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(54) **CORONAVIRUS ISOLATED FROM HUMANS**

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(57) **ABSTRACT**

Disclosed herein is a newly isolated human coronavirus (SARS-CoV), the causative agent of severe acute respiratory syndrome (SARS). Also provided are the nucleic acid sequence of the SARS-CoV genome and the amino acid sequences of the SARS-CoV open reading frames, as well as methods of using these molecules to detect a SARS-CoV and detect infections therewith. Immune stimulatory compositions are also provided, along with methods of their use.

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(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 0 days.

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(22) Filed: **Apr. 12, 2004**

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C12N 15/50 (2006.01)
C12N 7/00 (2006.01)

(52) **U.S. Cl.** **536/23.72**; 435/235.1

(58) **Field of Classification Search** **536/23.72**;
514/44; 435/235.1, 320.1
See application file for complete search history.

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1 Claim, 7 Drawing Sheets

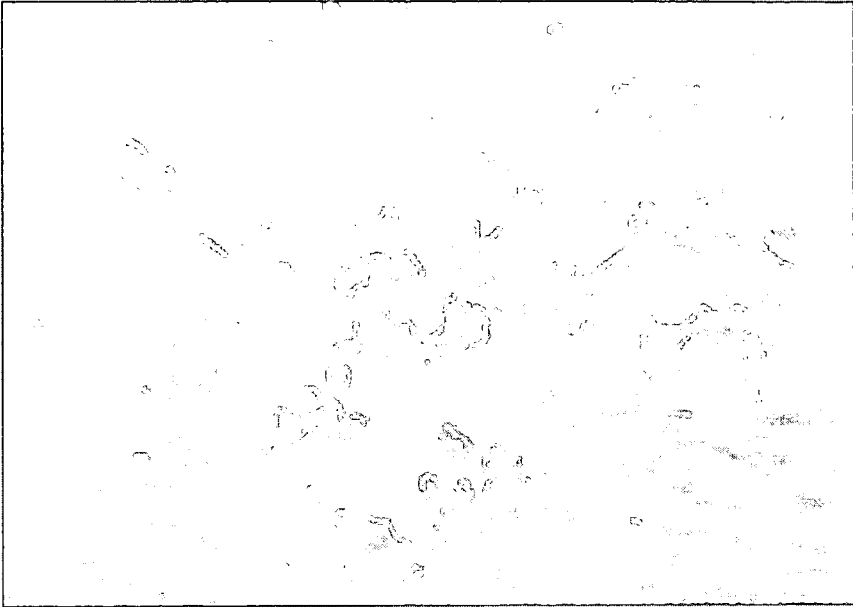


FIG. 1A

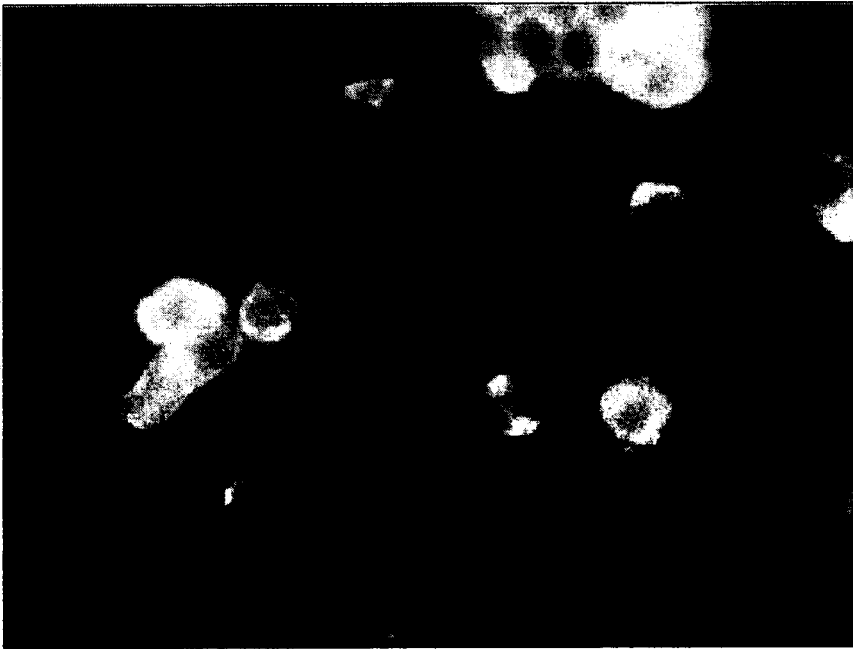


FIG. 1B

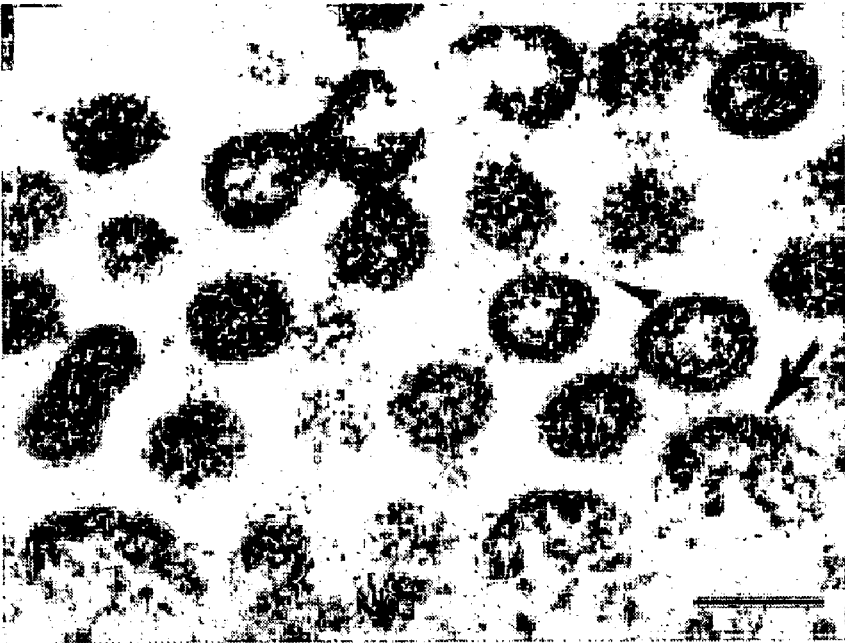


FIG. 2A

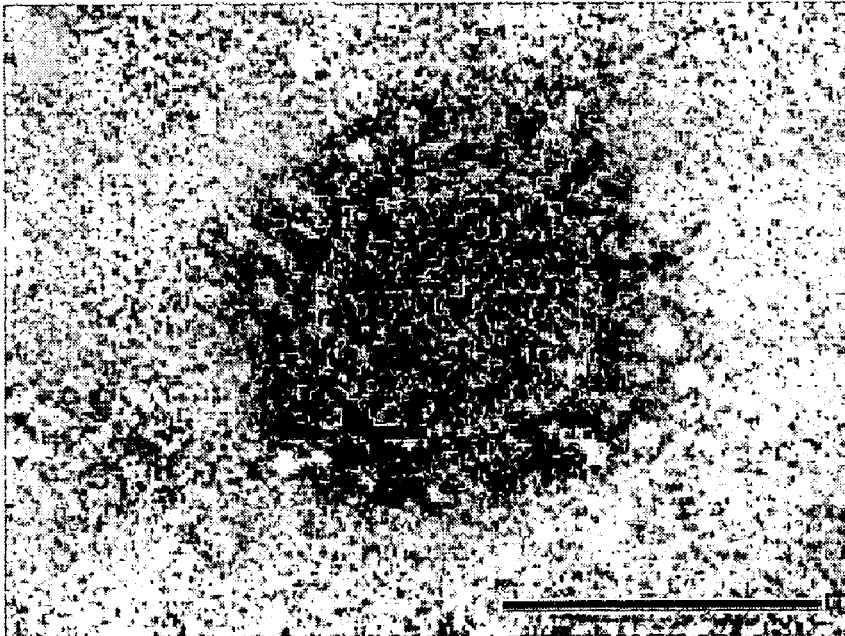


FIG. 2B

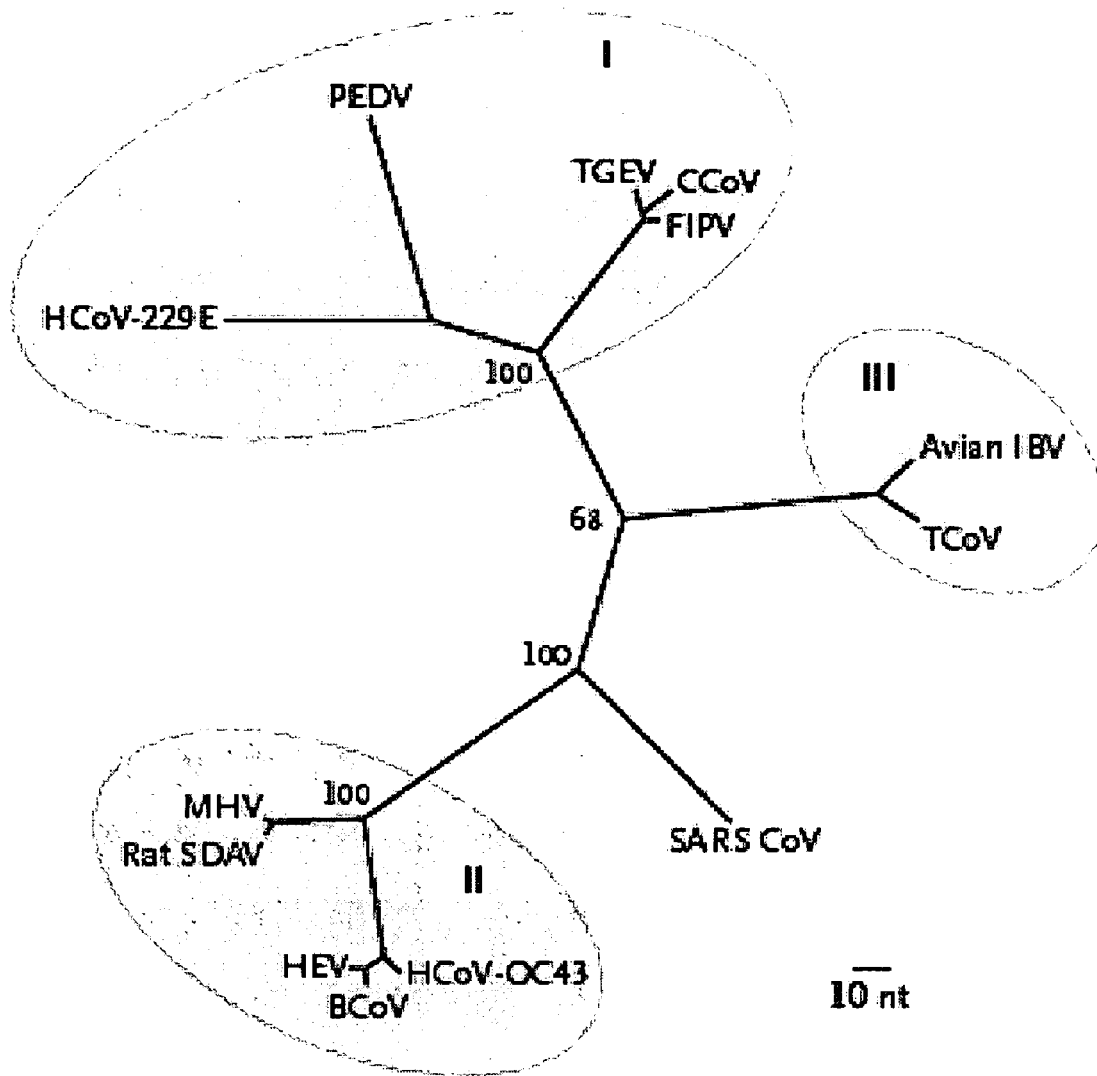


FIG. 3

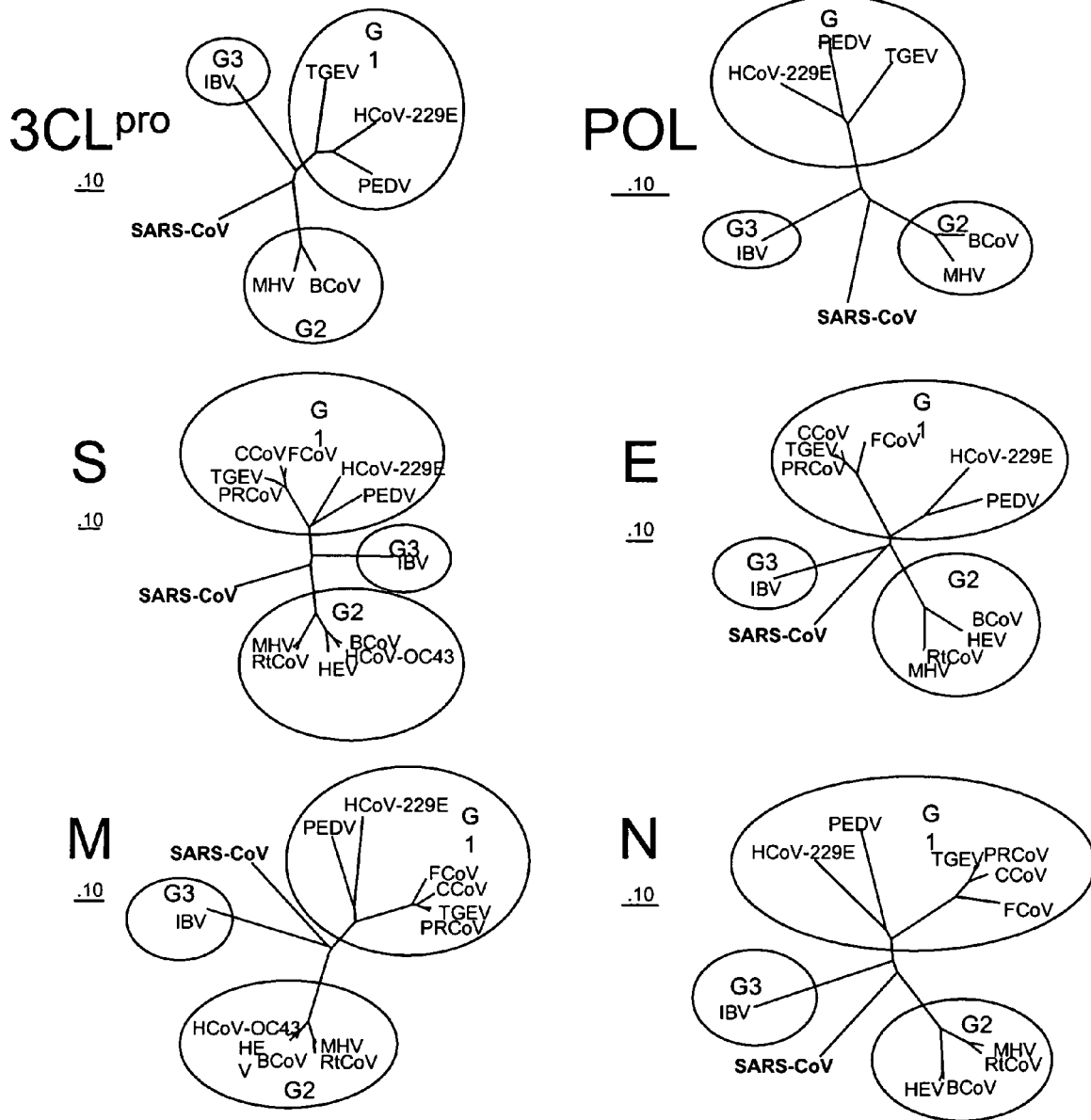


FIG. 4

FIG. 5A

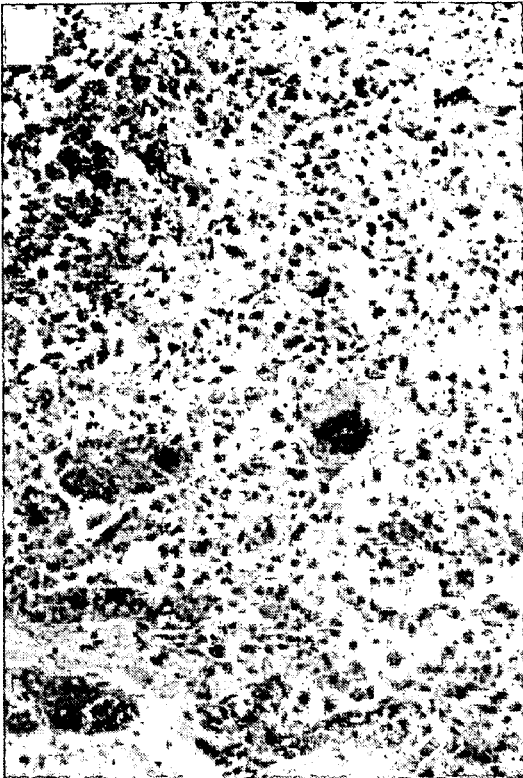


FIG. 5B

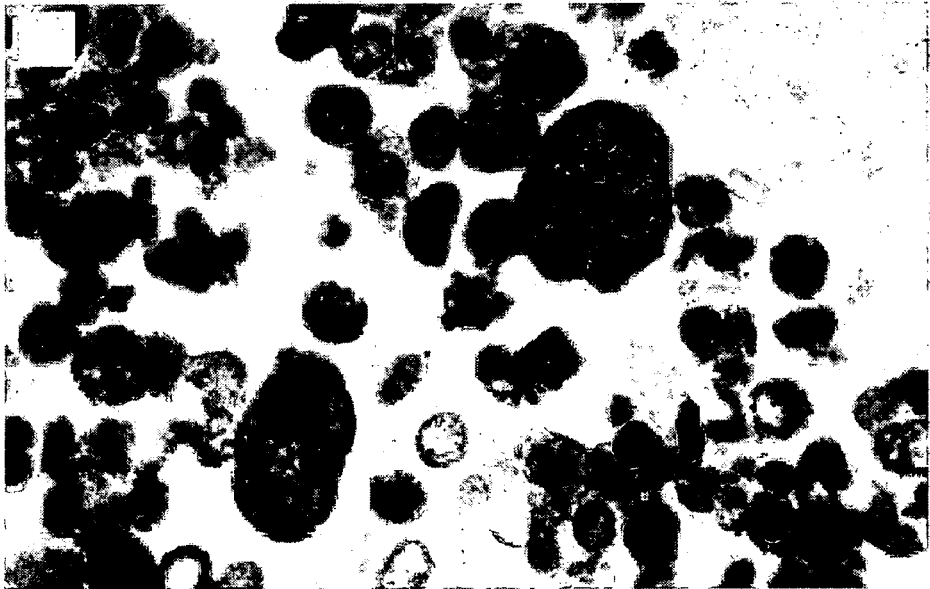
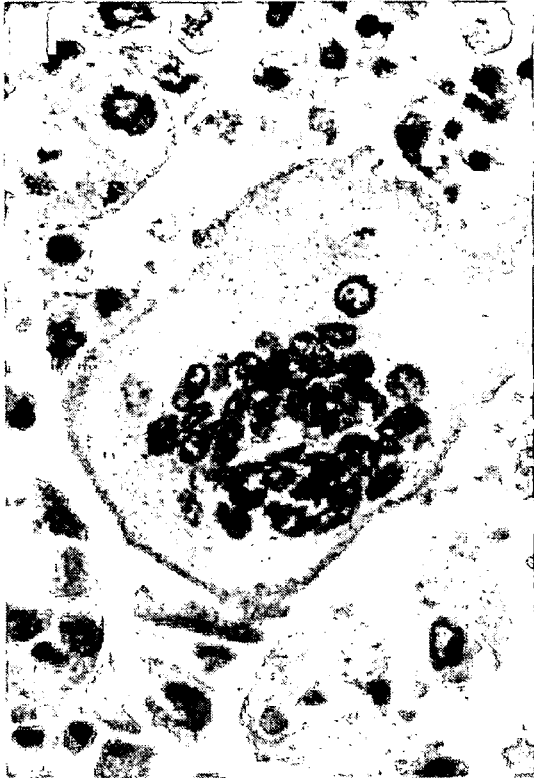


