: 881, and a CDR3 region of SEQ ID NO: 882; [0363] 148) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 883, a CDR2 region of SEQ ID NO: 884, and a CDR3 region of SEQ ID NO: 885, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 886, a CDR2 region of SEQ ID NO: 887, and a CDR3 region of SEQ ID NO: 888; [0364] 149) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 889, a CDR2 region of SEQ ID NO: 890, and a CDR3 region of SEQ ID NO: 891, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 892, a CDR2 region of SEQ ID NO: 893, and a CDR3 region of SEQ ID NO: 894; [0365] 150) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 895, a CDR2 region of SEQ ID NO: 896, and a CDR3 region of SEQ ID NO: 897, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 898, a CDR2 region of SEQ ID NO: 899, and a CDR3 region of SEQ ID NO: 900; [0366] 151) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 901, a CDR2 region of SEQ ID NO: 902, and a CDR3 region of SEQ ID NO: 903, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 904, a CDR2 region of SEQ ID NO: 905, and a CDR3 region of SEQ ID NO: 906; [0367] 152) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 907, a CDR2 region of SEQ ID NO: 908, and a CDR3 region of SEQ ID NO: 909, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 910, a CDR2 region of SEQ ID NO: 911, and a CDR3 region of SEQ ID NO: 912; [0368] 153) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 913, a CDR2 region of SEQ ID NO: 914, and a CDR3 region of SEQ ID NO: 915, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 916, a CDR2 region of SEQ ID NO: 917, and a CDR3 region of SEQ ID NO: 918; [0369] 154) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 919, a CDR2 region of SEQ ID NO: 920, and a CDR3 region of SEQ ID NO: 921, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 922, a CDR2 region of SEQ ID NO: 923, and a CDR3 region of SEQ ID NO: 924; [0370] 155) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 925, a CDR2 region of SEQ ID NO: 926, and a CDR3 region of SEQ ID NO: 927, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 928, a CDR2 region of SEQ ID NO: 929, and a CDR3 region of SEQ ID NO: 930; [0371] 156) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 931, a CDR2 region of SEQ ID NO: 932, and a CDR3 region of SEQ ID NO: 933, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 934, a CDR2 region of SEQ ID NO: 935, and a CDR3 region of SEQ ID NO: 936; [0372] 157) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 937, a CDR2 region of SEQ ID NO: 938, and a CDR3 region of SEQ ID NO: 939, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 940, a CDR2 region of SEQ ID NO: 941, and a CDR3 region of SEQ ID NO: 942; [0373] 158) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 943, a CDR2 region of SEQ ID NO: 944, and a CDR3 region of SEQ ID NO: 945, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 946, a CDR2 region of SEQ ID NO: 947, and a CDR3 region of SEQ ID NO: 948; [0374] 159) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 949, a CDR2 region of SEQ ID NO: 950, and a CDR3 region of SEQ ID NO: 951, and b) a

heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 952, a CDR2 region of SEQ ID NO: 953, and a CDR3 region of SEQ ID NO: 954; [0375] 160) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 955, a CDR2 region of SEQ ID NO: 956, and a CDR3 region of SEQ ID NO: 957, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 958, a CDR2 region of SEQ ID NO: 959, and a CDR3 region of SEQ ID NO: 960; [0376] 161) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 961, a CDR2 region of SEQ ID NO: 962, and a CDR3 region of SEQ ID NO: 963, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 964, a CDR2 region of SEQ ID NO: 965, and a CDR3 region of SEQ ID NO: 966; [0377] 162) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 967, a CDR2 region of SEQ ID NO: 968, and a CDR3 region of SEQ ID NO: 969, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 970, a CDR2 region of SEQ ID NO: 971, and a CDR3 region of SEQ ID NO: 972; [0378] 163) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 973, a CDR2 region of SEQ ID NO: 974, and a CDR3 region of SEQ ID NO: 975, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 976, a CDR2 region of SEQ ID NO: 977, and a CDR3 region of SEQ ID NO: 978; [0379] 164) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 979, a CDR2 region of SEQ ID NO: 980, and a CDR3 region of SEQ ID NO: 981, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 982, a CDR2 region of SEQ ID NO: 983, and a CDR3 region of SEQ ID NO: 984; [0380] 165) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 985, a CDR2 region of SEQ ID NO: 986, and a CDR3 region of SEQ ID NO: 987, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 988, a CDR2 region of SEQ ID NO: 989, and a CDR3 region of SEQ ID NO: 990; [0381] 166) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 991, a CDR2 region of SEQ ID NO: 992, and a CDR3 region of SEQ ID NO: 993, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 994, a CDR2 region of SEQ ID NO: 995, and a CDR3 region of SEQ ID NO: 996; [0382] 167) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 997, a CDR2 region of SEQ ID NO: 998, and a CDR3 region of SEQ ID NO: 999, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 1,000, a CDR2 region of SEQ ID NO: 1,001, and a CDR3 region of SEQ ID NO: 1,002; [0383] 168) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 1,003, a CDR2 region of SEQ ID NO: 1,004, and a CDR3 region of SEQ ID NO: 1,005, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 1,006, a CDR2 region of SEQ ID NO: 1,007, and a CDR3 region of SEQ ID NO: 1,008; [0384] 169) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 1,009, a CDR2 region of SEQ ID NO: 1,010, and a CDR3 region of SEQ ID NO: 1,011, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 1,012, a CDR2 region of SEQ ID NO: 1,013, and a CDR3 region of SEQ ID NO: 1,014; [0385] 170) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 1,015, a CDR2 region of SEQ ID NO: 1,016, and a CDR3 region of SEQ ID NO: 1,017, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 1,018, a CDR2 region of SEQ ID NO: 1,019, and a CDR3 region of SEQ ID NO: 1,020; [0386] 171) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 1,021, a CDR2 region of SEQ ID NO: 1,022, and a CDR3 region of SEQ ID NO: 1,023, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 1,024, a CDR2 region of SEQ ID NO: 1,025, and a CDR3 region of SEQ ID NO: 1,026; [0387] 172) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 1,027, a CDR2 region of SEQ ID NO: 1,028, and a CDR3 region of SEQ ID NO: 1,029, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 1,030, a CDR2 region of SEQ ID NO: 1,031, and a CDR3 region of SEQ ID NO: 1,032; [0388] 173) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 1,033, a CDR2 region of SEQ ID NO: 1,034, and a CDR3 region of SEQ ID NO: 1,035, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 1,036, a CDR2 region of SEQ ID NO: 1,037, and a CDR3 region of SEQ ID NO: 1,038; [0389] 174) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 1,039, a CDR2 region of SEQ ID NO: 1,040, and a CDR3 region of SEQ ID NO: 1,041, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 1,042, a CDR2 region of SEQ ID NO: 1,043, and a CDR3 region of SEQ ID NO: 1,044; [0390] 175) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 1,045, a CDR2 region of SEQ ID NO: 1,046, and a CDR3 region of SEQ ID NO: 1,047, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 1,048, a CDR2 region of SEQ ID NO: 1,049, and a CDR3 region of SEQ ID NO: 1,050; [0391] 176) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 1,051, a CDR2 region of SEQ ID NO: 1,052, and a CDR3 region of SEQ ID NO: 1,053, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 1,054, a CDR2 region of SEQ ID NO: 1,055, and a CDR3 region of SEQ ID NO: 1,056; [0392] 177) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 1,057, a CDR2 region of SEQ ID NO: 1,058, and a CDR3 region of SEQ ID NO: 1,059, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 1,060, a CDR2 region of SEQ ID NO: 1,061, and a CDR3 region of SEQ ID NO: 1,062; [0393] 178) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 1,063, a CDR2 region of SEQ ID NO: 1,064, and a CDR3 region of SEQ ID NO: 1,065, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 1,066, a CDR2 region of SEQ ID NO: 1,067, and a CDR3 region of SEQ ID NO: 1,068; [0394] 179) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 1,069, a CDR2 region of SEQ ID NO: 1,070, and a CDR3 region of SEQ ID NO: 1,071, and b) a heavy-

chain variable region comprising a CDR1 region of SEQ ID NO: 1,072, a CDR2 region of SEQ ID NO: 1,073, and a CDR3 region of SEQ ID NO: 1,074; [0395] 180) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 1,075, a CDR2 region of SEQ ID NO: 1,076, and a CDR3 region of SEQ ID NO: 1,077, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 1,078, a CDR2 region of SEQ ID NO: 1,079, and a CDR3 region of SEQ ID NO: 1,080; [0396] 181) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 1,081, a CDR2 region of SEQ ID NO: 1,082, and a CDR3 region of SEQ ID NO: 1,083, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 1,084, a CDR2 region of SEQ ID NO: 1,085, and a CDR3 region of SEQ ID NO: 1,086; [0397] 182) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 1,087, a CDR2 region of SEQ ID NO: 1,088, and a CDR3 region of SEQ ID NO: 1,089, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 1,090, a CDR2 region of SEQ ID NO: 1,091, and a CDR3 region of SEQ ID NO: 1,092; [0398] 183) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 1,093, a CDR2 region of SEQ ID NO: 1,094, and a CDR3 region of SEQ ID NO: 1,095, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 1,096, a CDR2 region of SEQ ID NO: 1,097, and a CDR3 region of SEQ ID NO: 1,098; [0399] 184) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 1,099, a CDR2 region of SEQ ID NO: 1,100, and a CDR3 region of SEQ ID NO: 1,101, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 1,102, a CDR2 region of SEQ ID NO: 1,103, and a CDR3 region of SEQ ID NO: 1,104; [0400] 185) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 1,105, a CDR2 region of SEQ ID NO: 1,106, and a CDR3 region of SEQ ID NO: 1,107, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 1,108, a CDR2 region of SEQ ID NO: 1,109, and a CDR3 region of SEQ ID NO: 1,110; [0401] 186) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 1,111, a CDR2 region of SEQ ID NO: 1,112, and a CDR3 region of SEQ ID NO: 1,113, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 1,114, a CDR2 region of SEQ ID NO: 1,115, and a CDR3 region of SEQ ID NO: 1,116; [0402] 187) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 1,117, a CDR2 region of SEQ ID NO: 1,118, and a CDR3 region of SEQ ID NO: 1,119, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 1,120, a CDR2 region of SEQ ID NO: 1,121, and a CDR3 region of SEQ ID NO: 1,122; [0403] 188) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 1,123, a CDR2 region of SEQ ID NO: 1,124, and a CDR3 region of SEQ ID NO: 1,125, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 1,126, a CDR2 region of SEQ ID NO: 1,127, and a CDR3 region of SEQ ID NO: 1,128; [0404] 189) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 1,129, a CDR2 region of SEQ ID NO: 1,130, and a CDR3 region of SEQ ID NO: 1,131, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 1,132, a CDR2 region of SEQ ID NO: 1,133, and a CDR3 region of SEQ ID NO: 1,134; and [0405] 190) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 1,135, a CDR2 region of SEQ ID NO: 1,136, and a CDR3 region of SEQ ID NO: 1,137, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 1,138, a CDR2 region of SEQ ID NO: 1,139, and a CDR3 region of SEQ ID NO: 1,140.

[0406] In one embodiment of the present invention, the binding molecule is a binding molecule that binds to a spike protein (S protein) on the surface of SARS-coronavirus-2 (SARS-CoV-2), and comprises a binding molecule that competes with any one binding molecule selected from the group consisting of the following binding molecules 1) to 49), and this binding molecule is included within the scope of the present invention as long as it achieves the purposes and effects of the present invention: [0407] 1) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 7, a CDR2 region of SEQ ID NO: 8, and a CDR3 region of SEQ ID NO: 9, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 10, a CDR2 region of SEQ ID NO: 11, and a CDR3 region of SEQ ID NO: 12; [0408] 2) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 13, a CDR2 region of SEQ ID NO: 14, and a CDR3 region of SEQ ID NO: 15, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 16, a CDR2 region of SEQ ID NO: 17, and a CDR3 region of SEQ ID NO: 18; [0409] 3) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 67, a CDR2 region of SEQ ID NO: 68, and a CDR3 region of SEQ ID NO: 69, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 70, a CDR2 region of SEQ ID NO: 71, and a CDR3 region of SEQ ID NO: 72; [0410] 4) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 85, a CDR2 region of SEQ ID NO: 86, and a CDR3 region of SEQ ID NO: 87, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 88, a CDR2 region of SEQ ID NO: 89, and a CDR3 region of SEQ ID NO: 90; [0411] 5) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 91, a CDR2 region of SEQ ID NO: 92, and a CDR3 region of SEQ ID NO: 93, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 94, a CDR2 region of SEQ ID NO: 95, and a CDR3 region of SEQ ID NO: 96; [0412] 6) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 103, a CDR2 region of SEQ ID NO: 104, and a CDR3 region of SEQ ID NO: 105, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 106, a CDR2 region of SEQ ID NO: 107, and a CDR3 region of SEQ ID NO: 108; [0413] 7) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 109, CDR2 region of SEQ ID NO: 110, and CDR3 region of SEQ ID NO: 111, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 112, a CDR2 region of SEQ ID NO: 113, and a CDR3 region of SEQ ID NO: 114; [0414] 8)

a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 115, a CDR2 region of SEQ ID NO: 116, and a CDR3 region of SEQ ID NO: 117, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 118, a CDR2 region of SEQ ID NO: 119, and a CDR3 region of SEQ ID NO: 120; [0415] 9) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 127, a CDR2 region of SEQ ID NO: 128, and a CDR3 region of SEQ ID NO: 129, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 130, a CDR2 region of SEQ ID NO: 131, and a CDR3 region of SEQ ID NO: 132; [0416] 10) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 133, a CDR2 region of SEQ ID NO: 134, and a CDR3 region of SEQ ID NO: 135, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 136, a CDR2 region of SEQ ID NO: 137, and a CDR3 region of SEQ ID NO: 138; [0417] 11) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 139, a CDR2 region of SEQ ID NO: 140, and a CDR3 region of SEQ ID NO: 141, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 142, a CDR2 region of SEQ ID NO: 143, and a CDR3 region of SEQ ID NO: 144; [0418] 12) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 151, a CDR2 region of SEQ ID NO: 152, and a CDR3 region of SEQ ID NO: 153, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 154, a CDR2 region of SEQ ID NO: 155, and a CDR3 region of SEQ ID NO: 156; [0419] 13) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 181, a CDR2 region of SEQ ID NO: 182, and a CDR3 region of SEQ ID NO: 183, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 184, a CDR2 region of SEQ ID NO: 185, and a CDR3 region of SEQ ID NO: 186; [0420] 14) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 187, a CDR2 region of SEQ ID NO: 188, and a CDR3 region of SEQ ID NO: 189, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 190, a CDR2 region of SEQ ID NO: 191, and a CDR3 region of SEQ ID NO: 192; [0421] 15) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 193, a CDR2 region of SEQ ID NO: 194, and a CDR3 region of SEQ ID NO: 195, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 196, a CDR2 region of SEQ ID NO: 197, and a CDR3 region of SEQ ID NO: 198; [0422] 16) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 199, a CDR2 region of SEQ ID NO: 200, and a CDR3 region of SEQ ID NO: 201, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 202, a CDR2 region of SEQ ID NO: 203, and a CDR3 region of SEQ ID NO: 204; [0423] 17) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 217, a CDR2 region of SEQ ID NO: 218, and a CDR3 region of SEQ ID NO: 219, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 220, a CDR2 region of SEQ ID NO: 221, and a CDR3 region of SEQ ID NO: 222; [0424] 18) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 253, a CDR2 region of SEQ ID NO: 254, and a CDR3 region of SEQ ID NO: 255, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 256, a CDR2 region of SEQ ID NO: 257, and a CDR3 region of SEQ ID NO: 258; [0425] 19) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 265, a CDR2 region of SEQ ID NO: 266, and a CDR3 region of SEQ ID NO: 267, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 268, a CDR2 region of SEQ ID NO: 269, and a CDR3 region of SEQ ID NO: 270; [0426] 20) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 283, a CDR2 region of SEQ ID NO: 284, and a CDR3 region of SEQ ID NO: 285, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 286, a CDR2 region of SEQ ID NO: 287, and a CDR3 region of SEQ ID NO: 288; [0427] 21) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 295, a CDR2 region of SEQ ID NO: 296, and a CDR3 region of SEQ ID NO: 297, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 298, a CDR2 region of SEQ ID NO: 299, and a CDR3 region of SEQ ID NO: 300; [0428] 22) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 301, a CDR2 region of SEQ ID NO: 302, and a CDR3 region of SEQ ID NO: 303, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 304, a CDR2 region of SEQ ID NO: 305, and a CDR3 region of SEQ ID NO: 306; [0429] 23) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 313, a CDR2 region of SEQ ID NO: 314, and a CDR3 region of SEQ ID NO: 315, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 316, a CDR2 region of SEQ ID NO: 317, and a CDR3 region of SEQ ID NO: 318; [0430] 24) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 319, a CDR2 region of SEQ ID NO: 320, and a CDR3 region of SEQ ID NO: 321, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 322, a CDR2 region of SEQ ID NO: 323, and a CDR3 region of SEQ ID NO: 324; [0431] 25) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 325, a CDR2 region of SEQ ID NO: 326, and a CDR3 region of SEQ ID NO: 327, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 328, a CDR2 region of SEQ ID NO: 329, and a CDR3 region of SEQ ID NO: 330; [0432] 26) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 331, a CDR2 region of SEQ ID NO: 332, and a CDR3 region of SEQ ID NO: 333, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 334, a CDR2 region of SEQ ID NO: 335, and a CDR3 region of SEQ ID NO: 336; [0433] 27) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 349, a CDR2 region of SEQ ID NO: 350, and a CDR3 region of SEQ ID NO: 351, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 352, a CDR2 region of SEQ ID NO: 353, and a CDR3 region of SEQ ID NO: 354; [0434] 28) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 355, a CDR2 region of SEQ ID NO: 356, and a CDR3 region of SEQ ID NO: 357, and b) a heavy-chain variable region

comprising a CDR1 region of SEQ ID NO: 358, a CDR2 region of SEQ ID NO: 359, and a CDR3 region of SEQ ID NO: 360; [0435] 29) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 361, a CDR2 region of SEQ ID NO: 362, and a CDR3 region of SEQ ID NO: 363, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 364, a CDR2 region of SEQ ID NO: 365, and a CDR3 region of SEQ ID NO: 366; [0436] 30) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 391, a CDR2 region of SEQ ID NO: 392, and a CDR3 region of SEQ ID NO: 393, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 394, a CDR2 region of SEQ ID NO: 395, and a CDR3 region of SEQ ID NO: 396; [0437] 31) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 409, a CDR2 region of SEQ ID NO: 410, and a CDR3 region of SEQ ID NO: 411, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 412, a CDR2 region of SEQ ID NO: 413, and a CDR3 region of SEQ ID NO: 414; [0438] 32) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 439, a CDR2 region of SEQ ID NO: 440, and a CDR3 region of SEQ ID NO: 441, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 442, a CDR2 region of SEQ ID NO: 443, and a CDR3 region of SEQ ID NO: 444; [0439] 33) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 445, a CDR2 region of SEQ ID NO: 446, and a CDR3 region of SEQ ID NO: 447, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 448, a CDR2 region of SEQ ID NO: 449, and a CDR3 region of SEQ ID NO: 450; [0440] 34) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 451, a CDR2 region of SEQ ID NO: 452, and a CDR3 region of SEQ ID NO: 453, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 454, a CDR2 region of SEQ ID NO: 455, and a CDR3 region of SEQ ID NO: 456; [0441] 35) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 481, a CDR2 region of SEQ ID NO: 482, and a CDR3 region of SEQ ID NO: 483, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 484, a CDR2 region of SEQ ID NO: 485, and a CDR3 region of SEQ ID NO: 486; [0442] 36) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 487, a CDR2 region of SEQ ID NO: 488, and a CDR3 region of SEQ ID NO: 489, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 490, a CDR2 region of SEQ ID NO: 491, and a CDR3 region of SEQ ID NO: 492; [0443] 37) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 493, a CDR2 region of SEQ ID NO: 494, and a CDR3 region of SEQ ID NO: 495, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 496, a CDR2 region of SEQ ID NO: 497, and a CDR3 region of SEQ ID NO: 498; [0444] 38) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 505, a CDR2 region of SEQ ID NO: 506, and a CDR3 region of SEQ ID NO: 507, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 508, a CDR2 region of SEQ ID NO: 509, and a CDR3 region of SEQ ID NO: 510; [0445] 39) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 511, a CDR2 region of SEQ ID NO: 512, and a CDR3 region of SEQ ID NO: 513, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 514, a CDR2 region of SEQ ID NO: 515, and a CDR3 region of SEQ ID NO: 516; [0446] 40) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 517, a CDR2 region of SEQ ID NO: 518, and a CDR3 region of SEQ ID NO: 519, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 520, a CDR2 region of SEQ ID NO: 521, and a CDR3 region of SEQ ID NO: 522; [0447] 41) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 553, a CDR2 region of SEQ ID NO: 554, and a CDR3 region of SEQ ID NO: 555, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 556, a CDR2 region of SEQ ID NO: 557, and a CDR3 region of SEQ ID NO: 558; [0448] 42) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 559, a CDR2 region of SEQ ID NO: 560, and a CDR3 region of SEQ ID NO: 561, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 562, a CDR2 region of SEQ ID NO: 563, and a CDR3 region of SEQ ID NO: 564; [0449] 43) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 565, a CDR2 region of SEQ ID NO: 566, and a CDR3 region of SEQ ID NO: 567, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 568, a CDR2 region of SEQ ID NO: 569, and a CDR3 region of SEQ ID NO: 570; [0450] 44) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 571, a CDR2 region of SEQ ID NO: 572, and a CDR3 region of SEQ ID NO: 573, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 574, a CDR2 region of SEQ ID NO: 575, and a CDR3 region of SEQ ID NO: 576; [0451] 45) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 583, a CDR2 region of SEQ ID NO: 584, and a CDR3 region of SEQ ID NO: 585, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 586, a CDR2 region of SEQ ID NO: 587, and a CDR3 region of SEQ ID NO: 588; [0452] 46) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 607, a CDR2 region of SEQ ID NO: 608, and a CDR3 region of SEQ ID NO: 609, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 610, a CDR2 region of SEQ ID NO: 611, and a CDR3 region of SEQ ID NO: 612; [0453] 47) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 613, a CDR2 region of SEQ ID NO: 614, and a CDR3 region of SEQ ID NO: 615, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 616, a CDR2 region of SEQ ID NO: 617, and a CDR3 region of SEQ ID NO: 618; [0454] 48) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 619, a CDR2 region of SEQ ID NO: 620, and a CDR3 region of SEQ ID NO: 621, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 622, a CDR2 region of SEQ ID NO: 623, and a CDR3 region of SEQ ID NO: 624; and [0455] 49) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID

NO: 643, a CDR2 region of SEQ ID NO: 644, and a CDR3 region of SEQ ID NO: 645, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 646, a CDR2 region of SEQ ID NO: 647, and a CDR3 region of SEQ ID NO: 648.

[0456] In one embodiment of the present invention, the binding molecule may be a binding molecule comprising a light-chain variable region comprising the following LC CDR1, LC CDR2 and LC CDR3, and a heavy-chain variable region comprising the following HC CDR1, HC CDR2 and HC CDR3.

[0457] The LC CDR1 is: [0458] the sequence SGSX.sub.1SNIGX.sub.2NTVN, where X.sub.1 is S or T, and X.sub.2 is S or T; or [0459] the sequence X.sub.13GSX.sub.14SX.sub.15IX.sub.16X.sub.17X.sub.18X.sub.19VS, where X.sub.13 is S or T, X.sub.14 is S or N, X.sub.15 is N or S, X.sub.16 is G or E, X.sub.17 is N or S, X.sub.18 is N or S, and X.sub.19 is Y or F; or [0460] the sequence RASQSVX.sub.32X.sub.33X.sub.34X.sub.35A, where X.sub.32 is S, N or R, X.sub.33 is S or N, X.sub.34 is Y or N, and X.sub.35 is L or S; or [0461] the sequence RASQSVX.sub.48X.sub.49X.sub.50YLA, where X.sub.48 is S or G, X.sub.49 is S or R, and X.sub.50 is S or N; or [0462] the sequence TGTSSX.sub.62VGX.sub.63YX.sub.64X.sub.65VS, where X.sub.62 is N or D, X.sub.63 is D or G, X.sub.64 is N or S, and X.sub.65 is Y or H; or [0463] the sequence SGX.sub.69X.sub.70SNIGSNX.sub.71VX.sub.72, where X.sub.69 is S or L, X.sub.70 is S or T, X.sub.71 is Y, T or F, and X.sub.72 is Y, H or N; or [0464] the sequence TGTSSDVGGYNYVS; or [0465] the sequence RASQSVSSSYLA; or [0466] the sequence TGX.sub.89X.sub.90SDX.sub.91GGYNX.sub.92X.sub.93S, where X.sub.89 is N or T, X.sub.90 is R or S, X.sub.91 is I or V, X.sub.92 is S or Y, and X.sub.93 is L or V; or [0467] the sequence SGSSSNIGNNYVS; or [0468] the sequence GGNNIGSKSVH; or [0469] the sequence X.sub.106GTX.sub.107SDVGGYNYVS, where X.sub.106 is T or S, and X.sub.107 is S or N; or [0470] the sequence SGSSSNIGSNX.sub.111VN, where X.sub.111 is A or T; or [0471] the sequence TGSSSNIGAGYDVH; or [0472] the sequence RASQSVSSYLA; or [0473] the sequence X.sub.121GSX.sub.122SNIGX.sub.123NX.sub.124VX.sub.125, where X.sub.121 is S or T, X.sub.122 is S or R, X.sub.123 is S or I, X.sub.124 is T or S, and X.sub.125 is S or N; or [0474] the sequence SGSSSNIGSNTVN; or [0475] the sequence TGTSSDIGGYNYVS; or [0476] the sequence RASQSVSX.sub.134X.sub.135LA, where X.sub.134 is S or T, and X.sub.135 is Y or F; or [0477] the sequence TGTSX.sub.142DX.sub.143GX.sub.144YNYVS, where X.sub.142 is T or S, X.sub.143 is I or V, and X.sub.144 is R or A; or [0478] the sequence RASQX.sub.161X.sub.162X.sub.163X.sub.164X.sub.165X.sub.166A, where X.sub.161 is S or G, X.sub.162 is V or I, X.sub.163 is S or R, X.sub.164 is S or N, X.sub.165 is Y, S or D, and X.sub.166 is L or I; or [0479] the sequence X.sub.173ASQX.sub.174ISSYLN, where X.sub.173 is R or Q, and X.sub.174 is S or D; or [0480] the sequence SGSX.sub.177SNIGX.sub.178NYVX.sub.179, where X.sub.177 is S or G, X.sub.178 is N or S, and X.sub.179 is S or H; or [0481] the sequence TGTRGDIGAYDGVS; or [0482] the sequence TGTX.sub.187X.sub.188DX.sub.189GX.sub.190YX.sub.191X.sub.192VS, where X.sub.187 is S or R, X.sub.188 is S or G, X.sub.189 is V or I, X.sub.190 is G or A, X.sub.191 is N or D, and X.sub.192 is Y or G; or [0483] the sequence SGSSSNIGX.sub.205NX.sub.206VX.sub.207, where X.sub.205 is S or N, X.sub.206 is T or Y, and X.sub.207 is N or S; or [0484] the sequence TGTSX.sub.213DVGX.sub.214YNX.sub.215VS, where X.sub.213 is T or S, X.sub.214 is G or S, and X.sub.215 is Y or L; or [0485] the sequence TGTSSDVGX.sub.232YNYVS, where X.sub.232 is N or G; or [0486] the sequence RASQSVSSNLA; or [0487] the sequence RASQGISNSL; or [0488] the sequence RASQSVSSX.sub.258LA, where X.sub.258 is Y or F; or [0489] the sequence SSSTGAVTRGHFPN; or [0490] the sequence CRASQSVSSSYLA; or [0491] the sequence RASQSISSYLN; or [0492] the sequence TGTSSDVGGYNX.sub.295VS, where X.sub.295 is Y or N; or [0493] the sequence SGSSSNIGX.sub.308NYVS, where X.sub.308 is R or N; or [0494] the sequence SGSSSX.sub.337X.sub.338GSNX.sub.339VN, where X.sub.337 is N or D, X.sub.338 is V or I, and X.sub.339 is I or T; or [0495] the sequence SGSSSNIGX.sub.353NYVX.sub.354, where X.sub.353 is N or S, and X.sub.354 is S or Y; or [0496] the sequence SGSSSNIGX.sub.373NYVX.sub.374, where X.sub.373 is N or S, and X.sub.374 is S or N.

[0497] The LC CDR2 is: [0498] the sequence X.sub.3X.sub.4NX.sub.5RPS, where X.sub.3 is S or T, X.sub.4 is N or D, and X.sub.5 Q is R; or [0499] the sequence X.sub.20NX.sub.21X.sub.22RPS, where X.sub.20 is D or R, X.sub.21 is N or S, and X.sub.22 is K, R, Q or V; or [0500] the sequence X.sub.36ASX.sub.37RAT, where X.sub.36 is D or G, and X.sub.37 is N, T or S; or [0501] the sequence X.sub.51ASX.sub.52RAT, where X.sub.51 is G or D, and X.sub.52 is S or T or [0502] the sequence X.sub.66VX.sub.67X.sub.68RPS, where X.sub.66 is D or E, X.sub.67 is T or S, and X.sub.68 is N or D; or [0503] the sequence X.sub.73NX.sub.74X.sub.75RPS, where X.sub.73 is R or S, X.sub.74 is N or D, and X.sub.75 is Q or E; or [0504] the sequence X.sub.83VSNRPS, where X.sub.83 is D or E; or [0505] the sequence GASSRAT; or [0506] the sequence DVX.sub.94NRPS, where X.sub.94 is N or S; or [0507] the sequence DX.sub.98X.sub.99X.sub.100RPS, where X.sub.98 is N or D, X.sub.99 is N or S, and X.sub.100 is K or D; or [0508] the sequence DVX.sub.108KRPS, where X.sub.108 is S or T; or [0509] the sequence X.sub.112NSX.sub.113RPS, where X.sub.112 is G or S, and X.sub.113 is N or Y; or [0510] the sequence DASNRAT; or [0511] the sequence SNNQRPS; or [0512] the sequence X.sub.127NX.sub.128X.sub.129RPS, where X.sub.127 is G or S, X.sub.128 is S or N, and X.sub.129 is N or Q; or [0513] the sequence X.sub.132X.sub.133SKRPS, where X.sub.132 is A or Q, and X.sub.133 is V or D; or [0514] the sequence DASNRA; or [0515] the sequence DVSKRPS; or [0516] the sequence DNNKRPS; or [0517] the sequence X.sub.152NNX.sub.153RPS, where X.sub.152 is S, T or N, and X.sub.153 is Q or R; or [0518] the sequence DX.sub.167SX.sub.168X.sub.169X.sub.170T, where X.sub.167 is A or T, X.sub.168 is N or T, X.sub.169 is R or L, and X.sub.170 is A or E; or [0519] the sequence AASRLES; or [0520] the sequence X.sub.175ASSLX.sub.176S, where X.sub.175 is K or A, and X.sub.176 is E or Q; or [0521] the sequence X.sub.180NX.sub.181X.sub.182RPS, where X.sub.180 is D or R, X.sub.181 is N or S, and X.sub.182 is K or G; or [0522] the sequence AVTQRPS; or [0523] the

sequence X.sub.184NX.sub.185X.sub.186RPS, where X.sub.184 is G or D, X.sub.185 is S or N, and X.sub.186 is Nor K; or [0524] the sequence X.sub.193VX.sub.194X.sub.195RPS, where X.sub.193 is D or A, X.sub.194 is S or T, and X.sub.195 is K or Q; or [0525] the sequence X.sub.208NNX.sub.209RPS, where X.sub.218 is S or D, and X.sub.209 is Q or K; or [0526] the sequence DVSX.sub.216RPS, where X.sub.216 is K or N; or [0527] the sequence DVX.sub.217KRPS, where X.sub.217 is G or S; or [0528] the sequence GNSNRPS; or [0529] the sequence DVSX.sub.233RPS, where X.sub.233 is N or K; or [0530] the sequence X.sub.250AX.sub.251X.sub.252RX.sub.253X.sub.254, where X.sub.250 is W or A, X.sub.251 is S or A, X.sub.252 is T or S, X.sub.253 is E or L, and X.sub.254 is S or E; or [0531] the sequence YDSDRPS; or [0532] the sequence STSNKHS; or [0533] the sequence AASSLQS; or [0534] the sequence DVSX.sub.293RPS, where X.sub.293 is K or N; or [0535] the sequence DVSX.sub.296RPS, where X.sub.296 is N or K; or [0536] the sequence DNNX.sub.309RPS, where X.sub.309 is R or K; or [0537] the sequence X.sub.340NNQRPS, where X.sub.340 is N or S; or [0538] the sequence X.sub.355NNX.sub.356RPS, where X.sub.355 is D or R, and X.sub.356 is K or Q; or [0539] the sequence X.sub.375NNX.sub.376RPS, where X.sub.375 is D or S, and X.sub.376 is K or Q.

[0540] The LC CDR3 is: [0541] the sequence AX.sub.6X.sub.7DDX.sub.8LX.sub.9X.sub.10X.sub.11X.sub.12, where X.sub.6 is A or S, X.sub.7 is W or R, X.sub.8 is S or R, X.sub.9 is N or S, X.sub.10 is A or G, X.sub.11 is S, L, V, Y, P, A or T, X.sub.12 is L or V; or [0542] the sequence X.sub.23X.sub.24WDX.sub.25SLSX.sub.26X.sub.27V, where X.sub.23 is G or A, X.sub.24 is T or A, X.sub.25 is S, N, D or T, X.sub.26 is A, G or S, and X.sub.27 is W or Y; or [0543] the sequence GTWDSSLSAYWV; or [0544] the sequence X.sub.38QX.sub.39X.sub.40X.sub.41X.sub.42PX.sub.43T, where X.sub.38 is Q or H, X.sub.39 is Y or H, X.sub.40 is G, N, Y or H, X.sub.41 is S, N, T, Q or R, X.sub.42 is S, W or V, and X.sub.43 is L, F, I or Q; or [0545] the sequence QQYGSSPSIT; or [0546] the sequence QQYGX.sub.53SPX.sub.54X.sub.55, where X.sub.53 is S or T, X.sub.54 is L or I, and X.sub.55 is T or A; or [0547] the sequence SSYTSGSTPVV; or [0548] the sequence NSYTSSSTWV; or [0549] the sequence X.sub.76X.sub.77WDDX.sub.78LX.sub.79GX.sub.80V, where X.sub.76 is A or S, X.sub.77 is A or T, X.sub.78 is S or T, X.sub.79 is S, N or V, and X.sub.80 is R or K; or [0550] the sequence SSYAGSNYVV; or [0551] the sequence SSYTSSSTX.sub.84X.sub.85V, where X.sub.84 is L or R, and X.sub.85 is G or Y; or [0552] the sequence QQYGSSPX.sub.87T, where X.sub.87 is Y or F; or [0553] the sequence QQYGSSPALT; or [0554] the sequence X.sub.95SYTSX.sub.96X.sub.97TWV, where X.sub.95 is N or S, X.sub.96 is K or S, and X.sub.97 is Nor S; or [0555] the sequence GTWDSSLSAGWV; or [0556] the sequence X.sub.101X.sub.102WDSSX.sub.103X.sub.104X.sub.105VV, where X.sub.101 is G or Q, X.sub.102 is T or V, X.sub.103 is L or S, X.sub.104 is S or D, and X.sub.105 is A or H; or [0557] the sequence SSYTSSX.sub.109TWV, where X.sub.109 is S or R; or [0558] the sequence SSYTSSSTPWV; or [0559] the sequence QSYDSX.sub.114LX.sub.115X.sub.116X.sub.117X.sub.118, where X.sub.114 is S or A, X.sub.115 is S or R, X.sub.116 is D or G, X.sub.117 is V or P, and X.sub.118 is V or L; or [0560] the sequence QQRRNWPPX.sub.119X.sub.120T, where X.sub.119 is V or R, and X.sub.120 is L or I; or [0561] the sequence AAWDDSLNGX.sub.126V, where X.sub.126 is V or Y; or [0562] the sequence AAWDDSLX.sub.130GX.sub.131V, where X.sub.130 is G or N, and X.sub.131 is P or W; or [0563] the sequence SSYTSSSGTLNV; [0564] the sequence QAWDSSTV; [0565] the sequence QQRSNWPPX.sub.136X.sub.137T, where X.sub.136 is A, R, K or M, and X.sub.137 is L, I or Y; or [0566] the sequence SYTSSSTYA; or [0567] the sequence X.sub.145X.sub.146WDX.sub.147SLSX.sub.148X.sub.149X.sub.150, where X.sub.145 is G or E, X.sub.146 is T or A, X.sub.147 is S or T, X.sub.148 is A or D, X.sub.149 is V or G, and X.sub.150 is V or L; or [0568] the sequence AAWDDSLX.sub.154GX.sub.155V, where X.sub.154 is N or S, and X.sub.155 is L, P, W or V; or [0569] the sequence or AAWDDSLNGX.sub.156VV, where X.sub.156 is S or H; or [0570] the sequence QQYYX.sub.171TPX.sub.172T, where X.sub.171 is S or T, and X.sub.172 is F or I; or [0571] the sequence QQSYSTWT; or [0572] the sequence AAWDDSLX.sub.183GWV, where X.sub.183 is N or S; or [0573] the sequence AAWDDSLNGVV; or [0574] the sequence SSYTSSSSWV; or [0575] the sequence QSYDSSLSGLWV; or [0576] the sequence QSYDSSLSAWV; or [0577] the sequence SSYTX.sub.196SSX.sub.197WV, where X.sub.196 is T or S, and X.sub.197 is T or S; or [0578] the sequence AAWDDSLX.sub.210GPV, where X.sub.210 is N or S; or [0579] the sequence SSYTSSSTLV; or [0580] the sequence SSYTSSSTX.sub.218V, where X.sub.218 is W or L; or [0581] the sequence QSYDSSLSGX.sub.225WV, where X.sub.225 is P or S; or [0582] the sequence SSYTSSX.sub.234TX.sub.235V, where X.sub.234 is G or S, and X.sub.235 is L or Y; or [0583] the sequence QSYDSSLSGWV; or [0584] the sequence LQYFTIPWT; or [0585] the sequence SQQYYSTPYT; or [0586] the sequence QQYGSSPPIT; or [0587] the sequence QQRSNWPPSIT; or [0588] the sequence QVWDSSSDHWV; or [0589] the sequence LLYDAGAPGWV; or [0590] the sequence GAWDSSLSTPNW; [0591] the sequence AAWDDSLNGWV; [0592] the sequence QQYGSSPX.sub.269T, where X.sub.269 is Y or P; or [0593] the sequence QQSYSTPLT; or [0594] the sequence QQSYSTPX.sub.275T, where X.sub.275 is F or L; or [0595] the sequence QSYDSSLSGPNWV; or [0596] the sequence QSYDSRLRAVV; or [0597] the sequence QSYDSSLSGX.sub.294V, where X.sub.294 is V or P; or [0598] the sequence SSYTSSSPWV; or [0599] the sequence GTWDSSLSAVX.sub.310, where X.sub.310 is A or V; or [0600] the sequence GTWDSSLSAX.sub.321V, where X.sub.321 is G or V; or [0601] the sequence AAWDDSLNX.sub.341WV, where X.sub.341 is A or G; or [0602] the sequence X.sub.357X.sub.358WDX.sub.359SLSX.sub.360X.sub.361X.sub.362, where X.sub.357 is G or A, X.sub.358 is T or A, X.sub.359 is S or D, X.sub.360 is A or G, X.sub.361 is G or W, and X.sub.362 is P or V; or [0603] the sequence X.sub.377TWDX.sub.378SLX.sub.379X.sub.380X.sub.381V, where X.sub.377 is G or A, X.sub.378 is S or D, X.sub.379 is S or N, X.sub.380 is A or G, and X.sub.381 is G or Q.

[0604] The HC CDR1 is: [0605] the sequence GYYWS; or [0606] the sequence X.sub.28YYMH, where X.sub.28 is S or G; or [0607] the sequence X.sub.44SSYYWG, where X.sub.44 is S or G; or [0608] the sequence

SX.sub.56X.sub.57YYWX.sub.58, where X.sub.56 is S or G, X.sub.57 is S or G, and X.sub.58 is G or S; or [0609] the sequence SSSYYWG; or [0610] the sequence SYAIS; or [0611] the sequence SYAMX.sub.86, where X.sub.86 is S or N; or [0612] the sequence SSPMH; or [0613] the sequence DYGMH; or [0614] the sequence X.sub.110YAMH, where X.sub.110 is S or G; or [0615] the sequence SYGIS; or [0616] the sequence TYGMH; or [0617] the sequence SYAIX.sub.138, where X.sub.138 is S or I; or [0618] the sequence EVAIH; or [0619] the sequence RYAMS; or [0620] the sequence SX.sub.157WIX.sub.158, where X.sub.157 is H or Y, and X.sub.158 is A, V or G; or [0621] the sequence DYYIQ; or [0622] the sequence SYAMH; or [0623] the sequence SNYMS; or [0624] the sequence ELSX.sub.198H, where X.sub.198 is I or M; or [0625] the sequence X.sub.211YAMS, where X.sub.211 is S or R; or [0626] the sequence NYGMH; or [0627] the sequence X.sub.219YAIS, where X.sub.219 is F or R; or [0628] the sequence RYAIX.sub.226, where X.sub.226 is N or S; or [0629] the sequence ELSIH; or [0630] the sequence NYGIS; or [0631] the sequence NAWMX.sub.255, where X.sub.255 is S or T; or [0632] the sequence DYAMS; or [0633] the sequence SYYIH; or [0634] the sequence SYPMH; or [0635] the sequence X.sub.260X.sub.261AMX.sub.262, where X.sub.260 is S or N, X.sub.261 is F or Y, and X.sub.262 is H or N; or [0636] the sequence NYVIN; or [0637] the sequence SNYMX.sub.270, where X.sub.270 is T or S, or [0638] the sequence SX.sub.276AX.sub.277X.sub.278, where X.sub.276 is Y or S, X.sub.277 is M or I, and X.sub.278 is H or N, or [0639] the sequence TQYLH; or [0640] the sequence RGDYWG; or [0641] the sequence THALS; or [0642] the sequence DYAMH; or [0643] the sequence SYDIS; or [0644] the sequence SYAX.sub.297S, where X.sub.297 is M or I; or [0645] the sequence SYX.sub.311X.sub.312X.sub.313, where X.sub.311 is Y or A, X.sub.312 is M or I, and X.sub.313 is H or I; or [0646] the sequence SX.sub.322X.sub.323IX.sub.324, where X.sub.322 is N or Y, X.sub.323 is W or V, and X.sub.324 is A or S; or [0647] the sequence NHWIA; or [0648] the sequence NYAIN; or [0649] the sequence TSGVGVG; or [0650] the sequence ELPIH; or [0651] the sequence DYX.sub.382MX.sub.383, where X.sub.382 is G or W, and X.sub.383 is H or S.