FIG. 5C

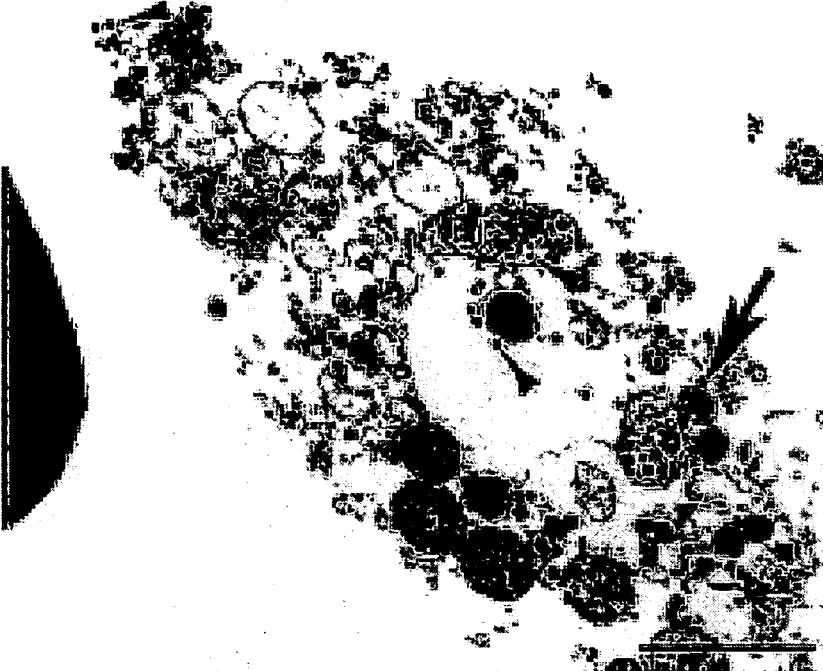


FIG. 6A

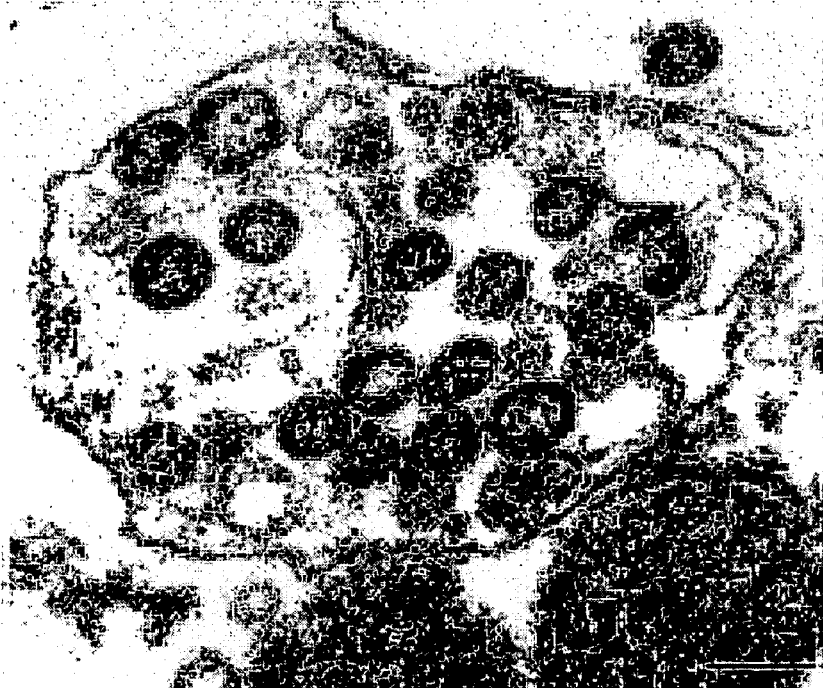
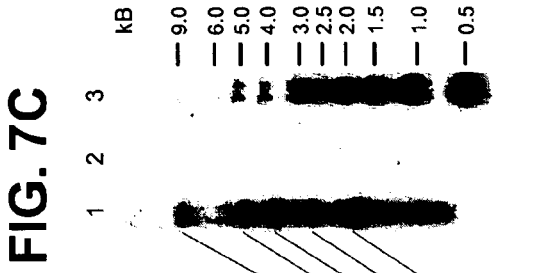
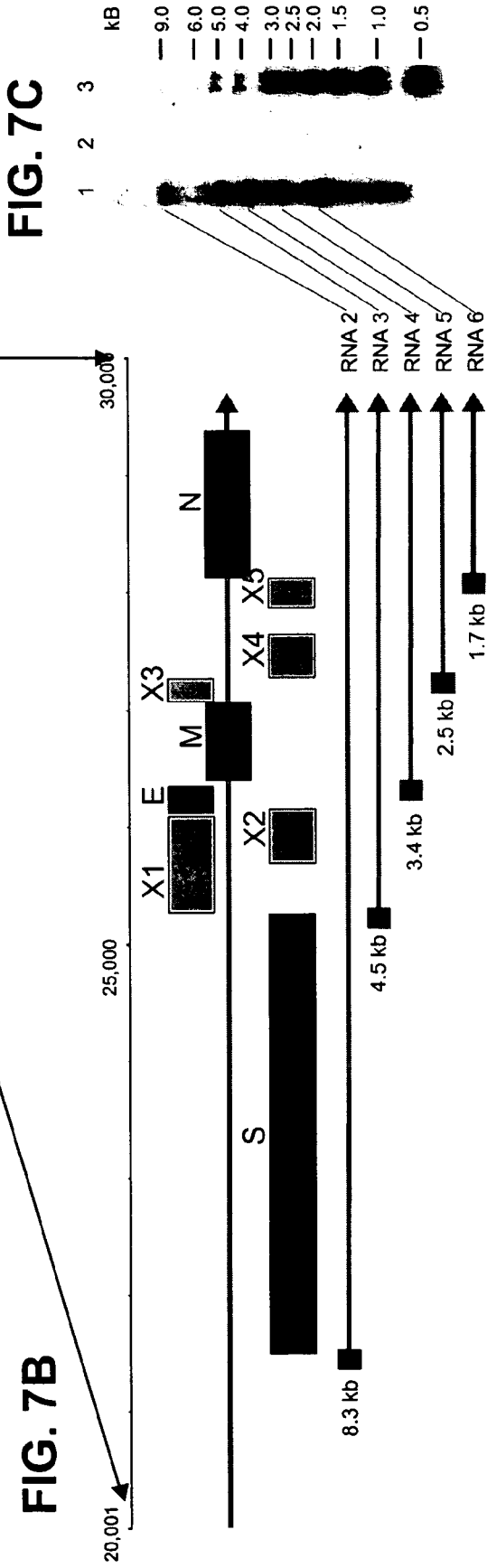
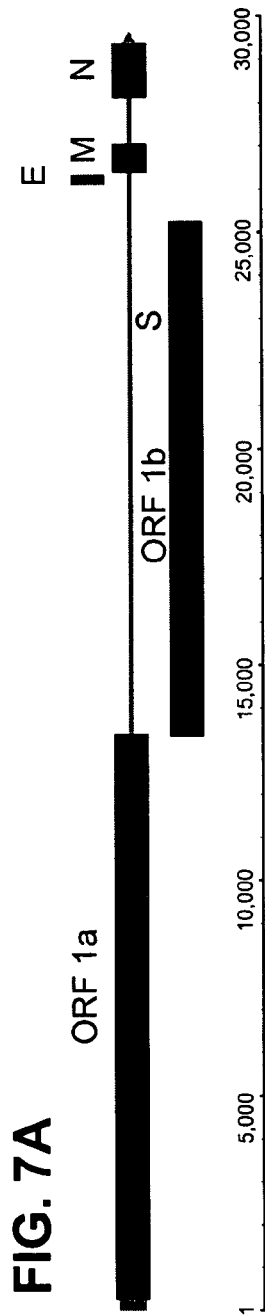


FIG. 6B



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CORONAVIRUS ISOLATED FROM HUMANS

PRIORITY CLAIM

This application claims the benefit of U.S. Provisional Patent Application No. 60/465,927 filed Apr. 25, 2003, which is incorporated herein by reference in its entirety.

STATEMENT OF GOVERNMENT SUPPORT

This invention was made by the Centers for Disease Control and Prevention, an agency of the United States Government. Therefore, the U.S. Government has certain rights in this invention.

FIELD OF THE DISCLOSURE

This invention relates to a newly isolated human coronavirus. More particularly, it relates to an isolated coronavirus genome, isolated coronavirus proteins, and isolated nucleic acid molecules encoding the same. The disclosure further relates to methods of detecting a severe acute respiratory syndrome-associated coronavirus and compositions comprising immunogenic coronavirus compounds.

BACKGROUND

The coronaviruses (order Nidovirales, family Coronaviridae, genus Coronavirus) are a diverse group of large, enveloped, positive-stranded RNA viruses that cause respiratory and enteric diseases in humans and other animals. At approximately 30,000 nucleotides (nt), their genome is the largest found