[0652] The HC CDR2 is: [0653] the sequence EINHSGSTNYNPSLKS; or [0654] the sequence X.sub.29INRSGGSTIYAQTFQX.sub.30, where X.sub.29 is I or V, X.sub.30 is G or S; or [0655] the sequence X.sub.45IX.sub.46YSGSTYYNPSLKS, where X.sub.45 is S or N, and X.sub.46 is Y or F; or [0656] the sequence X.sub.59IX.sub.60YSGSTYYNPSLKS, where X.sub.59 is S, Y or N, and X.sub.60 is Y or F; or [0657] the sequence NIFYSGSTYYNPSLKS; [0658] the sequence GIIPIFGTANYAQX.sub.81FQX.sub.82, where X.sub.81 is K or R, and X.sub.82 is G or D; or [0659] the sequence AISGSGGTTYYADSVKG; or [0660] the sequence VISYX.sub.88GSNKYYADSVKG, where X.sub.88 is D or G; or [0661] the sequence VISYDGSNKYYADSVKG; or [0662] the sequence AISYDGSNKYYADSVKG; or [0663] the sequence VISYDGSHKNYADSVKG; or [0664] the sequence GIIPILATTKFAQKFQG; or [0665] the sequence GIIPIFGTANYAQKFQG; or [0666] the sequence VISYDGFNKYYADSVKG; [0667] the sequence GFDPEDGETSYAQKFQG; or [0668] the sequence AISGSGGX.sub.151TYYADSVKG, where X.sub.151 is S or T; or [0669] the sequence X.sub.159IYPGDSDSRYSPSFQG, where X.sub.159 is I or T; or [0670] the sequence WINPNSGDTNYAHKFQG; or [0671] the sequence GIIPMFGTTNYAQKFQG; or [0672] the sequence AISGSGGSTYYADSVKG; or [0673] the sequence VIYPGGSTFFADSVQG; or [0674] the sequence GFDPEDX.sub.199ETIYAQKFQG, where X.sub.199 is G or A; or [0675] the sequence AISGSGGX.sub.212TYYADSVKG, where X.sub.212 is D or S; or [0676] the sequence VMSYDGSNKYYADSVKG; or [0677] the sequence GIIPX.sub.220FGX.sub.221X.sub.222X.sub.223YAQX.sub.224FQD, where X.sub.220 is L or I, X.sub.221 is T or K, X.sub.222 is A or V, X.sub.223 is K or N, and X.sub.224 is R or K; or [0678] the sequence GIIPX.sub.227X.sub.228GTX.sub.229X.sub.230YX.sub.231QKFQG, where X.sub.227 is L or I, X.sub.228 is L or F, X.sub.229 is A or G, X.sub.230 is D or N, and X.sub.231 is P or A; or [0679] the sequence GFDPEX.sub.236X.sub.237ETIX.sub.238AQX.sub.239FQG, where X.sub.236 is N or D, X.sub.237 is G or A, X.sub.238 is H or Y, and X.sub.239 is R or K; or [0680] the sequence X.sub.246ISX.sub.247X.sub.248NGNTX.sub.249YAQKLQG, where X.sub.246 is G or W, X.sub.247 is S or A, X.sub.248 is H or Y, and X.sub.249 is K or N; or [0681] the sequence RIKTKTDGGTTDYAAPVKG; or [0682] the sequence GIIPIFGTX.sub.259NYAQKFQG, where X.sub.259 is T or A; or [0683] the sequence VISGSGGSTSNADSVKG; or [0684] the sequence FINPSDVTTYYAQKFQG; or [0685] the sequence VISYDGSLKYYVDSVKG; or [0686] the sequence X.sub.263ISX.sub.264X.sub.265GX.sub.266X.sub.267X.sub.268YYADSVKG, where X.sub.263 is V or T, X.sub.264 is F or G, X.sub.265 is D or S, X.sub.266 is S or G, X.sub.267 is N or S, and X.sub.268 is K or T; or [0687] the sequence GFIPVFGIADYAQKFQG; or [0688] the sequence X.sub.271IYPGGSTX.sub.272X.sub.273ADSVX.sub.274G, where X.sub.271 is I or V, X.sub.272 is Y or F, X.sub.273 is Y or F, and X.sub.274 is K or Q; or [0689] the sequence VISYDGINKYYADSVKG; or [0690] the sequence GIIPIFGTVNYAQKFQG; or [0691] the sequence X.sub.286IX.sub.287PX.sub.288X.sub.289GX.sub.290X.sub.291X.sub.292YAQKFQG, where X.sub.286 is G or I, X.sub.287 is I or N, X.sub.288 is F or Y, X.sub.289 is F or G, X.sub.290 is T or S, X.sub.291 is S or T, and X.sub.292 is N or T; or [0692] the sequence SIYHSGSTYYNPSLKS; or [0693] the sequence GIIPIFGPADYAQKFQG; or [0694] the sequence GISWNSGTIGYADSVKG; or [0695] the sequence GIIPILGIPNYAQKFQG; or [0696] the sequence GIX.sub.298X.sub.299X.sub.300X.sub.301GX.sub.302TX.sub.303YAX.sub.304X.sub.305X.sub.306X.sub.307G, where X.sub.295 is S or I, X.sub.299 is G or P, X.sub.300 is S or M, X.sub.301 is G or F, X.sub.302 is S or T, X.sub.303 is Y or N, X.sub.304 is D or Q, X.sub.305 is S or K, X.sub.306 is V or F, and X.sub.307 is K or Q; or [0697] the sequence X.sub.314IX.sub.315PX.sub.316X.sub.317GX.sub.318X.sub.319X.sub.320YAQKFQG, where X.sub.314 is I or G, X.sub.315 is N or I, X.sub.316 is S or I, X.sub.317 is G or F, X.sub.318 is S or T, X.sub.319 is T or A, and X.sub.320 is S or N; or [0698] the sequence

X.sub.325IX.sub.326PX.sub.327X.sub.328X.sub.329X.sub.330X.sub.331X.sub.332X.sub.333X.sub.334X.sub.335X.sub.336FQG where X.sub.325 is I or R, X.sub.326 is Y or I, X.sub.327 is G or I, X.sub.328 is D or F, X.sub.329 is S or G, X.sub.330 is D or T, X.sub.331 is T or V, X.sub.332 is R or K, X.sub.333 is N or Y, X.sub.334 is S or A, X.sub.335 is P or Q, and X.sub.336 is S or K; or [0699] the sequence X.sub.342IX.sub.343PX.sub.344X.sub.345X.sub.346X.sub.347X.sub.348X.sub.349YX.sub.350X.sub.351X.sub.352FQG, where X.sub.342 is I or G, X.sub.343 is Y or I, X.sub.344 is Y or I, X.sub.345 is D or F, X.sub.346 is S or G, X.sub.347 is D or T, X.sub.348 is T or A, X.sub.349 is K or N, X.sub.350 is S or A, X.sub.351 is P or Q, and X.sub.352 is S or K; or [0700] the sequence LIDWDDNKYYTTSLKT; or [0701] the sequence RFDPEDGETIYAQNFQG; or [0702] the sequence X.sub.384IX.sub.385X.sub.386DGSX.sub.387KYYX.sub.388DSVKG, where X.sub.384 is A or N, X.sub.385 is S or K, X.sub.386 is Y or E, X.sub.387 is N or E, and X.sub.388 is A or V.

[0703] The HC CDR3 is: [0704] the sequence GRYSSNWYEAWTPRGIGMDV; or [0705] the sequence GGRHSLDX.sub.31, where X.sub.31 is V or A; or [0706] the sequence GSRGYYDX.sub.47LTGYSTGGFDY, where X.sub.47 is F or I; or [0707] the sequence GSRGYYDX.sub.61LTGYSTGGFDY, where X.sub.61 is F or I; or [0708] the sequence GSRGYYDILTGYSTGGFDY; or [0709] the sequence DGVVVPAVMYDTTDPYYYGMDV; or [0710] the sequence APSDLSFIWTGYYSEYYFDY; [0711] the sequence EIALNNYYGMDV; or [0712] the sequence DSGLYGSGWSTYQYYAMDV; or [0713] the sequence DNCGGDCGGGMDV; or [0714] the sequence GWGLRLFGEFSVWFDP; or [0715] the sequence VEGYDSSGYYLDY; or [0716] the sequence RYSSNWYEAWTPRGIGMDV; or [0717] the sequence SLGGNYYYGMDV; or [0718] the sequence VX.sub.139GYDX.sub.140SGYYQX.sub.141Y, where X.sub.139 is T or S, X.sub.140 is S or G, and X.sub.141 is D or E; or [0719] the sequence GPVLGLSKWLEFDP; or [0720] the sequence GPRGQDYGDYGFLDY; or [0721] the sequence GPNX.sub.160YNWFDS, where X.sub.160 is L or I; or [0722] the sequence GGSYYNVMYWFDP; or [0723] the sequence ARGGSYLYGMDV; or [0724] the sequence DPTSRSTYYYYSGSYYP; or [0725] the sequence SYDFLTDYTDAFDI; [0726] the sequence SPAX.sub.200X.sub.201X.sub.202X.sub.203X.sub.204WFDP, where X.sub.200 is V or I, X.sub.201 is T or I, X.sub.202 is T or R, X.sub.203 is A or V, and X.sub.204 is G or D; or [0727] the sequence VRYYDFWSGWDVMDV; or [0728] the sequence PDDSSGYYPDY; or [0729] the sequence GGWIYRGNWFDP; or [0730] the sequence GGSTWYGGNWFDP; or [0731] the sequence TLYYYDRSGNARTDDYFDH; or [0732] the sequence SLYYYDRSGYPISEDYFDY; or [0733] the sequence SX.sub.240X.sub.241X.sub.242X.sub.243X.sub.244AX.sub.245WFDP, where X.sub.240 is T or P, X.sub.241 is P or A, X.sub.242 is M or V, X.sub.243 is I or T, X.sub.244 is R or T, and X.sub.245 is S or G; or [0734] the sequence EGGYYYGSGSYYNPRFAFDI; or [0735] the sequence PRGYSGYGSNWYF; or [0736] the sequence X.sub.256SX.sub.257PDY, where X.sub.255 is F or H, and X.sub.257 is T or R; or [0737] the sequence DPTGWYSGYFDY; or [0738] the sequence VGTYDSSGYSFDY; or [0739] the sequence VYCGDDCYPVVGTPGDAFDI; or [0740] the sequence SRIAPTEDFFDY; or [0741] the sequence DSSCSGGSCFDY; or [0742] the sequence GDYYGSGSYYNPSPFFDY; or [0743] the sequence GYALNP; or [0744] the sequence SGLFDWLLPRSRHRDYFDY; or [0745] the sequence DLPLTGTTLDY; or [0746] the sequence X.sub.279X.sub.280X.sub.281X.sub.282X.sub.283X.sub.284X.sub.285YGMDV, where X.sub.279 is A or D, X.sub.280 is L or H, X.sub.281 is G or I, X.sub.282 is G or V, X.sub.283 is N or S, X.sub.284 is Y or P, and X.sub.285 is Y or L; or [0747] the sequence GQFSDSSGYQHPYYDYGMD; or [0748] the sequence SPSGYYGDYEGDAFDI; or [0749] the sequence HGTSGYYYPNWFDP; or [0750] the sequence GLSLGFCSAGSCYDYLDY; or [0751] the sequence EELGPYSNRWYSSSDGMDV; or [0752] the sequence SRGYSGYGANWYFDL; or [0753] the sequence GVVTADWYFDL; or [0754] the sequence GGDHGMDV; or [0755] the sequence VTGYDSSGYYQDY; or [0756] the sequence LAYFHPQRNGGYEYYFDY; or [0757] the sequence DLPGDSRDGYNYDAFDI; or [0758] the sequence NPTVTNWFDS; or [0759] the sequence DRYPGYYDILTGQIGTGERNAMDV; or [0760] the sequence X.sub.363X.sub.364X.sub.365X.sub.366X.sub.367X.sub.368X.sub.369X.sub.370X.sub.371X.sub.372YYYYGMDV, where X.sub.363 is I or D, X.sub.364 is P or L, X.sub.365 is G or T, X.sub.366 is F or T, X.sub.367 is L or V, X.sub.368 is R or T, X.sub.369 is Y or N, X.sub.370 is R or P, X.sub.371 is N or L, and X.sub.372 is R or N; or [0761] the sequence GYSGNF.

[0762] In another embodiment of the present invention, the binding molecule may be a binding molecule that binds to a spike protein (S protein) on the surface of SARS-coronavirus-2 (SARS-CoV-2), wherein the binding molecule comprises a light-chain variable region comprising LC CDR1, LC CDR2 and LC CDR3, and a heavy-chain variable region comprising HC CDR1, HC CDR2 and HC CDR3, and is any one selected from the group consisting of the following binding molecules 1) to 49): [0763] 1) a binding molecule in which the LC CDR1 comprises the sequence SGSX.sub.1SNIGX.sub.2NTVN, where X.sub.1 is S or T, and X.sub.2 is S or T, [0764] the LC CDR2 comprises the sequence X.sub.3X.sub.4NX.sub.5RPS, where X.sub.3 is S or T, X.sub.4 is N or D, and X.sub.5 is Q or R, [0765] the LC CDR3 comprises the sequence AX.sub.6X.sub.7DDX.sub.8LX.sub.9X.sub.10X.sub.11X.sub.12, where X.sub.6 is A or S, X.sub.7 is W or R, X.sub.8 is S or R, X.sub.9 is N or S, X.sub.10 is A or G, X.sub.11 is S, L, V, Y, P, A or T, X.sub.12 is L or V, [0766] the HC CDR1 comprises the sequence GYYWS, [0767] the HC CDR2 comprises the sequence EINHSGSTNYNPSLKS, and [0768] the HC CDR3 comprises the sequence GRYSSNWYEAWTPRGIGMDV; [0769] 2) a binding molecule in which the LC CDR1 comprises the sequence X.sub.13GSX.sub.14SX.sub.15IX.sub.16X.sub.17X.sub.18X.sub.19VS, where X.sub.13 is S or T, X.sub.14 is S or N, X.sub.15 is N or S, X.sub.16 is G or E, X.sub.17 is N or S, X.sub.18 is N or S, and X.sub.19 is Y or F, [0770] the LC CDR2 comprises the sequence X.sub.20NX.sub.21X.sub.22RPS, where X.sub.20 is D or R, X.sub.21 is N or S, and

X.sub.22 is K, R, Q or V, [0771] the LC CDR3 comprises the sequence X.sub.23X.sub.24WDX.sub.25SLSX.sub.26X.sub.27V or GTWDSSLSAYWV, where X.sub.23 is G or A, X.sub.24 is T or A, X.sub.25 is S, N, D or T, X.sub.26 is A, G or S, and X.sub.27 is W or Y, [0772] the HC CDR1 comprises the sequence X.sub.28YYMH, where X.sub.28 is S or G, [0773] the HC CDR2 comprises the sequence X.sub.29INRSGGSTIYAQTFQX.sub.30, where X.sub.29 is I or V, X.sub.30 is G or S, and [0774] the HC CDR3 comprises the sequence GGRHSLDX.sub.31, where X.sub.31 is V or A; [0775] 3) a binding molecule in which the LC CDR1 comprises the sequence RASQSVX.sub.32X.sub.33X.sub.34X.sub.35A, where X.sub.32 is S, N or R, X.sub.33 is S or N, X.sub.34 is Y or N, and X.sub.35 is L or S, [0776] the LC CDR2 comprises the sequence X.sub.36ASX.sub.37RAT, where X.sub.36 is D or G, and X.sub.37 is N, T or S, [0777] the LC CDR3 comprises the sequence X.sub.38QX.sub.39X.sub.40X.sub.41X.sub.42PX.sub.43T or QQYGSSPSIT, where X.sub.38 is Q or H, X.sub.39 is Y or H, X.sub.40 is G, N, Y or H, X.sub.41 is S, N, T, Q or R, X.sub.42 is S, W or V, and X.sub.43 is L, F, I or Q, [0778] the HC CDR1 comprises the sequence X.sub.44SSYYWG, where X.sub.44 is S or G, [0779] the HC CDR2 comprises the sequence X.sub.45IX.sub.46YSGSTYYNPSLKS, where X.sub.45 is S or N, and X.sub.46 is Y or F, and [0780] the HC CDR3 comprises the sequence GSRGYYDX.sub.47LTGYSTGGFDY, where X.sub.47 is F or I; [0781] 4) a binding molecule in which the LC CDR1 comprises the sequence RASQSVX.sub.48X.sub.49X.sub.50YLA, where X.sub.48 is S or G, X.sub.49 is S or R, and X.sub.50 is S or N, [0782] the LC CDR2 comprises the sequence X.sub.51ASX.sub.52RAT, where X.sub.51 is G or D, and X.sub.52 is S or T, [0783] the LC CDR3 comprises the sequence QQYGX.sub.53SPX.sub.54X.sub.55, where X.sub.53 is S or T, X.sub.54 is L or I, and X.sub.55 is T or A, [0784] the HC CDR1 comprises the sequence SX.sub.56X.sub.57YYWX.sub.58, where X.sub.56 is S or G, X.sub.57 is S or G, and X.sub.58 is G or S, [0785] the HC CDR2 comprises the sequence X.sub.59IX.sub.60YSGSTYYNPSLKS, where X.sub.59 is S, Y or N, and X.sub.60 is Y or F, and [0786] the HC CDR3 comprises the sequence GSRGYYDX.sub.61LTGYSTGGFDY, where X.sub.61 is F or I; [0787] 5) a binding molecule in which the LC CDR1 comprises the sequence TGTSSX.sub.62VGX.sub.63YX.sub.64X.sub.65VS, where X.sub.62 is N or D, X.sub.63 is D or G, X.sub.64 is N or S, and X.sub.65 is Y or H, [0788] the LC CDR2 comprises the sequence X.sub.66VX.sub.67X.sub.68RPS, where X.sub.66 is D or E, X.sub.67 is T or S, and X.sub.68 is N or D, [0789] the LC CDR3 comprises the sequence SSYTSGSTPVV or NSYTSSSTWV, [0790] the HC CDR1 comprises the sequence SSSYYWG, [0791] the HC CDR2 comprises the sequence NIFYSGSTYYNPSLKS, and [0792] the HC CDR3 comprises the sequence GSRGYYDILTGYSTGGFDY; [0793] 6) a binding molecule in which the LC CDR1 comprises the sequence SGX.sub.69X.sub.70SNIGSNX.sub.71VX.sub.72, where X.sub.69 is S or L, X.sub.70 is S or T, X.sub.71 is Y, T or F, and X.sub.72 is Y, H or N, [0794] the LC CDR2 comprises the sequence X.sub.73NX.sub.74X.sub.75RPS, where X.sub.73 is R or S, X.sub.74 is N or D, and X.sub.75 is Q or E, [0795] the LC CDR3 comprises the sequence X.sub.76X.sub.77WDDX.sub.78LX.sub.79GX.sub.80V, where X.sub.76 is A or S, X.sub.77 is A or T, X.sub.78 is S or T, X.sub.79 is S, N or V, and X.sub.80 is R or K, [0796] the HC CDR1 comprises the sequence SYAIS, [0797] the HC CDR2 comprises the sequence GIIPIFGTANYAQX.sub.81FQX.sub.82, where X.sub.81 is K or R, and X.sub.82 is G or D, and [0798] the HC CDR3 comprises the sequence DGVVVPAVMYDTTDPYYYGMDV; [0799] 7) a binding molecule in which the LC CDR1 comprises the sequence TGTSSDVGGYNYVS, [0800] the LC CDR2 comprises the sequence X.sub.83VSNRPS, where X.sub.83 is D or E, [0801] the LC CDR3 comprises the sequence SSYAGSNYVV or SSYTSSSTX.sub.84X.sub.85V, where X.sub.84 is L or R, and X.sub.85 is G or Y, [0802] the HC CDR1 comprises the sequence SYAMX.sub.86, where X.sub.86 is S or N, [0803] the HC CDR2 comprises the sequence AISGSGGTTYYADSVKG, and [0804] the HC CDR3 comprises the sequence APSDLSFIWTGYYSEYYFDY; [0805] 8) a binding molecule in which the LC CDR1 comprises the sequence RASQSVSSSYLA, [0806] the LC CDR2 comprises the sequence GASSRAT, [0807] the LC CDR3 comprises the sequence QQYGSSPX.sub.87T or QQYGSSPALT, where X.sub.87 is Y or F, [0808] the HC CDR1 comprises the sequence SSPMH, [0809] the HC CDR2 comprises the sequence VISYX.sub.88GSNKYYADSVKG, where X.sub.88 is D or G, and [0810] the HC CDR3 comprises the sequence EIALNNYYGMDV; [0811] 9) a binding molecule in which the LC CDR1 comprises the sequence TGX.sub.89X.sub.90SDX.sub.91GGYNX.sub.92X.sub.93S, where X.sub.89 is N or T, X.sub.90 is R or S, X.sub.91 is I or V, X.sub.92 is S or Y, and X.sub.93 is L or V, [0812] the LC CDR2 comprises the sequence DVX.sub.94NRPS, where X.sub.94 is N or S, [0813] the LC CDR3 comprises the sequence X.sub.95SYTSX.sub.96X.sub.97TWV, where X.sub.95 is N or S, X.sub.96 is K or S, and X.sub.97 is N or S, [0814] the HC CDR1 comprises the sequence SSPMH, [0815] the HC CDR2 comprises the sequence VISYDGSNKYYADSVKG, and [0816] the HC CDR3 comprises the sequence EIALNNYYGMDV; [0817] 10) a binding molecule in which the LC CDR1 comprises the sequence SGSSSNIGNNYVS or GGNNIGSKSVH, [0818] the LC CDR2 comprises the sequence DX.sub.98X.sub.99X.sub.100RPS, where X.sub.98 is N or D, X.sub.99 is N or S, and X.sub.100 is K or D, [0819] the LC CDR3 comprises the sequence GTWDSSLSAGWV or X.sub.101X.sub.102WDSSX.sub.103X.sub.104X.sub.105VV, where X.sub.101 is G or Q, X.sub.102 is T or V, X.sub.103 is L or S, X.sub.104 is S or D, and X.sub.105 is A or H, [0820] the HC CDR1 comprises the sequence DYGMH, [0821] the sequence HC CDR2 comprises the sequence AISYDGSNKYYADSVKG, and [0822] the HC CDR3 comprises the sequence DSGLYGSGWSTYQYYAMDV; [0823] 11) a binding molecule in which the LC CDR1 comprises the sequence X.sub.106GTX.sub.107SDVGGYNYVS, where X.sub.106 is T or S, and X.sub.107 is S or N, [0824] the LC CDR2 comprises the sequence DVX.sub.108KRPS, where X.sub.108 is S or T, [0825] the LC CDR3 comprises the sequence SSYTSSX.sub.109TWV or SSYTSSSTPWV, where X.sub.109 is S or R, [0826] the HC CDR1 comprises the sequence X.sub.110YAMH, where X.sub.110 is S or G, [0827] the HC CDR2 comprises the sequence VISYDGSHKNYADSVKG, and [0828] the HC CDR3 comprises the sequence DNCGGDCGGGMDV; [0829] 12) a binding molecule in which the LC

CDR1 comprises the sequence SGSSSNIGSNX.sub.111VN or TGSSSNIGAGYDVH, where X.sub.111 is A or T, [0830] the LC CDR2 comprises the sequence X.sub.112NSX.sub.113RPS, where X.sub.112 is G or S, and X.sub.113 is N or Y, [0831] the LC CDR3 comprises the sequence QSYDSX.sub.114LX.sub.115X.sub.116X.sub.117X.sub.118, where X.sub.114 is S or A, X.sub.115 is S or R, X.sub.116 is D or G, X.sub.117 is V or P, and X.sub.118 is V or L, [0832] the HC CDR1 comprises the sequence SYGIS, [0833] the HC CDR2 comprises the sequence GIIPILATTKFAQKFQG, and [0834] the HC CDR3 comprises the sequence GWGLRLFGEFSVWFDP; [0835] 13) a binding molecule in which the LC CDR1 comprises the sequence RASQSVSSYLA, [0836] the LC CDR2 comprises the sequence DASNRAT, [0837] the LC CDR3 comprises the sequence QQRRNWPPX.sub.119X.sub.120T, where X.sub.119 is V or R, and X.sub.120 is L or I, [0838] the HC CDR1 comprises the sequence SYAIS, [0839] the HC CDR2 comprises the sequence GIIPIFGTANYAQKFQG, and [0840] the HC CDR3 comprises the sequence VEGYDSSGYYLDY; [0841] 14) a binding molecule in which the LC CDR1 comprises the sequence X.sub.121GSX.sub.122SNIGX.sub.123NX.sub.124VX.sub.125, where X.sub.121 is S or T, X.sub.122 is S or R, X.sub.123 is S or I, X.sub.124 is T or S, and X.sub.125 is S or N, [0842] the LC CDR2 comprises the sequence SNNQRPS, [0843] the LC CDR3 comprises the sequence AAWDDSLNGX.sub.126V, where X.sub.126 is V or Y, [0844] the HC CDR1 comprises the sequence GYYWS, [0845] the HC CDR2 comprises the sequence EINHSGSTNYNPSLKSG, and [0846] the HC CDR3 comprises the sequence RYSSNWYEAWTPRGIGMDV; [0847] 15) a binding molecule in which the LC CDR1 comprises the sequence TGSSSNIGAGYDVH or SGSSSNIGSNTVN, [0848] the LC CDR2 comprises the sequence X.sub.127NX.sub.128X.sub.129RPS, where X.sub.127 is G or S, X.sub.128 is S or N, and X.sub.129 is N or Q, [0849] the LC CDR3 comprises the sequence AAWDDSLX.sub.130GX.sub.131V, where X.sub.130 is G or N, and X.sub.131 is P or W, [0850] the HC CDR1 comprises the sequence TYGMH, [0851] the HC CDR2 comprises the sequence VISYDGFNKYYADSVKG, and [0852] the HC CDR3 comprises the sequence SLGGNYYYGMDV; [0853] 16) a binding molecule in which the LC CDR1 comprises the sequence TGTSSDIGGYNYVS or GGNNIGSKSVH, [0854] the LC CDR2 comprises the sequence X.sub.132X.sub.133SKRPS, where X.sub.132 is A or Q, and X.sub.133 is V or D, [0855] the LC CDR3 comprises the sequence SSYTSSSGTLNV or QAWDSSTV, [0856] the HC CDR1 comprises the sequence TYGMH, [0857] the HC CDR2 comprises the sequence VISYDGFNKYYADSVKG, and [0858] the HC CDR3 comprises the sequence SLGGNYYYGMDV; [0859] 17) a binding molecule in which the LC CDR1 comprises the sequence RASQSVSX.sub.134X.sub.135LA, where X.sub.134 is S or T, and X.sub.135 is Y or F, [0860] the LC CDR2 comprises the sequence DASNRAT, [0861] the LC CDR3 comprises the sequence QQRSNWPPX.sub.136X.sub.137T, where X.sub.136 is A, R, K or M, and X.sub.137 is L, I or Y, [0862] the HC CDR1 comprises the sequence SYAIX.sub.138, where X.sub.138 is S or I, [0863] the HC CDR2 comprises the sequence GIIPIFGTANYAQKFQG, and [0864] the HC CDR3 comprises the sequence VX.sub.139GYDX.sub.140SGYYQX.sub.141Y, where X.sub.139 is T or S, X.sub.140 is S or G, and X.sub.141 is D or E; [0865] 18) a binding molecule in which the LC CDR1 comprises the sequence TGTSX.sub.142DX.sub.143GX.sub.144YNYVS, where X.sub.142 is T or S, X.sub.143 is I or V, and X.sub.144 is R or A, [0866] the LC CDR2 comprises the sequence DVSKRPS, [0867] the LC CDR3 comprises the sequence SYTSSSTYA or NSYTSSSTWV, [0868] the HC CDR1 comprises the sequence EVAIH, [0869] the HC CDR2 comprises the sequence GFDPEDGETSYAQKFQG, and [0870] the HC CDR3 comprises the sequence GPVLGLSKWLEFDP; [0871] 19) a binding molecule in which the LC CDR1 comprises the sequence SGSSSNIGNNYVS, [0872] the LC CDR2 comprises the sequence DNNKRPS, [0873] the LC CDR3 comprises the sequence X.sub.145X.sub.146WDX.sub.147SLSX.sub.148X.sub.149X.sub.150, where X.sub.145 is G or E, X.sub.146 is T or A, X.sub.147 is S or T, X.sub.148 is A or D, X.sub.149 is V or G, and X.sub.150 is V or L, [0874] the HC CDR1 comprises the sequence RYAMS, [0875] the HC CDR2 comprises the sequence AISGSGGX.sub.151TYYADSVKG, where X.sub.151 is S or T, and [0876] the HC CDR3 comprises the sequence GPRGQDYGDYGFLDY; [0877] 20) a binding molecule in which the LC CDR1 comprises the sequence SGSSSNIGSNTVN, [0878] the LC CDR2 comprises the sequence X.sub.152NNX.sub.153RPS, where X.sub.152 is S, T or N, and X.sub.153 is Q or R, [0879] the LC CDR3 comprises the sequence AAWDDSLX.sub.154GX.sub.155V or AAWDDSLNGX.sub.156VV, where X.sub.154 is N or S, X.sub.155 is L, P, W or V, and X.sub.156 is S or H, [0880] the HC CDR1 comprises the sequence SX.sub.157WIX.sub.158, where X.sub.157 is H or Y, and X.sub.158 is A, V or G, [0881] the HC CDR2 comprises the sequence X.sub.159IYPGDSDSRYSPSFQG, where X.sub.159 is I or T, and [0882] the HC CDR3 comprises the sequence GPNX.sub.160YNWFDS, where X.sub.160 is L or I; [0883] 21) a binding molecule in which the LC CDR1 comprises the sequence RASQX.sub.161X.sub.162X.sub.163X.sub.164X.sub.165X.sub.166A, where X.sub.161 is S or G, X.sub.162 is V or I, X.sub.163 is S or R, X.sub.164 is S or N, X.sub.165 is Y, S or D, and X.sub.166 is L or I, [0884] the LC CDR2 comprises the sequence DX.sub.167SX.sub.168X.sub.169X.sub.170T or AASRLES, where X.sub.167 is A or T, X.sub.168 is N or T, X.sub.169 is R or L, and X.sub.170 is A or E, [0885] the LC CDR3 comprises the sequence QQYYX.sub.171TPX.sub.172T, where X.sub.171 is S or T, and X.sub.172 is F or I, [0886] the HC CDR1 comprises the sequence DYYIQ, [0887] the HC CDR2 comprises the sequence WINPNSGDTNYAHKFQG, and [0888] the HC CDR3 comprises the sequence GGSYYNVMYWFDP; [0889] 22) a binding molecule in which the LC CDR1 comprises the sequence X.sub.173ASQX.sub.174ISSYLN, where X.sub.173 is R or Q, and X.sub.174 is S or D, [0890] the LC CDR2 comprises the sequence X.sub.175ASSLX.sub.176S, where X.sub.175 is K or A, and X.sub.176 is E or Q, [0891] the LC CDR3 comprises the sequence QQSYSTWT, [0892] the HC CDR1 comprises the sequence SYAMH, [0893] the HC CDR2 comprises the sequence VISYDGSNKYYADSVKG, and [0894] the HC CDR3 comprises the sequence ARGGSYLYGMDV; [0895] 23) a binding molecule in which the LC CDR1 comprises the sequence SGSX.sub.177SNIGX.sub.178NYVX.sub.179, where X.sub.177 is S or G, X.sub.178 is N or S, and X.sub.179 is S or H,

[0896] the LC CDR2 comprises the sequence X.sub.180NX.sub.181X.sub.182RPS, where X.sub.180 is D or R, X.sub.181 is N or S, and X.sub.182 is K or G, [0897] the LC CDR3 comprises the sequence AAWDDSLX.sub.183GWV, where X.sub.183 is N or S, [0898] the HC CDR1 comprises the sequence SYAIS, [0899] the HC CDR2 comprises the sequence GIIPMFGTTNYAQKFQG, and [0900] the HC CDR3 comprises the sequence DPTSRSTYYYYSGSYYP; [0901] 24) a binding molecule in which the LC CDR1 comprises the sequence SGSSSNIGNNYVS or TGTRGDIGAYDGVS, [0902] the LC CDR2 comprises the sequence DNNKRPS or AVTQRPS, [0903] the LC CDR3 comprises the sequence AAWDDSLNGVV or SSYTSSSSWV, [0904] the HC CDR1 comprises the sequence RYAMS, [0905] the HC CDR2 comprises the sequence AISGSGGSTYYADSVKG, and [0906] the HC CDR3 comprises the sequence GPRGQDYGDYGFLDY; [0907] 25) a binding molecule in which the LC CDR1 comprises the sequence TGSSSNIGAGYDVH or SGSSSNIGNNYVS, [0908] the LC CDR2 comprises the sequence X.sub.184NX.sub.185X.sub.186RPS, where X.sub.184 is G or D, X.sub.185 is S or N, and X.sub.186 is N or K, [0909] the LC CDR3 comprises the sequence QSYDSSLSGLWV or QSYDSSLSAWV, [0910] the HC CDR1 comprises the sequence SNYMS, [0911] the HC CDR2 comprises the sequence VIYPGGSTFFADSVQG, and [0912] the HC CDR3 comprises the sequence SYDFLTDYTDAFDI; [0913] 26) a binding molecule in which the LC CDR1 comprises the sequence TGTX.sub.187X.sub.188DX.sub.189GX.sub.190YX.sub.191X.sub.192VS, where X.sub.187 is S or R, X.sub.188 is S or G, X.sub.189 is V or I, X.sub.190 is G or A, X.sub.191 is N or D, and X.sub.192 is Y or G, [0914] the LC CDR2 comprises the sequence X.sub.193VX.sub.194X.sub.195RPS, where X.sub.193 is D or A, X.sub.194 is S or T, and X.sub.195 is K or Q, [0915] the LC CDR3 comprises the sequence SSYTX.sub.196SSX.sub.197WV, where X.sub.196 is T or S, and X.sub.197 is T or S, [0916] the HC CDR1 comprises the sequence ELSX.sub.198H, where X.sub.198 is I or M, [0917] the HC CDR2 comprises the sequence GFDPEDX.sub.199ETIYAQKFQG, where X.sub.199 is G or A, and [0918] the HC CDR3 comprises the sequence SPAX.sub.200X.sub.201X.sub.202X.sub.203X.sub.204WFDP, where X.sub.200 is V or I, X.sub.201 is T or I, X.sub.202 is T or R, X.sub.203 is A or V, and X.sub.204 is G or D; [0919] 27) a binding molecule in which the LC CDR1 comprises the sequence SGSSSNIGX.sub.205NX.sub.206VX.sub.207, where X.sub.205 is S or N, X.sub.206 is T or Y, and X.sub.207 is N or S, [0920] the LC CDR2 comprises the sequence X.sub.208NNX.sub.209RPS, where X.sub.208 is S or D, and X.sub.209 is Q or K, [0921] the LC CDR3 comprises the sequence AAWDDSLX.sub.210GPV, where X.sub.210 is N or S, [0922] the HC CDR1 comprises the sequence X.sub.211YAMS, where X.sub.211 is S or R, [0923] the HC CDR2 comprises the sequence AISGSGGX.sub.212TYYADSVKG, where X.sub.212 is D or S, and [0924] the HC CDR3 comprises the sequence VRYYDFWSGWDVMDV; [0925] 28) a binding molecule in which the LC CDR1 comprises the sequence TGTSX.sub.213DVGX.sub.214YNX.sub.215VS, where X.sub.213 is T or S, X.sub.214 is G or S, and X.sub.215 is Y or L, [0926] the LC CDR2 comprises the sequence DVSX.sub.216RPS, where X.sub.216 is K or N, [0927] the LC CDR3 comprises the sequence SSYTSSSTLV, [0928] the HC CDR1 comprises the sequence NYGMH, [0929] the HC CDR2 comprises the sequence VMSYDGSNKYYADSVKG, and [0930] the HC CDR3 comprises the sequence PDDSSGYYPDY; [0931] 29) a binding molecule in which the LC CDR1 comprises the sequence TGTSSDVGGYNYVS, [0932] the LC CDR2 comprises the sequence DVX.sub.217KRPS, where X.sub.217 is G or S, [0933] the LC CDR3 comprises the sequence SSYTSSSTX.sub.218V, where X.sub.218 is W OR L, [0934] the HC CDR1 comprises the sequence X.sub.219YAIS, where X.sub.219 is F or R, [0935] the HC CDR2 comprises the sequence GIIPX.sub.220FGX.sub.221X.sub.222X.sub.223YAQX.sub.224FQD, where X.sub.220 is L or I, X.sub.221 is T or K, X.sub.222 is A or V, X.sub.223 is K or N, and X.sub.224 is R or K, and [0936] the HC CDR3 comprises the sequence GGWIYRGNWFDP or GGSTWYGGNWFDP; [0937] 30) a binding molecule in which the LC CDR1 comprises the sequence TGSSSNIGAGYDVH, [0938] the LC CDR2 comprises the sequence GNSNRPS, [0939] the LC CDR3 comprises the sequence QSYDSSLSGX.sub.225WV, where X.sub.225 is P or S, [0940] the HC CDR1 comprises the sequence RYAIX.sub.226, where X.sub.226 is N or S, [0941] the HC CDR2 comprises the sequence GIIPX.sub.227X.sub.228GTX.sub.229X.sub.230YX.sub.231QKFQG, where X.sub.227 is L or I, X.sub.228 is L or F, X.sub.229 is A or G, X.sub.230 is D or N, and X.sub.231 is P or A, and [0942] the HC CDR3 comprises the sequence TLYYYDRSGNARTDDYFDH or SLYYYDRSGYPISEDYFDY; [0943] 31) a binding molecule in which the LC CDR1 comprises the sequence TGTSSDVGX.sub.232YNYVS, where X.sub.232 is N or G, [0944] the LC CDR2 comprises the sequence DVSX.sub.233RPS, where X.sub.233 is N or K, [0945] the LC CDR3 comprises the sequence SSYTSSX.sub.234TX.sub.235V, where X.sub.234 is G or S, and X.sub.235 is L or Y, [0946] the HC CDR1 comprises the sequence ELSIH, [0947] the HC CDR2 comprises the sequence GFDPEX.sub.236X.sub.237ETIX.sub.238AQX.sub.239FQG, where X.sub.236 is N or D, X.sub.237 is G or A, X.sub.238 is H or Y, and X.sub.239 is R or K, and [0948] the HC CDR3 comprises the sequence SX.sub.240X.sub.241X.sub.242X.sub.243X.sub.244AX.sub.245WFDP, where X.sub.240 is T or P, X.sub.241 is P or A, X.sub.242 is M or V, X.sub.243 is I or T, X.sub.244 is R or T, and X.sub.245 is S or G; [0949] 32) a binding molecule in which the LC CDR1 comprises the sequence TGSSSNIGAGYDVH, [0950] the LC CDR2 comprises the sequence GNSNRPS, [0951] the LC CDR3 comprises the sequence QSYDSSLSGWV, [0952] the HC CDR1 comprises the sequence NYGIS, [0953] the HC CDR2 comprises the sequence X.sub.246ISX.sub.247X.sub.248NGNTX.sub.249YAQKLQG, where X.sub.246 is G or W, X.sub.247 is S or A, X.sub.248 is H or Y, and X.sub.249 is K or N, and [0954] the HC CDR3 comprises the sequence EGGYYYGSGSYYNPRFAFDI or PRGYSGYGSNWYF; [0955] 33) a binding molecule in which the LC CDR1 comprises the sequence RASQSVSSNLA or RASQGISNSL, [0956] the LC CDR2 comprises the sequence X.sub.250AX.sub.251X.sub.252RX.sub.253X.sub.254, where X.sub.250 is W or A, X.sub.251 is S or A, X.sub.252 is T or S, X.sub.253 is E or L, and X.sub.254 is S or E, [0957] the LC CDR3 comprises the sequence LQYFTIPWT or SQQYYSTPYT, [0958] the HC CDR1 comprises the sequence