in any of the RNA viruses. Coronaviruses are spherical, 100–160 nm in diameter with 20–40 nm complex club shaped surface projections surrounding the periphery. Coronaviruses share common structural proteins including a spike protein (S), membrane protein (M), envelope protein (E), and, in a subset of coronaviruses, a hemagglutinin-esterase protein (HE). The S protein, a glycoprotein which protrudes from the virus membrane, is involved in host cell receptor binding and is a target for neutralizing antibodies. The E and M proteins are involved in virion formation and release from the host cell. Coronavirus particles are found within the cisternae of the rough endoplasmic reticulum and in vesicles of infected host cells where virions are assembled. The coronavirus genome consists of two open reading frames (ORF1a and ORF1b) yielding an RNA polymerase and a nested set of subgenomic mRNAs encoding structural and nonstructural proteins, including the S, E, M, and nucleocapsid (N) proteins. The genus Coronavirus includes at least 13 species which have been subdivided into at least three groups (groups I, II, and III) on the basis of serological and genetic properties (deVries et al., *Sem. Virol.* 8:33–47, 1997; Fields et al. eds. *Fields Virology*, 3rd edition, Raven Press, Philadelphia, 1323–1341, 1996; Mahey and Collier eds. *Microbiology and Microbial Infections*, Volume 1 Virology, 9th edition, Oxford University Press, 463–479, 1998).