NAWMX.sub.255, where X.sub.255 is S or T, [0959] the HC CDR2 comprises the sequence RIKTKTDGGTTDYAAPVKG, and [0960] the HC CDR3 comprises the sequence X.sub.256SX.sub.257PDY, where X.sub.255 is F or H, and X.sub.257 is T or R; [0961] 34) a binding molecule in which the LC CDR1 comprises the sequence RASQSVSSX.sub.258LA, where X.sub.258 is Y or F, [0962] the LC CDR2 comprises the sequence DASNRAT, [0963] the LC CDR3 comprises the sequence QQYGSSPPIT or QQRSNWPPSIT, [0964] the HC CDR1 comprises the sequence SYAIS, [0965] the HC CDR2 comprises the sequence GIIPIFGTX.sub.259NYAQKFQG, where X.sub.259 is T or A, and [0966] the HC CDR3 comprises the sequence DPTGWYSGYFDY or VGTYDSSGYSFDY; [0967] 35) a binding molecule in which the LC CDR1 comprises the sequence GGNNIGSKSVH, [0968] the LC CDR2 comprises the sequence YDSDRPS, [0969] the LC CDR3 comprises the sequence QVWDSSSDHWV, [0970] the HC CDR1 comprises the sequence DYAMS or SYYIH, [0971] the HC CDR2 comprises the sequence VISGSGGSTSNADSVKG or FINPSDVTTYYAQKFQG, and [0972] the HC CDR3 comprises the sequence VYCGDDCYPVVGTPGDAFDI or SRIAPTEDFFDY; [0973] 36) a binding molecule in which the LC CDR1 comprises the sequence SSSTGAVTRGHFPN or SGSSSNIGNNYVS, [0974] the LC CDR2 comprises the sequence STSNKHS or DNNKRPS, [0975] the LC CDR3 comprises the sequence LLYDAGAPGWV or GAWDSSLSTPNW, [0976] the HC CDR1 comprises the sequence SYPMH, [0977] the HC CDR2 comprises the sequence VISYDGSLKYYVDSVKG, and [0978] the HC CDR3 comprises the sequence DSSCSGGSCFDY; [0979] 37) a binding molecule in which the LC CDR1 comprises the sequence SGSSSNIGSNTVN, [0980] the LC CDR2 comprises the sequence SNNQRPS, [0981] the LC CDR3 comprises the sequence AAWDDSLNGWV, [0982] the HC CDR1 comprises the sequence X.sub.260X.sub.261AMX.sub.262, where X.sub.260 is S or N, X.sub.261 is F or Y, and X.sub.262 is H or N, [0983] the HC CDR2 comprises the sequence X.sub.263ISX.sub.264X.sub.265GX.sub.266X.sub.267X.sub.268YYADSVKG, where X.sub.263 is V or T, X.sub.264 is F or G, X.sub.265 is D or S, X.sub.266 is S or G, X.sub.267 is N or S, and X.sub.268 is K or T, and [0984] the HC CDR3 comprises the sequence GDYYGSGSYYNPSPFFDY or GYALNP; [0985] 38) a binding molecule in which the LC CDR1 comprises the sequence CRASQSVSSSYLA, [0986] the LC CDR2 comprises the sequence GASSRAT, [0987] the LC CDR3 comprises the sequence QQYGSSPX.sub.269T, where X.sub.269 is Y or P, [0988] the HC CDR1 comprises the sequence SSPMH or NYVIN, [0989] the HC CDR2 comprises the sequence VISYDGSNKYYADSVKG or GFIPVFGIADYAQKFQG, and [0990] the HC CDR3 comprises the sequence EIALNNYYGMDV or SGLFDWLLPRSRHRDYFDY; [0991] 39) a binding molecule in which the LC CDR1 comprises the sequence RASQSISSYLN, [0992] the LC CDR2 comprises the sequence AASSLQS, [0993] the LC CDR3 comprises the sequence QQSYSTPLT, [0994] the HC CDR1 comprises the sequence SNYMX.sub.270, where X.sub.270 is T or S, [0995] the HC CDR2 comprises the sequence X.sub.271IYPGGSTX.sub.272X.sub.273ADSVX.sub.274G, where X.sub.271 is I or V, X.sub.272 is Y or F, X.sub.273 is Y or F, and X.sub.274 is K or Q, and [0996] the HC CDR3 comprises the sequence DLPLTGTTLDY or SYDFLTDYTDAFDI; [0997] 40) a binding molecule in which the LC CDR1 comprises the sequence RASQSISSYLN, [0998] the LC CDR2 comprises the sequence AASSLQS, [0999] the LC CDR3 comprises the sequence QQSYSTPX.sub.275T, where X.sub.275 is F or L, [1000] the HC CDR1 comprises the sequence SX.sub.276AX.sub.277X.sub.278, where X.sub.276 is Y or S, X.sub.277 is M or I, and X.sub.278 is H or N, [1001] the HC CDR2 comprises the sequence VISYDGINKYYADSVKG or GIIPIFGTVNYAQKFQG, and [1002] the HC CDR3 comprises the sequence X.sub.279X.sub.280X.sub.281X.sub.282X.sub.283X.sub.284X.sub.285YGMDV, where X.sub.279 is A or D, X.sub.280 is L or H, X.sub.281 is G or I, X.sub.282 is G or V, X.sub.283 is N or S, X.sub.284 is Y or P, and X.sub.285 is Y or L; [1003] 41) a binding molecule in which the LC CDR1 comprises the sequence TGSSSNIGAGYDVH, [1004] the LC CDR2 comprises the sequence GNSNRPS, [1005] the LC CDR3 comprises the sequence QSYDSSLSGPNWV or QSYDSRLRAVV, [1006] the HC CDR1 comprises the sequence SYAIS or TQYLH, [1007] the HC CDR2 comprises the sequence X.sub.286IX.sub.287PX.sub.288X.sub.289GX.sub.290X.sub.291X.sub.292YAQKFQG, where X.sub.286 is G or I, X.sub.287 is I or N, X.sub.288 is F or Y, X.sub.289 is F or G, X.sub.290 is T or S, X.sub.291 is S or T, and X.sub.292 is N or T, and [1008] the HC CDR3 comprises the sequence GQFSDSSGYQHPYYDYGMD or SPSGYYGDYEGDAFDI; [1009] 42) a binding molecule in which the LC CDR1 comprises the sequence TGTSSDVGGYNYVS, [1010] the LC CDR2 comprises the sequence DVSX.sub.293RPS, where X.sub.293 is K or N, [1011] the LC CDR3 comprises the sequence SSYTSSSTLV, [1012] the HC CDR1 comprises the sequence RGDYWG or THALS, [1013] the HC CDR2 comprises the sequence SIYHSGSTYYNPSLKS or GIIPIFGPADYAQKFQG, and [1014] the HC CDR3 comprises the sequence HGTSGYYYPNWFDP or GLSLGFCSAGSCYDYLDY; [1015] 43) a binding molecule in which the LC CDR1 comprises the sequence TGSSSNIGAGYDVH, [1016] the LC CDR2 comprises the sequence GNSNRPS, [1017] the LC CDR3 comprises the sequence QSYDSSLSGX.sub.294V, where X.sub.294 is V or P, [1018] the HC CDR1 comprises the sequence DYAMH or SYDIS, [1019] the HC CDR2 comprises the sequence GISWNSGTIGYADSVKG or GIIPILGIPNYAQKFQG, and [1020] the HC CDR3 comprises the sequence EELGPYSNRWYSSSDGMDV or SRGYSGYGANWYFDL; [1021] 44) a binding molecule in which the LC CDR1 comprises the sequence TGTSSDVGGYNX.sub.295VS, where X.sub.295 is Y or N, [1022] the LC CDR2 comprises the sequence DVSX.sub.296RPS, where X.sub.296 is N or K, [1023] the LC CDR3 comprises the sequence SSYTSSSPWV, [1024] the HC CDR1 comprises the sequence SYAX.sub.297S, where X.sub.297 is M or I, [1025] the HC CDR2 comprises the sequence GIX.sub.298X.sub.299X.sub.300X.sub.301GX.sub.302TX.sub.303YAX.sub.304X.sub.305X.sub.306X.sub.307G, where X.sub.295 is S or I, X.sub.299 is G or P, X.sub.300 is S or M, X.sub.301 is G or F, X.sub.302 is S or T, X.sub.303 is Y or N, X.sub.304 is D or Q, X.sub.305 is S or K, X.sub.306 is V or F, and X.sub.307 is K or Q, and [1026] the HC CDR3

comprises the sequence GVVTADWYFDL or DPTSRSTYYYYSGSYYP; [1027] 45) a binding molecule in which the LC CDR1 comprises the sequence SGSSSNIGX.sub.308NYVS, where X.sub.308 is R or N, [1028] the LC CDR2 comprises the sequence DNNX.sub.309RPS, where X.sub.309 is R or K, [1029] the LC CDR3 comprises the sequence GTWDSSLSAVX.sub.310, where X.sub.310 is A or V, [1030] the HC CDR1 comprises the sequence SYX.sub.311X.sub.312X.sub.313, where X.sub.311 is Y or A, X.sub.312 is M or I, and X.sub.313 is H or I, [1031] the HC CDR2 comprises the sequence X.sub.314IX.sub.315PX.sub.316X.sub.317GX.sub.318X.sub.319X.sub.320YAQKFQG, where X.sub.314 is I or G, X.sub.315 is N or I, X.sub.316 is S or I, X.sub.317 is G or F, X.sub.318 is S or T, X.sub.319 is T or A, and X.sub.320 is S or N, and [1032] the HC CDR3 comprises the sequence GGDHGMDV or VTGYDSSGYYQDY; [1033] 46) a binding molecule in which the LC CDR1 comprises the sequence SGSSSNIGNNYVS, [1034] the LC CDR2 comprises the sequence DNNKRPS, [1035] the LC CDR3 comprises the sequence GTWDSSLSAX.sub.321V, where X.sub.321 is G or V, [1036] the HC CDR1 comprises the sequence SX.sub.322X.sub.323IX.sub.324, where X.sub.322 is N or Y, X.sub.323 is W or V, and X.sub.324 is A or S, [1037] the HC CDR2 comprises the sequence X.sub.3251X.sub.326PX.sub.327X.sub.328X.sub.329X.sub.330X.sub.331X.sub.332X.sub.333X.sub.334X.sub.335X.sub.336FQG where X.sub.325 is I or R, X.sub.326 is Y or n, X.sub.327 is G or I, X.sub.328 is D or F, X.sub.329 is S or G, X.sub.330 is D or T, X.sub.331 is T or V, X.sub.332 is R or K, X.sub.333 is N or Y, X.sub.334 is S or A, X.sub.335 is P or Q, and X.sub.336 is S or K, and [1038] the HC CDR3 comprises the sequence LAYFHPQRNGGYEYYFDY or DLPGDSRDGYNYDAFDI; [1039] 47) a binding molecule in which the LC CDR1 comprises the sequence SGSSSX.sub.337X.sub.338GSNX.sub.339VN, where X.sub.337 is N or D, X.sub.338 is V or I, and X.sub.339 is I or T, [1040] the LC CDR2 comprises the sequence X.sub.340NNQRPS, where X.sub.340 is N or S, [1041] the LC CDR3 comprises the sequence AAWDDSLNX.sub.341WV, where X.sub.341 is A or G, [1042] the HC CDR1 comprises the sequence NHWIA or NYAIN, [1043] the HC CDR2 comprises the sequence X.sub.342IX.sub.343PX.sub.344X.sub.345X.sub.346X.sub.347X.sub.348X.sub.349YX.sub.350X.sub.351X.sub.352FQG, where X.sub.342 is I or G, X.sub.343 is Y or I, X.sub.344 is Y or I, X.sub.345 is D or F, X.sub.346 is S or G, X.sub.347 is D or T, X.sub.348 is T or A, X.sub.349 is K or N, X.sub.350 is S or A, X.sub.351 is P or Q, and X.sub.352 is S or K, and [1044] the HC CDR3 comprises the sequence NPTVTNWFDS or DRYPGYYDILTGQIGTGERNAMD V; [1045] 48) a binding molecule in which the LC CDR1 comprises the sequence SGSSSNIGX.sub.353NYVX.sub.354, where X.sub.353 is N or S, and X.sub.354 is S or Y, [1046] the LC CDR2 comprises the sequence X.sub.355NNX.sub.356RPS, where X.sub.355 is D or R, and X.sub.356 is K or Q, [1047] the LC CDR3 comprises the sequence X.sub.357X.sub.358WDX.sub.359SLSX.sub.360X.sub.361X.sub.362, where X.sub.357 is G or A, X.sub.358 is T or A, X.sub.359 is S or D, X.sub.360 is A or G, X.sub.361 is G or W, and X.sub.362 is P or V, [1048] the HC CDR1 comprises the sequence TSGVGVG or ELPIH, [1049] the HC CDR2 comprises the sequence LIDWDDNKYYTTSLKT or RFDPEDGETIYAQNFQG, and [1050] the HC CDR3 comprises the sequence X.sub.363X.sub.364X.sub.365X.sub.366X.sub.367X.sub.368X.sub.369X.sub.370X.sub.371X.sub.372YYYYGMDV, where X.sub.363 is I or D, X.sub.364 is P or L, X.sub.365 is G or T, X.sub.366 is F or T, X.sub.367 is L or V, X.sub.368 is R or T, X.sub.369 is Y or N, X.sub.370 is R or P, X.sub.371 is N or L, and X.sub.372 is R or N; and [1051] 49) a binding molecule in which the LC CDR1 comprises the sequence SGSSSNIGX.sub.373NYVX.sub.374, where X.sub.373 is N or S, and X.sub.374 is S or N, [1052] the LC CDR2 comprises the sequence X.sub.375NNX.sub.376RPS, where X.sub.375 is D or S, and X.sub.376 is K or Q, [1053] the LC CDR3 comprises the sequence X.sub.377TWDX.sub.378SLX.sub.379X.sub.380X.sub.381V, where X.sub.377 is G or A, X.sub.378 is S or D, X.sub.379 is S or N, X.sub.380 is A or G, and X.sub.381 is G or Q, [1054] the HC CDR1 comprises the sequence DYX.sub.382MX.sub.383, where X.sub.382 is G or W, and X.sub.383 is H or S, [1055] the HC CDR2 comprises the sequence X.sub.384IX.sub.385X.sub.386DGSX.sub.387KYYX.sub.388DSVKG, where X.sub.384 is A or N, X.sub.385 is S or K, X.sub.386 is Y or E, X.sub.387 is N or E, and X.sub.388 is A or V, and [1056] the HC CDR3 comprises the sequence DSGLYGSGWSTYQYYAMDV or GYSGNF.

[1057] In one embodiment of the present invention, the binding molecule according to the present invention may have an IC.sub.50 value of preferably 200 ng/ml or less, more preferably 100 ng/ml or less, even more preferably 50 ng/ml or less, even more preferably 25 ng/ml or less, even more preferably 10 ng/ml or less, as evaluated according to a plaque reduction neutralization test (PRNT) method for SARS-coronavirus-2 (SARS-CoV-2), without being limited thereto. Here, the IC.sub.50 value refers to the antibody concentration at which the antibody exhibits 50% of neutralizing activity against the virus.

[1058] In one embodiment of the present invention, the minimum concentration value of the binding molecule according to the present invention that neutralizes 100 TCID50 of virus for SARS-coronavirus-2 (SARS-CoV-2) may be preferably 2 μg/ml or less, more preferably 1 μg/ml or less, even more preferably 0.5 μg/ml or less, even more preferably 0.25 μg/ml or less, even more preferably 0.125 μg/ml or less, without being limited thereto.

[1059] In one embodiment of the present invention, the binding molecule according to the present invention is able to bind to a receptor-binding domain (RBD) of the spike protein of SARS-coronavirus-2 with an equilibrium dissociation constant (K.sub.D) of preferably 1.0×10.sup.−8M or less, more preferably 1.0×10.sup.−9M or less, even more preferably 1.0×10.sup.−10 M or less, without being limited thereto.

[1060] In one embodiment of the present invention, the binding molecule may be a polypeptide, particularly an antibody or an antigen-binding fragment thereof. The antibody may be a monoclonal antibody, preferably a chimeric antibody, a humanized antibody, or a human antibody, without being limited thereto. The antigen-binding fragment may be Fab, F(ab′), F(ab′)2, Fv, dAb, Fd, a single-chain antibody fragment (scFv), scFv-Fc, a complementarity-determining region

(CDR) fragment, a bivalent single-chain antibody fragment, a single-chain phage antibody fragment, a diabody, a triabody, or a tetrabody, without being limited thereto. [1061] An embodiment of the present invention provides scFv-Fc that binds to the S protein of SARS-CoV-2. Another embodiment of the present invention provides a fully human antibody (full IgG) that binds to the S protein of SARS-CoV-2.
[1062] An embodiment of the present invention provides scFv-Fc that binds to the S protein of SARS-CoV-1. Another embodiment of the present invention provides a fully human antibody (full IgG) that binds to the S protein of SARS-CoV-1.
[1063] An embodiment of the present invention provides scFv-Fc that binds to the S protein of MERS-CoV. Another embodiment of the present invention provides a fully human antibody (full IgG) that binds to the S protein of MERS-CoV.
[1064] In the present invention, the binding molecules include those that exist in the human body and those that are not present in the human body but are wholly or partially artificially produced. In particular, the binding molecule of the present invention may be one that is wholly or partially artificially produced. Wholly or partially artificially produced examples include, but are not limited to, those produced in vitro or isolated, those produced by mammalian cell culture, those artificially produced by transformed cells, or those artificially produced through shuffling recombination of genetic information of light-chain and/or heavy-chain variable regions of the antibody.
[1065] As used herein, the term “antibody” is used in the broadest sense, and particularly includes an intact monoclonal antibody, a polyclonal antibody, a multispecific antibody (e.g., a bispecific antibody) formed from two or more intact antibodies, and an antibody fragment that shows a desired biological activity. The antibody is a protein that is produced by an immune system capable of recognizing and binding to a specific antigen. Structurally, the antibody generally has a Y-shaped protein comprising four amino acid chains (two heavy chains and two light chains). Each antibody generally has two regions (a variable region and a constant region). The variable region, which is located at the ends of the arms of the Y, binds to and interacts with a target antigen. The variable region includes a complementarity-determining region (CDR) that recognizes and binds to a specific binding site on a specific antigen. The constant region, which is located at the tail of the Y, is recognized by the immune system and interacts therewith. The target antigen generally has a plurality of binding sites called epitopes, which are recognized by CDRs on antibodies. Respective antibodies that specifically bind to different epitopes have different structures. Therefore, a single antigen may have at least one antibody corresponding thereto.
[1066] Moreover, the present invention includes functional variants of the binding molecule. Binding molecules are considered to be functional variants of the binding molecule of the present invention so long as the variants are capable of competing with the binding molecule of the present invention in order to specifically bind to coronavirus or to an S protein thereof and also have neutralizing activity against coronavirus. Such functional variants include, but are not limited to, derivatives that are substantially similar in primary structural sequence, and examples thereof include in-vitro or in-vivo modifications, chemicals and/or biochemicals, that are not found in the parental monoclonal antibody of the present invention. Such modifications include, for example, acetylation, acylation, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, cross-linking, disulfide bond formation, glycosylation, hydroxylation, methylation, oxidation, pegylation, proteolytic processing, phosphorylation, and the like. Alternatively, the functional variants may be antibodies comprising an amino acid sequence containing one or more substitutions, insertions, deletions or combinations thereof of one or more amino acids compared to the amino acid sequence of the parental antibody. Furthermore, the functional variants may comprise truncated forms of the amino acid sequence at either or both the amino or carboxyl termini. The functional variants of the present invention may have the same or different, either higher or lower, binding affinities compared to the parental antibody of the present invention but are still capable of binding to coronavirus or an S protein thereof. For instance, the amino acid sequences of the variable regions, including, but not limited to, framework regions, hypervariable regions, in particular, the light-chain or heavy-chain complementarity-determining regions (CDRs), may be modified. Generally, the light chain or heavy chain variable regions comprise three hypervariable regions, comprising three CDRs, and more conserved regions, the so-called framework regions (FRs). The hypervariable regions comprise amino acid residues from CDRs and amino acid residues from hypervariable loops. Functional variants falling within the scope of the present invention may have about 50% to 99%, about 60% to 99%, about 80% to 99%, about 90% to 99%, about 95% to 99%, or about 97% to 99% amino acid sequence identity with the parental antibody defined herein. Computer algorithms such as Gap or Bestfit known to a person skilled in the art may be used to optimally align amino acid sequences to be compared and to define similar or identical amino acid residues. The functional variants may be obtained by altering the parental antibodies or parts thereof by general molecular biology methods known in the art, including PCR, oligonucleotide-directed mutagenesis, and site-directed mutagenesis, or by organic synthesis processes, without being limited thereto.
[1067] The present invention also provides an immunoconjugate in which at least one tag is additionally conjugated to the binding molecule. In one embodiment, a drug may be additionally conjugated to the binding molecule. Specifically, the binding molecule according to the present invention may be used in the form of antibody-drug conjugates comprising a drug conjugated thereto. The use of antibody-drug conjugates (ADCs), i.e. immunoconjugates, for the local delivery of drugs, allows targeted delivery of the drug moiety to infected cells, because administration of unconjugated drug agents may result in unacceptable levels of toxicity to normal cells. The maximal efficacy and minimal toxicity of ADC can be achieved by increasing the selectivity of polyclonal and monoclonal antibodies (mAbs) as well as drug-linking and drug-releasing properties.
[1068] Conventional means of attaching, i.e., linking through covalent bonds, a drug moiety to an antibody generally leads to a heterogeneous mixture of molecules where the drug moieties are attached at a number of sites on the antibody. For

example, cytotoxic drugs have typically been conjugated to antibodies through the often-numerous lysine residues of an antibody, thereby generating a heterogeneous antibody-drug conjugate mixture. Depending on reaction conditions, the heterogeneous mixture typically contains a distribution of antibodies with from 0 to about 8 or more, attached to drug moieties. In addition, each subgroup of conjugates with a particular integer ratio of drug moieties to antibody is a potentially heterogeneous mixture where the drug moiety is attached at various sites on the antibody. Antibodies are large, complex and structurally diverse biomolecules, often with many reactive functional groups. Their reactivities with linker reagents and drug-linker intermediates are dependent on factors such as pH, concentration, salt concentration, and co-solvents.

[1069] Another embodiment of the present invention provides a nucleic acid molecule encoding the binding molecule.

[1070] The nucleic acid molecule of the present invention includes any nucleic acid molecule in which the amino acid sequence of the antibody provided in the present invention is translated into a polynucleotide sequence as known to those skilled in the art. Thus, various polynucleotide sequences may be produced using an ORF (open reading frame), and may also be included within the range of the nucleic acid molecule of the present invention.

[1071] Another embodiment of the present invention provides an expression vector into which the nucleic acid molecule has been inserted.

[1072] The expression vector may be any one expression vector selected from the group consisting of a MarEx vector (see Korean Patent No. 10-1076602), which is an expression vector available from Celltrion, and a commercially widely useful pCDNA vector, F, R1, RP1, Col, pBR322, ToL, and Ti vector; a cosmid; phages, such as lambda, lambdoid, M13, Mu, p1 P22, Qμ, T-even, T2, T3, T7, etc.; and plant viruses, without being limited thereto. Any expression vector known to those skilled in the art may be used in the present invention, and the expression vector may be selected depending on the properties of the host cell of interest. The introduction of the vector into the host cell may be performed by calcium phosphate transfection, viral infection, DEAE-dextran-mediated transfection, lipofectamine transfection, or electroporation, without being limited thereto, and those skilled in the art may adopt an introduction process suitable for the expression vector used and the host cell. For example, the expression vector may contain at least one selection marker, without being limited thereto, and even when a vector not containing a selection marker is used, selection is possible depending on whether or not the product is capable of being obtained. Choosing the selection marker depends on the host cell of interest, and is performed using any method known to those skilled in the art, and thus is not critical to the present invention.

[1073] In order to facilitate the purification of the binding molecule of the present invention, a tag sequence may be inserted into the expression vector and thus fused therewith. Examples of the tag include, but are not limited to, a hexa-histidine tag, a hemagglutinin tag, a myc tag or a flag tag, and any tag known to those in the art, which facilitates purification, may be used in the present invention.

[1074] The present invention also provides a cell line transformed with the expression vector. In one embodiment of the present invention, there is provided a cell line in which the expression vector is transformed into a host cell and which produces the binding molecule having ability to bind to and neutralize coronavirus.

[1075] In the present invention, the cell line may include cells of mammalian, plant, insect, fungal or cellular origin, without being limited thereto. As the mammalian cells, any one cell type selected from the group consisting of CHO cells, F2N cells, COS cells, BHK cells, Bowes melanoma cells, HeLa cells, 911 cells, HT1080 cells, A549 cells, HEK 293 cells and HEK293T cells may be used, without being limited thereto, and any cells may be used, as long as they are useful as mammalian host cells known to those skilled in the art.

[1076] The present invention also provides a composition for the diagnosis, amelioration, prevention and/or treatment of a disease caused by coronavirus, particularly SARS-coronavirus-2 (SARS-CoV-2), SARS-coronavirus-1 (SARS-CoV-1) or Middle East respiratory syndrome coronavirus (MERS-CoV), the composition comprising at least one of the binding molecule, the immunoconjugate, the nucleic acid molecule, the expression vector, and the cell line. Here, the disease caused by coronavirus may be coronavirus infection 2019 (COVID-19), severe acute respiratory syndrome, or Middle East respiratory syndrome, without being limited thereto. The above description of the binding molecule, the immunoconjugate, the nucleic acid molecule, the expression vector, and the cell line according to the present invention applies equally to the composition of the present invention. The composition of the present invention may comprise a pharmaceutically acceptable excipient, in addition to the binding molecule. As the pharmaceutically acceptable excipient, those already well known to those skilled in the art may be equally applied.

[1077] The composition of the present invention may further comprise one or more other therapeutic agents or diagnostic agents. For example, the composition of the present invention may further comprise, as an antiviral drug, interferon, an anti-S protein monoclonal antibody, an anti-S protein polyclonal antibody, a nucleoside analogue, a DNA polymerase inhibitor, a siRNA preparation, or a therapeutic vaccine, in addition to the binding molecule.

[1078] The composition comprising the binding molecule according to the present invention may be provided in the form of a formulation, such as a sterile injectable solution, a lyophilized formulation, a pre-filled syringe solution, an oral formulation, a formulation for external use, or a suppository, according to respective conventional methods, without being limited thereto.

[1079] Also, the composition comprising the binding molecule according to may be administered orally or parenterally. For example, the administration route may be intravenous administration, without being limited thereto.

[1080] The composition of the present invention may be administered to mammals including humans, thereby preventing and/or treating coronavirus infection, particularly SARS-coronavirus-2 (SARS-CoV-2), SARS-coronavirus-1 (SARS-CoV-

1) or Middle East respiratory syndrome coronavirus (MERS-CoV) infection, and a disease caused by the infection. Here, the administration dose of the binding molecule (e.g. antibody) depends on a subject to be treated, the severity of disease or condition, administration rate, and the judgment of the prescribing physician, and may be, for example, 0.1 to 300 mg/kg.

[1081] The present invention also provides a kit for the diagnosis, amelioration, prevention and/or treatment of a disease caused by coronavirus, particularly SARS-coronavirus-2 (SARS-CoV-2), SARS-coronavirus-1 (SARS-CoV-1) or Middle East respiratory syndrome coronavirus (MERS-CoV), the kit comprising at least one of the binding molecule, the immunoconjugate, the nucleic acid molecule, the expression vector, and the cell line. The above description of the binding molecule, the immunoconjugate, the nucleic acid molecule, the expression vector, and the cell line according to the present invention applies equally to the kit of the present invention.

[1082] In one embodiment of the present invention, the binding molecule or the like of the present invention, which is used in the diagnostic kit, may be detectably labeled. Various methods that may be used to label biomolecules are well known to those skilled in the art and are considered to fall within the scope of the present invention. Examples of labels that may be used in the present invention include enzymes, radioisotopes, colloidal metals, fluorescent compounds, chemiluminescent compounds and bioluminescent compounds. Commonly used labels include fluorescent substances (e.g., fluorescein, rhodamine, Texas red, etc.), enzymes (e.g., horseradish peroxidase, β-galactosidase, and alkaline phosphatase), radioisotopes (e.g., 32P or 125I), biotin, digoxigenin, colloidal metals, and chemiluminescent or bioluminescent compounds (e.g., dioxetane, luminol or acridinium). Labeling methods such as covalent bonding, iodination, phosphorylation, biotinylation, etc. of enzymes or biotinyl groups are well known in the art. Detection methods include, but are not limited to, autoradiography, fluorescence microscopy, direct and indirect enzyme reactions, and the like. As commonly used detection assays, radioisotopic or non-radioisotopic assays may be applied to the present invention. These assays include, inter alia, Western blotting, overlay analysis, RIA (radioimmunoassay), IRMA (immunoradioimmunometric assay), EIA (enzyme immunoassay), ELISA (enzyme-linked immunosorbent assay), FIA (fluorescent immunoassay) and CLIA (chemiluminescent immunoassay), without being limited thereto.

[1083] The diagnostic kit of the present invention may be used to detect the presence or absence of coronaviruses, including SARS-CoV-2, SARS-CoV-1, and MERS-CoV, by bringing the binding molecule into contact with a sample and then observing the reaction. The sample may be, but is not limited to, any one selected from the group consisting of sputum, saliva, blood, sweat, lung cells, lung tissue mucus, respiratory tissue, and spit, isolated from a subject, and the sample may be prepared using a conventional method known to those skilled in the art.

[1084] Another embodiment of the present invention also provides [1085] a kit for diagnosis, prevention or treatment of a disease caused by coronavirus, the kit comprising: [1086] a) the binding molecule; and [1087] b) a container.

[1088] Here, the disease caused by the coronavirus may be coronavirus infection 2019 (COVID-19), severe acute respiratory syndrome, or Middle East respiratory syndrome, without being limited thereto.

[1089] In the kit for diagnosis, amelioration, prevention and/or treatment according to the present invention, a solid carrier may be contained in the container of the kit. The antibody of the present invention may be attached to the solid carrier, and the solid carrier may be porous or non-porous, or may be planar or non-planar.

[1090] The present invention also provides a method of diagnosing, ameliorating, preventing and/or treating a disease caused by coronavirus, particularly, SARS-coronavirus-2 (SARS-CoV-2), SARS-coronavirus-1 (SARS-CoV-1) or Middle East respiratory syndrome coronavirus (MERS-CoV), the method comprising a step of administering a therapeutically effective amount of the binding molecule, immunoconjugate or composition of the present invention to either a subject having a disease caused by coronavirus, particularly, SARS-coronavirus-2 (SARS-CoV-2), SARS-coronavirus-1 (SARS-CoV-1) or Middle East respiratory syndrome coronavirus (MERS-CoV), or a subject suspected of or concerned about having the disease. Here, the disease caused by the coronavirus may be coronavirus infection 2019 (COVID-19), severe acute respiratory syndrome, or Middle East respiratory syndrome, without being limited thereto. The above description of the binding molecule, the immunoconjugate and the composition according to the present invention also applies equally to the method of the present invention. In one embodiment of the present invention, the method for diagnosis, amelioration, prevention and/or treatment may further comprise a step of administering an antiviral drug, a virus entry inhibitor or a virus adhesion inhibitor.

[1091] The present invention also provides a composition for diagnosing a disease caused by coronavirus, particularly, SARS-coronavirus-2 (SARS-CoV-2), SARS-coronavirus-1 (SARS-CoV-1) or Middle East respiratory syndrome coronavirus (MERS-CoV), the composition comprising at least one of the binding molecule, the immunoconjugate, the nucleic acid molecule, the expression vector and the cell line. Here, the disease caused by the coronavirus may be coronavirus infection 2019 (COVID-19), severe acute respiratory syndrome, or Middle East respiratory syndrome, without being limited thereto. The above description of the binding molecule, the immunoconjugate, the nucleic acid molecule, the expression vector and the cell line according to the present invention also applies equally to the composition of the present invention. The diagnostic composition of the present invention may comprise a pharmaceutically acceptable excipient, in addition to the binding molecule. As the pharmaceutically acceptable excipient, those already well known to those skilled in the art may be equally used.

[1092] The diagnostic composition of the present invention may further comprise one or more other diagnostic agents. For example, it may further comprise a binding molecule that binds to a nucleocapsid protein (N protein) on the surface of SARS-coronavirus-2 (SARS-CoV-2), in addition to the binding molecule described above.

[1093] In another embodiment of the present invention, the present invention also provides a strip for

immunochromatographic analysis, the strip comprising the binding molecule that binds to a spike protein (S protein) on the surface of coronavirus. The strip for immunochromatographic analysis may further comprise a binding molecule that binds to a nucleocapsid protein (N protein) of coronavirus. The coronavirus may be any one selected from the group consisting of SARS-coronavirus-2 (SARS-CoV-2), human coronavirus 229E (HCoV-229E), human coronavirus OC43 (HCoV-OC43), severe acute respiratory syndrome coronavirus-1 (SARS-CoV-1), human coronavirus NL63 (HCoV-NL63), human coronavirus HKU1, and Middle East respiratory syndrome coronavirus (MERS-CoV), without being limited thereto.
[1094] The strip for immunochromatographic analysis may comprise: [1095] i) a support; [1096] ii) a sample pad configured to accommodate a sample to be analyzed and comprising a buffer inlet and a sample inlet; [1097] iii) a conjugate pad containing a binding molecule that specifically binds to coronavirus contained in the sample introduced from the sample pad; [1098] iv) a signal detection pad comprising a signal detection part to configured to detect whether coronavirus is present in the sample and a control part configured to check whether the sample has moved to an absorbent pad regardless of the presence or absence of an analyte (coronavirus); and [1099] v) an absorbent pad configured to absorb the sample after completion of the signal detection reaction.
[1100] The strip may be configured such that a binding molecule that binds to a spike protein (S protein) on the surface of coronavirus is contained in each of the conjugate pad and the signal detection pad. The coronavirus S protein-binding molecule contained in the conjugate pad may be the same as or different from that contained in the signal detection pad. Also, the coronavirus S protein-binding molecule contained in each of the conjugate pad and the signal detection pad may be a binding molecule comprising the above-described sequence.
[1101] In the strip for immunochromatographic analysis, the binding molecule contained in the conjugate pad may be labeled with metal particles, latex particles, fluorescent materials, or enzymes. For example, the metal particles may be gold particles. The gold particles may be colloidal gold particles, without being limited thereto.
[1102] More specifically, the binding molecule of the present invention in the conjugate pad of the strip for immunochromatographic analysis may be detectably labeled. Various methods that may be used to label biomolecules are well known to those skilled in the art and are considered to fall within the scope of the present invention. Examples of labels that may be used in the present invention include enzymes, radioisotopes, colloidal metals, fluorescent compounds, chemiluminescent compounds and bioluminescent compounds. Commonly used labels include fluorescent substances (e.g., fluorescein, rhodamine, Texas red, etc.), enzymes (e.g., horseradish peroxidase, β-galactosidase, and alkaline phosphatase), radioisotopes (e.g., 32P or 125I), biotin, digoxigenin, colloidal metals, and chemiluminescent or bioluminescent compounds (e.g., dioxetane, luminol or acridinium). Labeling methods such as covalent bonding, iodination, phosphorylation, biotinylation, etc. of enzymes or biotinyl groups are well known in the art. Detection methods include, but are not limited to, autoradiography, fluorescence microscopy, direct and indirect enzyme reactions, and the like. As commonly used detection assays, radioisotopic or non-radioisotopic assays may be applied to the present invention. These assays include, inter alia, Western blotting, overlay analysis, RIA (radioimmunoassay), IRMA (immunoradioimmunometric assay), EIA (enzyme immunoassay), ELISA (enzyme-linked immunosorbent assay), FIA (fluorescent immunoassay) and CLIA (chemiluminescent immunoassay).
[1103] In the strip for immunochromatographic analysis, detection may be performed through visual observation, optical means, electrochemical means, or electrically conductive means, without being limited thereto.
[1104] In another embodiment of the present invention, the present invention provides a kit for diagnosing a disease caused by coronavirus, particularly SARS-coronavirus-2 (SARS-CoV-2), SARS-coronavirus-1 (SARS-CoV-1) or Middle East respiratory syndrome coronavirus (MERS-CoV), the kit comprising the strip for immunochromatographic analysis.
[1105] The diagnostic kit of the present invention may be used to detect the presence or absence of coronavirus by bringing the binding molecule into contact with a sample and then observing the reaction. The sample may be, but is not limited to, any one selected from the group consisting of sputum, saliva, blood, sweat, lung cells, lung tissue mucus, respiratory tissue, and spit, isolated from a subject, and the sample may be prepared using a conventional method known to those skilled in the art.
[1106] In another embodiment of the present invention, the present invention provides a method of detecting coronavirus, particularly SARS-coronavirus-2 (SARS-CoV-2), SARS-coronavirus-1 (SARS-CoV-1) or Middle East respiratory syndrome coronavirus (MERS-CoV), by using the diagnostic kit.
[1107] In another embodiment of the present invention, the present invention provides a method of detecting a disease caused by coronavirus, particularly SARS-coronavirus-2 (SARS-CoV-2), SARS-coronavirus-1 (SARS-CoV-1) or Middle East respiratory syndrome coronavirus (MERS-CoV), by using the diagnostic kit.
[1108] In another embodiment of the present invention, the present invention provides the use of the binding molecule for preparation of a composition for diagnosis, amelioration, prevention and/or treatment of a disease caused by coronavirus, particularly SARS-coronavirus-2 (SARS-CoV-2), SARS-coronavirus-1 (SARS-CoV-1) or Middle East respiratory syndrome coronavirus (MERS-CoV). Here, the disease caused by coronavirus may be coronavirus infection 2019 (COVID-19), severe acute respiratory syndrome, or Middle East respiratory syndrome, without being limited thereto. The above description of the binding molecule according to the present invention also applies equally to the use of the present invention.
[1109] In another embodiment of the present invention, the present invention provides the use of the composition for diagnosis, amelioration, prevention and/or treatment of a disease caused by coronavirus, particularly SARS-coronavirus-2 (SARS-CoV-2), SARS-coronavirus-1 (SARS-CoV-1) or Middle East respiratory syndrome coronavirus (MERS-CoV), the use comprising a step of administering a therapeutically effective amount of the binding molecule, immunoconjugate or

composition of the present invention to either a subject having a disease caused by coronavirus, particularly, SARS-coronavirus-2 (SARS-CoV-2), SARS-coronavirus-1 (SARS-CoV-1) or Middle East respiratory syndrome coronavirus (MERS-CoV), or a subject suspected of or concerned about having the disease. Here, the disease caused by coronavirus may be coronavirus infection 2019 (COVID-19), severe acute respiratory syndrome, or Middle East respiratory syndrome, without being limited thereto. The above description of the binding molecule, the immunoconjugate or the composition according to the present invention also applies equally to the use of the present invention.

[1110] In another embodiment of the present invention, the present invention provides a method of producing a binding molecule, the method comprising steps of: introducing a nucleic acid molecule encoding the binding molecule into a host cell; culturing the host cell under conditions that allow expression of the nucleic acid molecule; and selecting the binding molecule from the cultured host cell and/or a culture of the host cell. The above description of the binding molecule according to the present invention mentioned above applies equally to the production method of the present invention.

[1111] In another embodiment of the present invention, the present invention provides a binding molecule produced according to the method for producing the binding molecule.

[1112] Hereinafter, the terms used in the present invention will be defined as follows.

[1113] As used herein, the term “binding molecule” refers to intact immunoglobulins, including monoclonal antibodies, such as chimeric, humanized or human monoclonal antibodies, or antigen-binding fragments, which are immunoglobulins that bind to antigens. For example, the term indicates a variable domain, enzyme, receptor or protein comprising an immunoglobulin fragment that competes with the intact immunoglobulin in order to bind to a spike protein on SARS-CoV-2. Regardless of the structure, an antigen-binding fragment binds to the same antigen that is recognized by the intact immunoglobulin. The antigen-binding fragment may comprise a peptide or polypeptide comprising an antibody amino acid sequence comprising 2 or more contiguous amino acid residues, 20 or more contiguous amino acid residues, 25 or more contiguous amino acid residues, 30 or more contiguous amino acid residues, 35 or more contiguous amino acid residues, 40 or more contiguous amino acid residues, 50 or more contiguous amino acid residues, 60 or more contiguous amino acid residues, 70 or more contiguous amino acid residues, 80 or more contiguous amino acid residues, 90 or more contiguous amino acid residues, 100 or more contiguous amino acid residues, 125 or more contiguous amino acid residues, 150 or more contiguous amino acid residues, 175 or more contiguous amino acid residues, 200 or more contiguous amino acid residues, or 250 or more contiguous amino acid residues.

[1114] As used herein, the term “antigen-binding fragment” includes Fab, F(ab′), F(ab′)2, Fv, dAb, Fd, a complementarity-determining region (CDR) fragment, a single-chain antibody fragment (scFv), a bivalent single-chain antibody fragment, a single-chain phage antibody fragment, a diabody, a triabody, a tetrabody, a polypeptide that contains at least one fragment of an immunoglobulin that is sufficient to confer specific antigen binding to the polypeptide, etc. The above fragment may be produced synthetically or by enzymatic or chemical cleavage of intact immunoglobulins, or may be produced using a genetic engineering method by a recombinant DNA technique. Such production methods are well known in the art.

[1115] As used herein, the term “pharmaceutically acceptable excipient” refers to any inert substance that is combined with an active molecule such as a drug, agent, or antibody for preparing an agreeable or convenient dosage form. The pharmaceutically acceptable excipient is an excipient that is non-toxic, or at least of which the toxicity is acceptable for its intended use, to recipients at the dosages and concentrations employed and is compatible with other ingredients of the formulation comprising the drug, agent or binding molecule.

[1116] As used herein, the term “therapeutically effective amount” refers to an amount of the binding molecule of the present invention that is effective for prevention or treatment before or after exposure to coronavirus. In one embodiment of the present invention, the therapeutically effective amount may be, for example, 0.1 to 300 mg/kg.

[1117] As used herein, the term “culturing” means the in vitro maintenance, differentiation, growth, proliferation and/or reproduction of cells in a medium under suitable conditions.

[1118] As used herein, the term “comprises”, “comprising”, “includes” or “including” means that it may further comprise other components in addition to the corresponding component, and is different from the term “consisting of” that excludes further comprising other additional components.

[1119] The features described herein may be used in combination, and the fact that the features are set forth in different dependent claims of the claims does not indicate that they cannot be used in combination.

MODE FOR INVENTION

[1120] Hereinafter, the present invention will be described in detail with reference to examples. However, the following examples are merely illustrative of the content of the present invention, and the scope of the invention is not limited by the examples. Documents cited herein are incorporated herein by reference.

Example 1: Isolation of PBMCs from Blood of Patients Who Recovered from SARS-CoV-2

[1121] Blood donors were people (Korean adults) who were confirmed to have been infected with SARS-CoV-2 in 2020 and no longer exhibited viruses as a result of treatment, and the donor selection and blood collection processes were performed under the approval of the Institutional Review Board (IRB). After donor selection, about 30 ml of whole blood was collected, and PBMCs (peripheral blood mononuclear cells) were isolated using a Ficoll-Paque™ PLUS (GE Healthcare) method. The isolated PBMCs were washed twice with a phosphate buffer solution and then adjusted to a concentration of 1×10.sup.7 cells/ml in a freezing medium (RPMI:FBS:DMSO=5:4:1) and stored in a liquid nitrogen tank.

Example 2: Production of Antibody-Displayed Phage Library

[1122] Total RNA was extracted from the PBMCs (isolated in Example 1) using a TRIzol reagent (Invitrogen), and then cDNA was synthesized therefrom using a SuperScript™ III First-Strand cDNA synthesis system (Invitrogen, USA).

[1123] Production of the antibody library from the synthesized cDNA was performed with reference to the related literature (Barbas C. et. al. Phage Display: A Laboratory Manual. 2001. CSHL Press). Briefly, light-chain and heavy-chain variable regions of the antibody were amplified from the synthesized cDNA by a PCR (polymerase chain reaction) method using high-fidelity Taq polymerase (Roche) and a degenerative primer set (IDT). The isolated light-chain and heavy-chain variable-region fragments were made into an scFv gene by an overlap PCR method so as to be connected as one sequence in random combination, and the scFv gene was amplified, cleaved with restriction enzymes, and then isolated using 1% agarose gel electrophoresis and a gel extraction kit (Qiagen). A phage vector was cleaved with the same restriction enzymes, isolated, and mixed with the scFv gene, and T4 DNA ligase (New England Biolabs) was added thereto. The resulting mixture was allowed to react at 16° C. for 12 hours or more. The resulting reaction solution was mixed with ER2738 competent cells, and then transformed into the cells by an electroporation process. The transformed ER2738 cells were subjected to shaking culture, and then a VCSM13 helper phage (Agilent Technologies) was added thereto, followed by culturing for 12 hours or more.