The three known groups of coronavirus are associated with a variety of diseases of humans and domestic animals (for example, cattle, pigs, cats, dogs, rodents, and birds), including gastroenteritis and upper and lower respiratory tract disease. Known coronaviruses include human Coronavirus 229E (HCoV-229E), canine coronavirus (CCoV), feline infectious peritonitis virus (FIPV), porcine transmissible gastroenteritis virus (TGEV), porcine epidemic diarrhea virus (PEDV), human coronavirus OC43 (HCoV-

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OC43), bovine coronavirus (BCoV), porcine hemagglutinating encephalomyelitis virus (HEV), rat sialodacryoadenitis virus (SDAV), mouse hepatitis virus (MHV), turkey coronavirus (TCoV), and avian infectious bronchitis virus (IBV-Avian) (Fields et al. eds. *Fields Virology*, 3rd edition, Raven Press, Philadelphia, 1323–1341, 1996; Mahey and Collier eds. *Microbiology and Microbial Infections*, Volume 1 Virology, 9th edition, Oxford University Press, 463–479, 1998).

Coronavirus infections are generally host specific with respect to infectivity and clinical symptoms. Coronaviruses further exhibit marked tissue tropism; infection in the incorrect host species or tissue type may result in an abortive infection, mutant virus production and altered virulence. Coronaviruses generally do not grow well in cell culture, and animal models for human coronavirus infection are lacking. Therefore, little is known about them (Fields et al. eds. *Fields Virology*, 3rd edition, Raven Press, Philadelphia, 1323–1341, 1996). The known human coronaviruses are notably fastidious in cell culture, preferring select cell lines, organ culture, or suckling mice for propagation. Coronaviruses grown in cell culture exhibit varying degrees of virulence and/or cytopathic effect (CPE) depending on the host cell type and culture conditions. The only human or animal coronavirus which has been shown to grow in Vero E6 cells is PEDV, and it requires the addition of trypsin to culture medium for growth in Vero E6 cells. Moreover, PEDV adapted to Vero E6 cell culture results in a strikingly different CPE, with cytoplasmic vacuoles and the formation of large syncytia (Hofmann and Wyler, *J. Clin. Micro.* 26:2235–39, 1988; Kusanagi et al., *J. Vet. Med. Sci.* 55:4: 313–18, 1991).

Coronavirus have not previously been known to cause severe disease in humans, but have been identified as a major cause of upper respiratory tract illness, including the common cold. Repeat infections in humans are common within and across serotype, suggesting that immune response to coronavirus infection in humans is either incomplete or short lived. Coronavirus infection in animals can cause severe enteric or respiratory disease. Vaccination has been used successfully to prevent and control some coronavirus infections in animals. The ability of animal-specific coronaviruses to cause severe disease raises the possibility that coronavirus could also cause more severe disease in humans (Fields et al. eds. *Fields Virology*, 3rd edition, Raven Press, Philadelphia, 1323–1341, 1996; Mahey and Collier eds. *Microbiology and Microbial Infections*, Volume 1 Virology, 9th edition, Oxford University Press, 463–479, 1998).

In late 2002, cases of life-threatening respiratory disease with no identifiable etiology were reported from Guangdong Province, China, followed by reports from Vietnam, Canada, and Hong Kong of severe febrile respiratory illness that spread to household members and health care workers. The syndrome was designated “severe acute respiratory syndrome” (SARS) in February 2003 by the Centers for Disease Control and Prevention (*MMWR*, 52:241–48, 2003).

Past efforts to develop rapid diagnostics and vaccines for coronavirus infection in humans have been hampered by a lack of appropriate research models and the moderate course of disease in humans. Therefore, a need for rapid diagnostic tests and vaccines exists.

SUMMARY OF THE DISCLOSURE

A newly isolated human coronavirus has been identified as the causative agent of SARS, and is termed SARS-CoV.

The nucleic acid sequence of the SARS-CoV genome and the amino acid sequences of the SARS-CoV open reading frames are provided herein.

This disclosure provides methods and compositions useful in detecting the presence of a SARS-CoV nucleic acid in a sample and/or diagnosing a SARS-CoV infection in a subject. Also provided are methods and compositions useful in detecting the presence of a SARS-CoV antigen or antibody in a sample and/or diagnosing a SARS-CoV infection in a subject.

The foregoing and other features and advantages will become more apparent from the following detailed description of several embodiments, which proceeds with reference to the accompanying figures.

BRIEF DESCRIPTION OF THE FIGURES

FIGS. 1A–B are photomicrographs illustrating typical early cytopathic effects seen with coronavirus isolates and serum from SARS patients. FIG. 1A is a photomicrograph of Vero E6 cells inoculated with an oropharyngeal specimen from a SARS patient (×40). FIG. 1B is a photomicrograph of infected Vero E6 cells reacting with the serum of a convalescent SARS patient in an indirect fluorescent antibody (IFA) assay (×400).

FIGS. 2A–B are electronmicrographs illustrating ultrastructural characteristics of the SARS-associated coronavirus (SARS-CoV). FIG. 2A is a thin-section electron-microscopical view of viral nucleocapsids aligned along the membrane of the rough endoplasmic reticulum (arrow) as particles bud into the cisternae. Enveloped virions have surface projections (arrowhead) and an electron-lucent center. Directly under the viral envelope lies a characteristic ring formed by the helical nucleocapsid, often seen in cross-section. FIG. 2B is a negative stain (methylamine tungstate) electronmicrograph showing stain-penetrated coronavirus particle with the typical internal helical nucleocapsid-like structure and club-shaped surface projections surrounding the periphery of the particle. Bars: 100 nm.

FIG. 3 is an estimated maximum parsimony tree illustrating putative phylogenetic relationships between SARS-CoV and other human and animal coronaviruses. Phylogenetic relationships are based on sequence alignment of 405 nucleotides of the coronavirus polymerase gene ORF1b (nucleic acid 15,173 to 15,578 of SEQ ID NO: 1). The three major coronavirus antigenic groups (I, II and III), represented by HCoV-229E, CCoV, FIPV, TGEV, PEDV, HCoV-OC43, BCoV, HEV, SDAV, MHV, TCoV, and IBV-Avian, are shown shaded. Bootstrap values (100 replicates) obtained from a 50% majority rule consensus tree are plotted at the main internal branches of the phylogram. Branch lengths are proportionate to nucleotide differences.

FIG. 4 is a pictorial representation of neighbor joining trees illustrating putative phylogenetic relationships between SARS-CoV and other human and animal coronaviruses. Amino acid sequences of the indicated SARS-CoV proteins were compared with those from reference viruses representing each species in the three groups of coronaviruses for which complete genomic sequence information was available [group 1: HCoV-229E (AF304460); PEDV (AF353511); TGEV (AJ271965); group 2: BCoV (AF220295); MHV (AF201929); group 3: infectious bronchitis virus (M95169)]. Sequences for representative strains of other coronavirus species, for which partial sequence information was available, were included for some of the structural protein comparisons [group 1: CCoV (D13096); FCoV (AY204704); porcine respiratory coronavirus (Z24675); group 2: HCoV-OC43 (M76373, L14643, M93390); HEV (AY078417); rat coronavirus (AF207551)]. Sequence alignments and neighbor-joining trees were gen-

erated by using Clustalx 1.83 with the Gonnet protein comparison matrix. The resulting trees were adjusted for final output using treetool 2.0.1.

FIGS. 5A–C are photomicrographs illustrating diffuse alveolar damage in a patient with SARS (FIGS. 5A–B), and immunohistochemical staining of SARS-CoV-infected Vero E6 cells (FIG. 5C). FIG. 5A is a photomicrograph of lung tissue from a SARS patient (×50). Diffuse alveolar damage, abundant foamy macrophages and multinucleated syncytial cells are present; hematoxylin and eosin stain was used. FIG. 5B is a higher magnification photomicrograph of lung tissue from the same SARS patient (×250). Syncytial cells show no conspicuous viral inclusions. FIG. 5C is a photomicrograph of immunohistochemically stained SARS-CoV-infected cells (×250). Membranous and cytoplasmic immunostaining of individual and syncytial Vero E6 cells was achieved using feline anti-FIPV-1 ascitic fluid. Immunoalkaline phosphatase with naphthol-fast red substrate and hematoxylin counter stain was used.

FIG. 6A–B are electronmicrographs illustrating ultrastructural characteristics of a coronavirus-infected cell in bronchoalveolar lavage (BAL) from a SARS patient. FIG. 6A is an electronmicrograph of a coronavirus-infected cell. Numerous intracellular and extracellular particles are present; virions are indicated by the arrowheads. FIG. 6B is a higher magnification electronmicrograph of the area seen at the arrow in FIG. 6A (rotated clockwise approximately 90°). Bars: FIG. 6A, 1 μm; FIG. 6B, 100 nm.

FIGS. 7A–C illustrate the organization of the SARS-CoV genome. FIG. 7A is a diagram of the overall organization of the 29,727-nt SARS-CoV genomic RNA. The 72-nt leader sequence is represented as a small rectangle at the left-most end. ORFs1a and 1b, encoding the nonstructural polyproteins, and those ORFs encoding the S, E, M, and N structural proteins, are indicated. Vertical position of the boxes indicates the phase of the reading frame (phase 1 for proteins above the line, phase two for proteins on the line and phase three for proteins below the line). FIG. 7B is an expanded view of the structural protein encoding region and predicted mRNA transcripts. Known structural protein encoding regions (dark grey boxes) and regions and reading frames for potential products X1–X5 (light grey boxes) are indicated. Lengths and map locations of the 3'-coterminal mRNAs expressed by the SARS-CoV are indicated, as predicted by identification of conserved transcriptional regulatory sequences. FIG. 7C is a digitized image of a nylon membrane showing Northern blot analysis of SARS-CoV mRNAs. Poly(A)+ RNA from infected Vero E6 cells was separated on a formaldehyde-agarose gel, transferred to a nylon membrane, and hybridized with a digoxigenin-labeled riboprobe overlapping the 3'-untranslated region. Signals were visualized by chemiluminescence. Sizes of the SARS-CoV mRNAs were calculated by extrapolation from a log-linear fit of the molecular mass marker. Lane 1, SARS-CoV mRNA; lane 2, Vero E6 cell mRNA; lane 3, molecular mass marker, sizes in kB.

SEQUENCE LISTING

The nucleic and amino acid sequences listed in the accompanying sequence listing are shown using standard letter abbreviations for nucleotide bases, and three letter code for amino acids, as defined in 37 C.F.R. 1.822. Only one strand of each nucleic acid sequence is shown, but the complementary strand is understood as included by any reference to the displayed strand. In the accompanying sequence listing:

SEQ ID NO: 1 shows the nucleic acid sequence of the SARS-CoV genome.

SEQ ID NO: 2 shows the amino acid sequence of the SARS-CoV polyprotein 1a (encoded by nucleic acid 265 to nucleic acid 13,398 of SEQ ID NO: 1).

SEQ ID NO: 3 shows the amino acid sequence of the SARS-CoV polyprotein 1b (encoded by nucleic acid 13,398 to 21,482 of SEQ ID NO: 1).

SEQ ID NO: 4 shows the amino acid sequence of the SARS-CoV S protein (encoded by nucleic acid 21,492 to 25,256 of SEQ ID NO: 1).

SEQ ID NO: 5 shows the amino acid sequence of the SARS-CoV X1 protein (encoded by nucleic acid 25,268 to 26,089 of SEQ ID NO: 1).

SEQ ID NO: 6 shows the amino acid sequence of the SARS-CoV X2 protein (encoded by nucleic acid 25,689 to 26,150 of SEQ ID NO: 1).

SEQ ID NO: 7 shows the amino acid sequence of the SARS-CoV E protein (encoded by nucleic acid 26,117 to 26,344 of SEQ ID NO: 1).

SEQ ID NO: 8 shows the amino acid sequence of the SARS-CoV M protein (encoded by nucleic acid 26,398 to 27,060 of SEQ ID NO: 1).

SEQ ID NO: 9 shows the amino acid sequence of the SARS-CoV X3 protein (encoded by nucleic acid 27,074 to 27,262 of SEQ ID NO: 1).

SEQ ID NO: 10 shows the amino acid sequence of the SARS-CoV X4 protein (encoded by nucleic acid 27,273 to 27,638 of SEQ ID NO: 1).

SEQ ID NO: 11 shows the amino acid sequence of the SARS-CoV X5 protein (encoded by nucleic acid 27,864 to 28,115 of SEQ ID NO: 1).

SEQ ID NO: 12 shows the amino acid sequence of the SARS-CoV N protein (encoded by nucleic acid 28,120 to 29,385 of SEQ ID NO: 1).