Example 3: Selection Using Phage Enzyme Immunoassay

[1124] The phage library culture prepared in Example 2 was centrifuged to remove the host cells, and then 4% PEG and 0.5 M NaCl were added thereto. The phage was precipitated by centrifugation and the supernatant was removed. The precipitated phage was diluted with 1% BSA/TBS to afford a phage library, and then panning was independently performed through association to and dissociation from various SARS-CoV-2 spike proteins (S1, S2, S1+S2), SARS-CoV-1 spike proteins or MERS-CoV spike proteins, thereby isolating an scFv-phage having ability to bind to SARS-CoV-2, SARS-CoV-1 or MERS-CoV spike proteins. For example, the phage library was added to an ELISA plate to which an S2 domain (residues S686 to P1213 on S protein), which is a portion of the SARS-CoV-2 S protein, was attached, followed by reaction at room temperature for 2 hours. The reaction solution was removed, and then the ELISA plate was washed with PBS containing 0.05% Tween 20. Next, the scFv-phage bound to the antigen was detached by adding 60 μl of 0.1 M glycine-HCl (pH 2.2), and neutralized using 2M Tris (pH 9.1). The neutralized scFv-phage was infected into ER2738 cells, and then incubated with helper phage, and used for subsequent panning. A portion of the infected ER2738 was spread on an LB plate before the addition of the helper phage, and a colony was obtained the next day.

[1125] The colonies, formed in each panning round, were shake-cultured in a culture medium in a 96-well deep well plate (Axygen), and when the OD.sub.600 reached 0.7 or more, helper phage was added thereto, followed by shaking culture at 37° C. for 12 hours or more. The culture was centrifuged, the host cells were removed, and the supernatant containing the scFv-phage was collected.

[1126] The collected scFv-phage supernatant was diluted at 1:1 with 6% BSA/PBS, and then added to each well of a 96-well microtiter plate, which has been adsorbed with SARS-CoV-2 S proteins and then blocked, and each well was incubated at 37° C. for 2 hours. Each well was washed three times with PBS containing 0.05% Tween 20, and then incubated with an anti-M13 antibody labeled with HRP (horseradish peroxidase) 37° C. for 1 hour. Each well was washed three times with PBS containing 0.05% Tween 20, and then ABTS (2,2′-azinobis[3-ethylbenzothiazoline-6-sulfonic acid]-diammonium salt) was added thereto, and the absorbance at 405 nm was measured, thereby selecting scFv-phages having ability to bind to SARS-CoV-2 S antigen proteins.

Example 4: Evaluation of Neutralizing Activity of scFv-Fc Antibody Fragment Against SARS-CoV-2

[1127] For the scFv-phages selected in Example 3, DNA was obtained through shaking culture of colonies, and then sequences for antibody variable regions were analyzed. Among them, scFv-phages, selected by excluding clones with overlapping amino acid sequences, were cloned into vectors in the form of an scFv antibody fragment (scFv-Fc) in order to evaluate the expression levels of candidate antibodies in animal cell lines. The scFv-phages were transfected into CHO cells using a transfection reagent and expressed therein, and using the culture of the cells, the 190 scFv-Fc antibody fragments were evaluated against the Korean isolate SARS-CoV-2 virus S type (betaCoV/Korea/KCDC03/2020; NCCP43326) by CPE (cytopathic effect) assay. The 190 selected antibody fractions are shown in Tables 1 and 2.

[1128] For CPE assay, each antibody sample was diluted, mixed with an equal volume of 100TCID50 virus, incubated at 37° C. for 30 minutes, and infected into the VERO.E6 cell line, and viable cells were analyzed. After 4 days of incubation in an incubator at 37° C. under 5% CO.sub.2, the neutralizing activity of each antibody fragment was evaluated by analyzing viable cells. Two wells at one concentration were independently analyzed, and the neutralizing activity (%) of the antibody was expressed as 100% when the cells in the two wells were variable. 50% indicates a case in which the cells in only one well were viable, and 0% indicates a case in which the cells in the two wells were not viable.

[1129] As a result of the analysis, as shown in Table 3 below, antibody fragments having neutralizing activity were identified. No. in Table 3 below refers to the same binding molecule as the No. of each binding molecule shown in Tables 1 and 2 above. The positive control antibody in Table 3 below is Celltrion's CT-P59 COVID-19 neutralizing antibody (antibody No. 139 disclosed in Korean Patent No. 10-2205028).

TABLE-US-00003 TABLE 3 scFv-Fc dilution concentration (μg/ml) No. 2 1 0.5 0.25 0.125 2 0 0 50 0 0 3 50 0 0 0 0 0 12 50 0 0 0 0 15 0 0 0 50 0 16 50 0 0 0 0 18 50 0 0 0 0 19 50 0 0 0 0 20 100 100 100 100 100 22 0 50 0 0 0 23 50 0 0 0 0 24 100 100 100 0 0 26 0 0 50 50 0 31 50 0 0 0 0 32 100 100 100 100 100 33 50 50 0 0 0 34 100 100 100 50 0 37 50 50 50 50 0 43 100 0 0 0 0 45 100 50 50 50 0 48 100 100 100 100 100 50 0 50 0 0 0 51 50 0 0 0 0 53 50 50 50 0 0 54 100 100 100 100 100 55 0 0 50 0 0 56 0 0 50 50 0 59 50 50 0 0 0 60 50 50 0 0 0 61 100 100 100 50 0 66 50 50 50 0 0 69 50 0 0 0 0 74 50 0 0 0 0 75 50 50 0 0 0 76 100 50 0 0 0 81 100 100 100 100 100 82 50 0 0 0 0 83 50 0 0 0 0 85 50 0 0 0 0 86 50 0 0 0 0 87 50 50 50 0 0 93 50 50 50 0 0 94 100 0 0 0 0 95 100 0 0 0 0 96 100 0 0 0 0 98 50 50 0 0 0 102 100 0 0 0 0 103 0 0 100 100 50 104 100 100 50 0 0 108 0 50 0 0 0 Positive control 100 100 100 100 100 antibody

Example 5: Evaluation of Binding Affinity of Antibody after Conversion into Fully Human Antibody (Full IgG)

[1130] The selected antibody fragments (scFv-Fc) confirmed to have neutralizing activity in Example 4 above were converted into fully human antibodies (full IgG), and antibody-containing cultures were prepared according to the method of Example 4. The binding affinity (equilibrium dissociation constant, K.sub.D) of each fully human antibody to SARS-CoV-2 RBD was evaluated by biolayer interference (BLI) assay using Octet. As a result of analysis, it was confirmed that 11 fully human antibodies had excellent binding affinity to the SARS-CoV-2 virus surface protein (RBD) as shown in Table 4 below. No. in Table 4 below refers to the same binding molecule as the No. of each binding molecule shown in Tables 1 and 2 above.

TABLE-US-00004 TABLE 4 No. K.sub.D (M) 32 1.47E−10 33 4.31E−11 34 1.85E−10 37 5.70E−11 45 7.08E−11 48 1.84E−10 53 3.39E−09 54 3.13E−11 59 4.96E−11 61 2.26E−11 81 4.28E−11

Example 6: Evaluation of Neutralizing Activity of Fully Human Antibody (Full IgG)

6-1. Evaluation (1) of Neutralizing Activity of Fully Human Antibody (Full IgG)

[1131] The 11 fully human antibodies (full IgGs) selected based on their binding affinity to the SARS-CoV-2 S (RBD) protein and their expression level in Example 5 were evaluated for neutralizing activity against the Korean isolate SARS-CoV-2 virus GR type (hCoV-19/South Korea/KUMC17/2020) using a PRNT (plaque reduction neutralization test) method.

[1132] For PRNT, each antibody sample was diluted (10 concentrations, obtained through 1/4 serial dilution from 1 ng/ml, and 11 concentrations, obtained through 1/2 serial dilution from 0.5 ng/1l), mixed with an equal volume of a virus (0.05 MOI), incubated at 37° C. for 2 hours, and then infected into VERO.E6 cells, followed by plaque assay. After incubation in a 5% CO.sub.2 incubator at 37° C. for 60 hours, the neutralizing activity of each antibody sample was evaluated by staining with crystal violet and comparatively analyzing the number of formed plaques. The neutralizing activity (ng/ml) of each antibody is an average value obtained from the results of the neutralizing activity evaluation performed in duplicate, and was expressed as the IC.sub.50 value of the antibody-treated group. Here, the IC.sub.50 value is the antibody concentration at which the antibody exhibits 50% of the neutralizing activity against the virus. In Table 5 below, a lower value indicates the better neutralizing activity.

[1133] As a result of analysis, as shown in Table 5 below, fully human antibodies (full IgG) having excellent neutralizing activity were confirmed. In Table 5 below, No. refers to the same binding molecule as the No. of each binding molecule shown in Tables 1 and 2.

TABLE-US-00005 TABLE 5 No. IC.sub.50 (ng/ml) 32 92.17 33 >1000 34 448.9 37 542.8 45 434.5 48 155.8 53 381.4 54 63.8 59 >1000 61 798.6 81 669.9

6-2. Evaluation (2) of Neutralizing Activity of Fully Human Antibody (Full IgG)

[1134] 6 fully human antibodies (full IgGs), selected based on antibody characteristics such as antibody expression levels, were additionally evaluated for neutralizing activity against the SARS-CoV-2 GR type virus using a PRNT (plaque reduction neutralization test) method.

[1135] As a result of analysis, it was confirmed that the antibodies had neutralizing activity as shown in Table 6 below. In Table 6 below, No. refers to the same binding molecule as the No. of each binding molecule shown in Tables 1 and 2. The positive control antibody in Table 6 below is Celltrion's CT-P59 COVID-19 neutralizing antibody.

TABLE-US-00006 TABLE 6 No. IC.sub.50 (ng/ml) 32 21.1 34 499.4 37 1082.4 45 521.9 54 16.0 32 + 54 11.1 Positive control 2.0

6-3. Evaluation (3) of Neutralizing Activity of Fully Human Antibody (Full IgG)

[1136] Antibody No. 32, selected based on antibody characteristics such as antibody expression levels, was additionally evaluated against the Korean isolate GR type (hCoV-19/South Korea/KUMC17/2020), GH type (hCoV-19/Korea/KCDC10847/2020), the mutant virus strain from the UK (hCoV-19/South Korea/KDCA0838/2020) and the mutant virus strain from South African (hCoV-19/South Korea/KDCA0463/2020) by a PRNT (plaque reduction neutralization test) method according to the analysis method described in Example 6-1.

[1137] As a result of analysis, it was confirmed that the antibody had neutralizing activity against each virus strain as shown in Table 7 below.

TABLE-US-00007 TABLE 7 Type IC.sub.50 (ng/ml) GR 71.1 GH 176.2 Mutant virus strain from the UK 31.73 Mutant virus strain from South African 27.62

6-4. Evaluation (4) of Neutralizing Activity of Fully Human Antibody (Full IgG)

[1138] The antibodies, selected based on antibody characteristics such as antibody expression levels, were additionally evaluated for neutralizing activity against SARS-CoV-1 and MERS-CoV viruses.

[1139] As a result of analysis, it was confirmed that the antibodies had neutralizing activity as shown in Table 8 below. In Table 8 below, No. refers to the same binding molecule as the No. of each binding molecule shown in Tables 1 and 2 above. In Table 8 below, the positive control antibody against SARS-CoV-1 is CR3022 (Xiaolong Tian et al., Emerg Microbes Infect. 2020 Feb. 17; 9(1):382-385), and the positive control antibody against MERS-CoV is Celltrion's CT-P38 MERS neutralizing antibody (antibody 5 disclosed in Table 7 of Korean Patent Application Publication No. 10-2019-0093114).

TABLE-US-00008 TABLE 8 MERS-CoV SARS-CoV-1 No. IC.sub.50 (ng/ml) IC.sub.50 (ng/ml) 2 6682.3 4001.4 59 >10000 6729.5 95 9690.8 >10000 102 >10000 2314.7 103 8132.8 >10000 32 8377.7 >10000 CT-P59 8125.1 >10000 CR3022 >10000 6843.6 CT-P38 51.8 >10000

Example 6-5. Evaluation (1) of Neutralizing Activity of Fully Human Antibody (Full IgG) Against SARS-CoV-2 Mutant Pseudoviruses

[1140] A test was conducted to evaluate the neutralizing activity of a cocktail of antibody No. 32+antibody No. 54 against SARS-CoV-2 spike D614 and D614G and 20 prepared SARS-CoV-2 spike mutant pseudoviruses. Here, antibody No. 32 and antibody No. 54 respectively refer to binding molecule No. 32 and binding molecule No. 54 shown in Tables 1 and 2. The SARS-CoV-2 spike mutant pseudoviruses were prepared with reference to a portion of the epitope of the CT-P59 (Regdanvimab) antibody and the mutant viruses published in papers (A. Baum et al., Science, 2020 Aug. 21; 369(6506): 1014-1018, and Korber et al., 2020, Cell 182, 812-827). The amount of each mutant pseudovirus was fixed at 1.73×10.sup.7 copies, and the antibody was diluted in 10 steps of 3-fold dilutions to the highest concentration of 1,000 ng/mL. As a result of conducting a neutralization activity test using each mutant pseudovirus and each antibody dilution, it was confirmed that the antibody had neutralizing activity as shown in Table 9 below.

[1141] In Table 9 below, each mutation position was numbered from the N-terminus of the coronavirus spike protein (NCBI accession number: YP_009724390.1, SEQ ID NO: 1,521).

TABLE-US-00009 TABLE 9 SARS-CoV-2 mutant Backbone IC.sub.50 No. pseudovirus vector (ng/mL) 1 D614 — 5.229 2 S494P D614 13.42 3 R685H D614 5.046 4 S494P + R685H D614 2.676 5 E484K D614 13.63 6 Q493K D614 10.15 7 F490S D614 13.25 8 Y449N D614 12.55 9 L455F D614 6.989 10 F456L D614 3.056 11 L452R D614 25.73 12 E406Q D614 15.11 13 K444Q D614 8.646 14 V445A D614 7.124 15 N234Q D614 70.01 16 A475V D614 7.35 17 D614G — 6.723 18 S477N D614G 4.659 19 A222V D614G 6.404 20 V1176F D614G 9.035 21 N439K D614G 6.225 22 Y453F D614G 8.515

Example 6-6. Evaluation (2) of Neutralizing Activity of Fully Human Antibody (Full IgG) Against SARS-CoV-2 Mutant Pseudoviruses

[1142] A test was conducted to evaluate the neutralizing activities of antibody No. 32 and antibody No. 54 against 15 SARS-CoV-2 mutant pseudoviruses. Here, antibody No. 32 and antibody No. 54 respectively refer to binding molecule No. 32 and binding number 54 shown in Tables 1 and 2. The SARS-CoV-2 spike mutant pseudoviruses were prepared with reference to a portion of the epitope of the CT-P59 (Regdanvimab) antibody and the mutant viruses published in papers (A. Baum et al., Science, 2020 Aug. 21; 369(6506): 1014-1018, and Korber et al., 2020, Cell 182, 812-827). The amount of each mutant pseudovirus was fixed at 1.73×10.sup.7 copies, and the antibody was diluted in 10 steps of 3-fold dilutions to the highest concentration of 1,000 ng/mL. As a result of conducting a neutralization activity test using each mutant pseudovirus and each antibody dilution, as shown in Table 10 below, it was confirmed that the antibody had neutralizing activity.

[1143] In Table 10 below, each mutation position was numbered from the N-terminus of the coronavirus spike protein (NCBI accession number: YP_009724390.1, SEQ ID NO: 1521).

TABLE-US-00010 TABLE 10 SARS-CoV-2 mutant IC.sub.50 (ng/ml) No. pseudovirus No. 32 No. 54 1 D614G 7 100 2 K417N + E484K + N501Y 10 2870 3 501Y.V2 60 2180 4 D614G 3.25 12.84 5 K417N 1 4.817 6 E484K 5.9 >1000 7 L452R 3.39 >1000 8 Y449N 2.14 21.9 9 L455F 7.52 8.87 10 F456L 2.4 2.15 11 Q493K 5.62 9.92 12 S494P 6.29 5.85 13 E406Q 3.26 1.71 14 F490S 6.08 12 15 K417T 0.91 7.08

6-7. Evaluation of Neutralizing Activity of Antibody No. 32

[1144] Antibody No. 32 (corresponding to No. 32 in Tables 1 and 2), which is a fully human antibody (full IgG) selected based on its binding affinity to the SARS-CoV-2 S (RBD) protein and expression level and its neutralizing activity against the wild-type SARS-CoV-2 virus, was evaluated for neutralizing activity against the mutant virus strain from South Africa (hCoV-19/South Korea/KDCA0463/2020) by a PRNT (plaque reduction neutralization test) method.

[1145] For PRNT, the antibody sample was diluted (11 concentrations obtained through 1/2 serial dilution from 1 ng/μl), mixed with an equal volume of a virus (0.05 MOI), incubated at 37° C. for 2 hours, and then infected into VERO.E6 cells, followed by plaque assay. After incubation in a 5% CO.sub.2 incubator at 37° C. for 60 hours, the neutralizing activity of the antibody sample was evaluated by staining with crystal violet and comparatively analyzing the number of formed plaques. The neutralizing activity (ng/ml) of the antibody is an average value obtained from the results of the neutralizing activity evaluation performed in duplicate, and was expressed as the IC.sub.50 value and IC.sub.90 value of the antibody-treated group. Here, the IC.sub.50 value is the antibody concentration at which the antibody exhibits 50% of the neutralizing activity against the virus, and the IC.sub.90 value is the antibody concentration at which the antibody exhibits 90% of the neutralizing activity against the virus. In Table 11 below, a lower value indicates the better neutralizing activity.

[1146] As a result of analysis, it was confirmed that antibody No. 32 had neutralizing activity against the mutant virus strain from South Africa as shown in Table 11 below.

TABLE-US-00011 TABLE 11 Antibody IC.sub.50 (ng/ml) IC.sub.90 (ng/ml) No. 32 24.45 59.78

6-8. Evaluation of Neutralizing Activity of Antibody No. 32 Against SARS-CoV-2 Mutant Pseudoviruses

[1147] A test was conducted to evaluate the neutralizing activities of antibody No. 32 against SARS-CoV-2 spike D614 and 50 prepared SARS-CoV-2 spike mutant pseudoviruses. The SARS-CoV-2 spike mutant pseudoviruses were prepared with reference to a portion of the epitope of the CT-P59 (Regdanvimab) antibody and the mutant viruses published in papers (A. Baum et al., Science, 2020 Aug. 21; 369(6506):1014-1018., Korber et al., 2020, Cell 182, 812-827., and Wang et al., 2021, doi: 10.1038/s41586-021-03398-2.). The amount of each mutant pseudovirus was fixed at 1.73×10.sup.7 copies, and the antibody was diluted in 10 steps of 3-fold dilutions to the highest concentration of 100 ng/mL. As a result of conducting a neutralization activity test using each mutant pseudovirus and each antibody dilution, it was confirmed that the antibody had neutralizing activity as shown in Table 12 below.

[1148] In Table 12 below, each mutation position was numbered from the N-terminus of the coronavirus spike protein (NCBI accession number: YP_009724390.1, SEQ ID NO: 1,521). In addition, the position of each mutation in UK mutant

virus strain 501Y.V1 (B.1.1.7), South Africa mutant virus strain 501Y.V2 (B.1.351), Brazil mutant virus strain 501Y.V3 (P.1), California mutant virus strain (B.1.429), New York mutant virus strain (B.1.525) and New York mutant virus strain (B.1.526) is shown in Reference Table A below.

TABLE-US-00012 TABLE 12 SARS-CoV-2 mutant Backbone No. pseudovirus vector IC.sub.50 (ng/ml) 1 D614 — 4.342 2 D614G — 4.113 3 Q493R D614G 4.941 4 K417E D614G 1.133 5 G446V D614G 5.019 6 G476S D614G 6.036 7 F486V D614G 4.222 8 E406W D614G 7.836 9 N440D D614G 4.238 10 P681H D614G 3.011 11 K417N D614G 1.344 12 A701V D614G 4.139 13 D80A D614G 2.657 14 K417N + E484K + N501Y D614G 2.71 15 Q493M D614G 4.785 16 F486I D614G 3.18 17 Y489H D614G 8.358 18 N501Y D614G 4.838 19 HV69-70 del D614G 4.156 20 HV69-70del + N501Y D614G 4.633 21 N501T D614G 5.959 22 N501F D614G 5.952 23 Q677H D614G 4.84 24 Q498H D614G 2.558 25 N460T D614G 16.71 26 F486S D614G 2.275 27 F486L D614G 2.366 28 T478K D614G 2.575 29 K417T D614G 0.977 30 Q493Y D614G 1.124 31 Q493A D614G 5.745 32 A372V D614G 2.441 33 P384L D614G 4.404 34 S494L D614G 4.638 35 501Y.V3 (P.1) D614G 1.71 36 501Y.V2 (B.1.351) D614G 3.272 37 B.1.526 D614G 3.53 38 E484Q + L452R + P681R D614G 8.264 39 UK (B.1.1.7) D614G 5.413 40 California (B.1.429) D614G 6.723 41 New York (B.1.525) D614G 5.569 42 S477R D614G 8.772 43 D420N D614G — 44 Y473F D614G 5.248 45 S494Q D614G 2.756 46 E484G D614G 3.556 47 S477N D614G 4.561 48 S494P D614G 6.49 49 Y453F D614G 4.422 50 N439K D614G 5.352 51 A222V D614G 4.721 52 N234Q D614G 14.41

TABLE-US-00013 (Reference Table A) UK HV Y144del N501Y D614G T716I S982A D1118H 501Y.V1 69- (B.1.1.7) 70del A570D P681H South L18F D215G K417N N501Y D614G A701V Africa D80A LAL 242-244del E484K 501Y.V2 (B.1.351) Brazil L18F D138Y K417T N501Y D614G T1027I 501Y.V3 T20N R190S E484K H655Y V1176F (P.1) P26S California S13I W152C L452R D614G (B.1.429) A67V Y144del E484K D614G F888L New York HV Q677H (B.1.525) 69- 70del New York L5F D253G E484K D614G A701V (B.1.526) T95I

6-9. Evaluation of Neutralizing Activity of Antibody No. 32 Against SARS-CoV-2 Mutant Viruses from US and South Africa

[1149] Antibody No. 32, selected based on antibody characteristics such as antibody expression level, was additionally evaluated against the mutant virus strains from California, USA ((hCoV-19/Korea/KDCA49671/2021 (B.1.427) and hCoV-19/Korea/KDCA59777/2021 (B.1.429) and the mutant virus strain from South Africa (hCoV-19/South Korea/KDCA0463/2020, B.1.351) by a PRNT (plaque reduction neutralization test) method as described above. As a result, it was confirmed that the antibody had neutralizing activity as shown in Table 13 below.

TABLE-US-00014 TABLE 13 No. Mutant virus IC.sub.50 (ng/ml) 1 (B.1.427) from California, USA 58.48 2 (B.1.429) from California, USA 34.28 3 Mutant strain (B.1.351) from South Africa 20.58

6-10. Evaluation of Neutralizing Activity of Antibody No. 32 Against SARS-CoV-2 Mutant Viruses from New York and Nigeria

[1150] Antibody No. 32, selected based on antibody characteristics such as antibody expression level, was additionally evaluated against the Korean isolate GR type (B.1.1.119) as a control, the mutant virus strain from New York, USA (hCoV-19/Korea/KDCA82438/2021, B.1.526), and the mutant virus strain (B.1.525) from UK/Nigeria by a PRNT (plaque reduction neutralization test) method as described above. As a result, it was confirmed that the antibody had neutralizing activity as shown in Table 14 below.

TABLE-US-00015 TABLE 14 No. Mutant virus IC.sub.50 (ng/ml) 1 (B.1.526) from New York, USA 44.44 2 (B.1.525) from UK/Nigeria 14.53 3 GR (B.1.1.119) 50.5

6-11. Evaluation of Neutralizing Activity of Antibody No. 32 Against SARS-CoV-2 Mutant Virus (P.1) from Brazil

[1151] Antibody No. 32, selected based on antibody characteristics such as antibody expression level, was additionally evaluated against the mutant virus strain (P.1) from Brazil by a PRNT (plaque reduction neutralization test) method as described above. As a result of analysis, it was confirmed that the antibody had neutralizing activity as shown in Table 15 below.

TABLE-US-00016 TABLE 15 No. Mutant virus IC.sub.50 (ng/ml) 1 (P.1) from Brazil 7.21

6-12. Evaluation of Neutralizing Activity of Antibody No. 32 Against SARS-CoV-2 Mutant Viruses (B.1.617.1, and B.1.617.2) from India

[1152] Antibody No. 32, selected based on antibody characteristics such as antibody expression level, was additionally evaluated against the mutant virus strains (hCoV-19/Korea/KDCA2950/2021 (B.1.617.1), and hCoV-19/Korea/19861/KDCA/2021 (B.1.617.2)) from India by a PRNT (plaque reduction neutralization test) method as described above. As a result of analysis, it was confirmed that the antibody had neutralizing activity as shown in Table 16 below.

TABLE-US-00017 TABLE 16 No. Mutant virus IC.sub.50 (ng/ml) 1 (B.1.617.1) from India 25.84 2 (B.1.617.2) from India 18.88

Example 7. Evaluation of Binding Affinity and Mechanism of Action of Fully Human Antibody (Full IgG)

[1153] The binding affinity (antibody No. 32 and No. 54) and mechanism of action (antibody No. 32) of the antibodies (full IgG), selected in Examples 5 and 6, to SARS-CoV-2 RBD mutant proteins, were evaluated by performing Octet analysis.

[1154] SARS-CoV-2 virus can initiate infection of human cells by binding of the surface protein (RBD) thereof to the human receptor (ACE2). Thus, the mechanism of action of antibody No. 32 (full IgG) was evaluated by performing biolayer interference (BLI) assay using Octet. As a result of analysis, it was confirmed that the antibodies had excellent binding affinity even to mutant proteins of the SARS-CoV-2 virus surface protein (RBD) as shown in Table 17 below, and

that the binding of the SARS-CoV-2 virus surface protein (RBD) to the human receptor (ACE2) was completely inhibited by antibody No. 32 (full IgG) as shown in FIG. **1**.

TABLE-US-00018 TABLE 17 No. RBD type K.sub.D (M) kon (1/Ms) kdis (1/s) 32 3.05E−10 6.33E+05 1.93E−04 54 WT 1.33E−10 8.15E+05 1.08E−04 32 1.61E−10 5.48E+05 8.82E−05 54 S494P 1.84E−11 8.22E+05 1.51E−05 32 3.13E−10 4.74E+05 1.48E−04 54 K417N 6.63E−11 1.06E+06 7.04E−05 32 2.90E−10 6.63E+05 1.92E−04 54 E484K 1.73E−09 2.32E+05 4.01E−04 32 3.79E−10 4.72E+05 1.79E−04 54 N501Y 1.18E−10 8.13E+05 9.56E−05 32 + 54 WT 2.74E−10 3.72E+05 1.02E−04 32 + 54 S494P 1.99E−10 4.14E+05 8.22E−05 32 + 54 K417N 1.60E−10 4.62E+05 7.39E−05 32 + 54 E484K 6.90E−10 2.48E+05 1.71E−04 32 + 54 N501Y 2.35E−10 4.13E+05 9.68E−05

Example 8. Evaluation of Neutralizing Activity of Fully Human Antibody (Full IgG) Against SARS-CoV-2 Virus Through Animal Experiment

8-1. Experiment for Evaluation of Preventive Efficacy in Mice

[1155] Using TG mice (B6.Cg-Tg(K18-ACE2)2Prlmn/J [Stock No: 034860 K18-hACE2] from The Jackson Laboratory) as an animal model that is naturally infected with SARS-CoV-2 virus and shows clinical symptoms and lesions similar to those in humans, an experiment was conducted as follows in order to evaluate the in-vivo preventive efficacy of antibody No. 32 and No. 54.

[1156] Mice were divided into a total of 10 groups, including a non-infected group, an infected group, and administered groups (1 mg/kg or 10 mg/kg CT-P59, 1 mg/kg or 10 mg/kg antibody No. 32, 1 mg/kg or 10 mg/kg antibody No. 54, and 1 mg/kg or 10 mg/kg antibody No. 32+antibody No. 54 cocktail). The non-infected group consisted of 3 mice, and the infected group and the administered groups consisted of 6 mice per group. 24 hours after administration of DPBS or 1 mg/kg or 10 mg/kg of each antibody to each group, 1×10.sup.5 PFU/50 μL of SARS-CoV-2 virus (NMC-nCoV02) was inoculated into the nasal cavity, and observation was performed for a maximum of 6 days. Additionally, the body weight of each mouse in each group was evaluated before viral inoculation and daily for 6 days after viral inoculation. In order to measure the virus titer in the tissue, the mice were sacrificed on days 3 and 6 after viral inoculation, and the lung tissue and nasal lavage fluid were obtained therefrom. The virus titer of each tissue was measured through plaque assay using Vero cells.

[1157] As a result, antibody No. 32 (1 and 10 mg/kg) and antibody No. 54 (10 mg/kg) showed non-inferiority in terms of body weight change compared to CT-P59. A low dose (1 mg/kg) of antibody No. 54 showed significantly lower results in terms of body weight change compared to CT-P59 and antibody No. 32 (FIG. **2***a*).

[1158] The results of measuring the virus titer in the lungs by plaque assay are as follows. A high dose (10 mg/kg) of antibody No. 32 antibody and a high dose (10 mg/kg) of the cocktail of antibody No. 32 and antibody No. 54 showed the best preventive efficacy because the virus was not detected from day 3. On day 6, all of the antibody-administered groups showed preventive efficacy (FIG. **2***b*).

[1159] In addition, the results of measuring the viral titer in the nasal lavage fluid by plaque assay are as follows. On day 3, there was no difference in preventive efficacy between the low-dose (1 mg/kg) groups. Only the antibody No. 32+antibody No. 54 cocktail group showed the best preventive efficacy in comparison between the low-dose (1 mg/kg) groups because the virus was not detected on day 6. The high dose (10 mg/kg) showed preventive efficacy on day 6 in all of the administered groups (FIG. **2***c*).

Claims

1. A neutralizing binding molecule that binds to a spike protein (S protein) on a surface of coronavirus, wherein the binding molecule is any one selected from the group consisting of the following binding molecules 1) to 49): 1) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 7, a CDR2 region of SEQ ID NO: 8, and a CDR3 region of SEQ ID NO: 9, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 10, a CDR2 region of SEQ ID NO: 11, and a CDR3 region of SEQ ID NO: 12; 2) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 13, a CDR2 region of SEQ ID NO: 14, and a CDR3 region of SEQ ID NO: 15, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 16, a CDR2 region of SEQ ID NO: 17, and a CDR3 region of SEQ ID NO: 18; 3) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 67, a CDR2 region of SEQ ID NO: 68, and a CDR3 region of SEQ ID NO: 69, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 70, a CDR2 region of SEQ ID NO: 71, and a CDR3 region of SEQ ID NO: 72; 4) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 85, a CDR2 region of SEQ ID NO: 86, and a CDR3 region of SEQ ID NO: 87, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 88, a CDR2 region of SEQ ID NO: 89, and a CDR3 region of SEQ ID NO: 90; 5) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 91, a CDR2 region of SEQ ID NO: 92, and a CDR3 region of SEQ ID NO: 93, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 94, a CDR2 region of SEQ ID NO: 95, and a CDR3 region of SEQ ID NO: 96; 6) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 103, a CDR2 region of SEQ ID NO: 104, and a CDR3 region of SEQ ID NO: 105, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 106, a CDR2 region of SEQ ID NO: 107, and a CDR3 region of SEQ ID NO: 108; 7) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 109, CDR2 region of SEQ ID NO: 110, and CDR3 region of SEQ ID NO: 111, and b) a heavy-chain

variable region comprising a CDR1 region of SEQ ID NO: 112, a CDR2 region of SEQ ID NO: 113, and a CDR3 region of SEQ ID NO: 114; 8) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 115, a CDR2 region of SEQ ID NO: 116, and a CDR3 region of SEQ ID NO: 117, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 118, a CDR2 region of SEQ ID NO: 119, and a CDR3 region of SEQ ID NO: 120; 9) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 127, a CDR2 region of SEQ ID NO: 128, and a CDR3 region of SEQ ID NO: 129, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 130, a CDR2 region of SEQ ID NO: 131, and a CDR3 region of SEQ ID NO: 132; 10) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 133, a CDR2 region of SEQ ID NO: 134, and a CDR3 region of SEQ ID NO: 135, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 136, a CDR2 region of SEQ ID NO: 137, and a CDR3 region of SEQ ID NO: 138; 11) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 139, a CDR2 region of SEQ ID NO: 140, and a CDR3 region of SEQ ID NO: 141, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 142, a CDR2 region of SEQ ID NO: 143, and a CDR3 region of SEQ ID NO: 144; 12) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 151, a CDR2 region of SEQ ID NO: 152, and a CDR3 region of SEQ ID NO: 153, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 154, a CDR2 region of SEQ ID NO: 155, and a CDR3 region of SEQ ID NO: 156; 13) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 181, a CDR2 region of SEQ ID NO: 182, and a CDR3 region of SEQ ID NO: 183, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 184, a CDR2 region of SEQ ID NO: 185, and a CDR3 region of SEQ ID NO: 186; 14) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 187, a CDR2 region of SEQ ID NO: 188, and a CDR3 region of SEQ ID NO: 189, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 190, a CDR2 region of SEQ ID NO: 191, and a CDR3 region of SEQ ID NO: 192; 15) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 193, a CDR2 region of SEQ ID NO: 194, and a CDR3 region of SEQ ID NO: 195, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 196, a CDR2 region of SEQ ID NO: 197, and a CDR3 region of SEQ ID NO: 198; 16) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 199, a CDR2 region of SEQ ID NO: 200, and a CDR3 region of SEQ ID NO: 201, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 202, a CDR2 region of SEQ ID NO: 203, and a CDR3 region of SEQ ID NO: 204; 17) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 217, a CDR2 region of SEQ ID NO: 218, and a CDR3 region of SEQ ID NO: 219, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 220, a CDR2 region of SEQ ID NO: 221, and a CDR3 region of SEQ ID NO: 222; 18) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 253, a CDR2 region of SEQ ID NO: 254, and a CDR3 region of SEQ ID NO: 255, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 256, a CDR2 region of SEQ ID NO: 257, and a CDR3 region of SEQ ID NO: 258; 19) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 265, a CDR2 region of SEQ ID NO: 266, and a CDR3 region of SEQ ID NO: 267, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 268, a CDR2 region of SEQ ID NO: 269, and a CDR3 region of SEQ ID NO: 270; 20) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 283, a CDR2 region of SEQ ID NO: 284, and a CDR3 region of SEQ ID NO: 285, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 286, a CDR2 region of SEQ ID NO: 287, and a CDR3 region of SEQ ID NO: 288; 21) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 295, a CDR2 region of SEQ ID NO: 296, and a CDR3 region of SEQ ID NO: 297, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 298, a CDR2 region of SEQ ID NO: 299, and a CDR3 region of SEQ ID NO: 300; 22) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 301, a CDR2 region of SEQ ID NO: 302, and a CDR3 region of SEQ ID NO: 303, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 304, a CDR2 region of SEQ ID NO: 305, and a CDR3 region of SEQ ID NO: 306; 23) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 313, a CDR2 region of SEQ ID NO: 314, and a CDR3 region of SEQ ID NO: 315, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 316, a CDR2 region of SEQ ID NO: 317, and a CDR3 region of SEQ ID NO: 318; 24) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 319, a CDR2 region of SEQ ID NO: 320, and a CDR3 region of SEQ ID NO: 321, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 322, a CDR2 region of SEQ ID NO: 323, and a CDR3 region of SEQ ID NO: 324; 25) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 325, a CDR2 region of SEQ ID NO: 326, and a CDR3 region of SEQ ID NO: 327, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 328, a CDR2 region of SEQ ID NO: 329, and a CDR3 region of SEQ ID NO: 330; 26) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 331, a CDR2 region of SEQ ID NO: 332, and a CDR3 region of SEQ ID NO: 333, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 334, a CDR2 region of SEQ ID NO: 335, and a CDR3 region of SEQ ID NO: 336; 27) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 349, a CDR2 region of SEQ ID NO: 350, and a CDR3 region of SEQ ID NO: 351, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 352, a CDR2 region of SEQ ID NO: 353, and a CDR3 region of SEQ ID NO: 354; 28) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 355, a

CDR2 region of SEQ ID NO: 356, and a CDR3 region of SEQ ID NO: 357, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 358, a CDR2 region of SEQ ID NO: 359, and a CDR3 region of SEQ ID NO: 360; 29) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 361, a CDR2 region of SEQ ID NO: 362, and a CDR3 region of SEQ ID NO: 363, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 364, a CDR2 region of SEQ ID NO: 365, and a CDR3 region of SEQ ID NO: 366; 30) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 391, a CDR2 region of SEQ ID NO: 392, and a CDR3 region of SEQ ID NO: 393, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 394, a CDR2 region of SEQ ID NO: 395, and a CDR3 region of SEQ ID NO: 396; 31) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 409, a CDR2 region of SEQ ID NO: 410, and a CDR3 region of SEQ ID NO: 411, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 412, a CDR2 region of SEQ ID NO: 413, and a CDR3 region of SEQ ID NO: 414; 32) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 439, a CDR2 region of SEQ ID NO: 440, and a CDR3 region of SEQ ID NO: 441, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 442, a CDR2 region of SEQ ID NO: 443, and a CDR3 region of SEQ ID NO: 444; 33) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 445, a CDR2 region of SEQ ID NO: 446, and a CDR3 region of SEQ ID NO: 447, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 448, a CDR2 region of SEQ ID NO: 449, and a CDR3 region of SEQ ID NO: 450; 34) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 451, a CDR2 region of SEQ ID NO: 452, and a CDR3 region of SEQ ID NO: 453, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 454, a CDR2 region of SEQ ID NO: 455, and a CDR3 region of SEQ ID NO: 456; 35) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 481, a CDR2 region of SEQ ID NO: 482, and a CDR3 region of SEQ ID NO: 483, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 484, a CDR2 region of SEQ ID NO: 485, and a CDR3 region of SEQ ID NO: 486; 36) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 487, a CDR2 region of SEQ ID NO: 488, and a CDR3 region of SEQ ID NO: 489, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 490, a CDR2 region of SEQ ID NO: 491, and a CDR3 region of SEQ ID NO: 492; 37) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 493, a CDR2 region of SEQ ID NO: 494, and a CDR3 region of SEQ ID NO: 495, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 496, a CDR2 region of SEQ ID NO: 497, and a CDR3 region of SEQ ID NO: 498; 38) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 505, a CDR2 region of SEQ ID NO: 506, and a CDR3 region of SEQ ID NO: 507, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 508, a CDR2 region of SEQ ID NO: 509, and a CDR3 region of SEQ ID NO: 510; 39) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 511, a CDR2 region of SEQ ID NO: 512, and a CDR3 region of SEQ ID NO: 513, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 514, a CDR2 region of SEQ ID NO: 515, and a CDR3 region of SEQ ID NO: 516; 40) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 517, a CDR2 region of SEQ ID NO: 518, and a CDR3 region of SEQ ID NO: 519, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 520, a CDR2 region of SEQ ID NO: 521, and a CDR3 region of SEQ ID NO: 522; 41) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 553, a CDR2 region of SEQ ID NO: 554, and a CDR3 region of SEQ ID NO: 555, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 556, a CDR2 region of SEQ ID NO: 557, and a CDR3 region of SEQ ID NO: 558; 42) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 559, a CDR2 region of SEQ ID NO: 560, and a CDR3 region of SEQ ID NO: 561, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 562, a CDR2 region of SEQ ID NO: 563, and a CDR3 region of SEQ ID NO: 564; 43) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 565, a CDR2 region of SEQ ID NO: 566, and a CDR3 region of SEQ ID NO: 567, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 568, a CDR2 region of SEQ ID NO: 569, and a CDR3 region of SEQ ID NO: 570; 44) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 571, a CDR2 region of SEQ ID NO: 572, and a CDR3 region of SEQ ID NO: 573, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 574, a CDR2 region of SEQ ID NO: 575, and a CDR3 region of SEQ ID NO: 576; 45) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 583, a CDR2 region of SEQ ID NO: 584, and a CDR3 region of SEQ ID NO: 585, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 586, a CDR2 region of SEQ ID NO: 587, and a CDR3 region of SEQ ID NO: 588; 46) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 607, a CDR2 region of SEQ ID NO: 608, and a CDR3 region of SEQ ID NO: 609, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 610, a CDR2 region of SEQ ID NO: 611, and a CDR3 region of SEQ ID NO: 612; 47) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 613, a CDR2 region of SEQ ID NO: 614, and a CDR3 region of SEQ ID NO: 615, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 616, a CDR2 region of SEQ ID NO: 617, and a CDR3 region of SEQ ID NO: 618; 48) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 619, a CDR2 region of SEQ ID NO: 620, and a CDR3 region of SEQ ID NO: 621, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 622, a CDR2 region of SEQ ID NO: 623, and a CDR3 region of SEQ ID NO:

624; and 49) a binding molecule comprising a) a light-chain variable region comprising a CDR1 region of SEQ ID NO: 643, a CDR2 region of SEQ ID NO: 644, and a CDR3 region of SEQ ID NO: 645, and b) a heavy-chain variable region comprising a CDR1 region of SEQ ID NO: 646, a CDR2 region of SEQ ID NO: 647, and a CDR3 region of SEQ ID NO: 648.

2.-**9**. (canceled)

10. The binding molecule according to claim 1, wherein the binding molecule is an antibody or an antigen-binding fragment thereof.

11. The binding molecule according to claim 10, wherein the antibody is a monoclonal antibody.

12. The binding molecule according to claim 11, wherein the monoclonal antibody is a chimeric antibody, a humanized antibody, or a human antibody.

13. The binding molecule according to claim 10, wherein the antigen-binding fragment is Fab, F(ab′), F(ab′)2, Fv, dAb, Fd, a single-chain antibody fragment (scFv), scFv-Fc, a complementarity-determining region (CDR) fragment, a bivalent single-chain antibody fragment, a single-chain phage antibody fragment, diabody, triabody, or tetrabody.

14. The binding molecule according to claim 1, wherein the binding molecule has neutralizing activity against a mutant virus having a mutation in the spike protein of SARS-coronavirus-2.

15. The binding molecule according to claim 1, wherein the binding molecule has neutralizing activity against SARS-coronavirus-2 S-type, L-type, V-type, G-type, GH-type or GR-type.

16.-**40**. (canceled)