SEQ ID NOS: 13–15 show the nucleic acid sequence of several SARS-CoV-specific oligonucleotide primers.

SEQ ID NOS: 16–33 show the nucleic acid sequence of several oligonucleotide primers/probes used for real-time reverse transcription-polymerase chain reaction (RT-PCR) SARS-CoV assays.

SEQ ID NOS: 34–35 show the nucleic acid sequence of two degenerate primers designed to anneal to sites encoding conserved coronavirus amino acid motifs.

SEQ ID NOS: 36–38 show the nucleic acid sequence of several oligonucleotide primers/probe used as controls in real-time RT-PCR assays.

DETAILED DESCRIPTION OF SEVERAL EMBODIMENTS

I. Abbreviations

M:	coronavirus membrane protein
N:	coronavirus nucleoprotein
ORF:	open reading frame
PCR:	polymerase chain reaction
RACE:	5' rapid amplification of cDNA ends
RT-PCR:	reverse transcription-polymerase chain reaction
S:	coronavirus spike protein
SARS:	severe acute respiratory syndrome
SARS-CoV:	severe acute respiratory syndrome-associated coronavirus
TRS:	transcriptional regulatory sequence

II. Terms

Unless otherwise noted, technical terms are used according to conventional usage. Definitions of common terms in molecular biology may be found in Benjamin Lewin, *Genes*

VII, published by Oxford University Press, 2000 (ISBN 019879276X); Kendrew et al. (eds.), *The Encyclopedia of Molecular Biology*, published by Blackwell Publishers, 1994 (ISBN 0632021829); and Robert A. Meyers (ed.), *Molecular Biology and Biotechnology: a Comprehensive Desk Reference*, published by Wiley, John & Sons, Inc., 1995 (ISBN 0471186341); and other similar references.

As used herein, the singular terms “a,” “an,” and “the” include plural referents unless context clearly indicates otherwise. Similarly, the word “or” is intended to include “and” unless the context clearly indicates otherwise. Also, as used herein, the term “comprises” means “includes.” Hence “comprising A or B” means including A, B, or A and B. It is further to be understood that all nucleotide sizes or amino acid sizes, and all molecular weight or molecular mass values, given for nucleic acids or polypeptides are approximate, and are provided for description. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present specification, including explanations of terms, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

In order to facilitate review of the various embodiments of this disclosure, the following explanations of specific terms are provided:

Adjuvant: A substance that non-specifically enhances the immune response to an antigen. Development of vaccine adjuvants for use in humans is reviewed in Singh et al. (*Nat. Biotechnol.* 17:1075–1081, 1999), which discloses that, at the time of its publication, aluminum salts and the MF59 microemulsion are the only vaccine adjuvants approved for human use.

Amplification: Amplification of a nucleic acid molecule (e.g., a DNA or RNA molecule) refers to use of a laboratory technique that increases the number of copies of a nucleic acid molecule in a sample. An example of amplification is the polymerase chain reaction (PCR), in which a sample is contacted with a pair of oligonucleotide primers under conditions that allow for the hybridization of the primers to a nucleic acid template in the sample. The primers are extended under suitable conditions, dissociated from the template, re-annealed, extended, and dissociated to amplify the number of copies of the nucleic acid. The product of amplification can be characterized by such techniques as electrophoresis, restriction endonuclease cleavage patterns, oligonucleotide hybridization or ligation, and/or nucleic acid sequencing.

Other examples of amplification methods include strand displacement amplification, as disclosed in U.S. Pat. No. 5,744,311; transcription-free isothermal amplification, as disclosed in U.S. Pat. No. 6,033,881; repair chain reaction amplification, as disclosed in WO 90/01069; ligase chain reaction amplification, as disclosed in EP-A-320,308; gap filling ligase chain reaction amplification, as disclosed in U.S. Pat. No. 5,427,930; and NASBA™ RNA transcription-free amplification, as disclosed in U.S. Pat. No. 6,025,134. An amplification method can be modified, including for example by additional steps or coupling the amplification with another protocol.

Animal: Living multi-cellular vertebrate organisms, a category that includes, for example, mammals and birds. The term mammal includes both human and non-human mammals. Similarly, the term “subject” includes both human and veterinary subjects, for example, humans, non-human primates, dogs, cats, horses, and cows.

Antibody: A protein (or protein complex) that includes one or more polypeptides substantially encoded by immunoglobulin genes or fragments of immunoglobulin genes. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively.

The basic immunoglobulin (antibody) structural unit is generally a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kDa) and one "heavy" (about 50–70 kDa) chain. The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms "variable light chain" (V_L) and "variable heavy chain" (V_H) refer, respectively, to these light and heavy chains.

As used herein, the term "antibodies" includes intact immunoglobulins as well as a number of well-characterized fragments. For instance, Fabs, Fvs, and single-chain Fvs (SCFvs) that bind to target protein (or epitope within a protein or fusion protein) would also be specific binding agents for that protein (or epitope). These antibody fragments are defined as follows: (1) Fab, the fragment which contains a monovalent antigen-binding fragment of an antibody molecule produced by digestion of whole antibody with the enzyme papain to yield an intact light chain and a portion of one heavy chain; (2) Fab', the fragment of an antibody molecule obtained by treating whole antibody with pepsin, followed by reduction, to yield an intact light chain and a portion of the heavy chain; two Fab' fragments are obtained per antibody molecule; (3) (Fab')₂, the fragment of the antibody obtained by treating whole antibody with the enzyme pepsin without subsequent reduction; (4) F(ab')₂, a dimer of two Fab' fragments held together by two disulfide bonds; (5) Fv, a genetically engineered fragment containing the variable region of the light chain and the variable region of the heavy chain expressed as two chains; and (6) single chain antibody, a genetically engineered molecule containing the variable region of the light chain, the variable region of the heavy chain, linked by a suitable polypeptide linker as a genetically fused single chain molecule. Methods of making these fragments are routine (see, for example, Harlow and Lane, *Using Antibodies: A Laboratory Manual*, CSHL, New York, 1999).

Antibodies for use in the methods and devices of this disclosure can be monoclonal or polyclonal. Merely by way of example, monoclonal antibodies can be prepared from murine hybridomas according to the classical method of Kohler and Milstein (*Nature* 256:495–97, 1975) or derivative methods thereof. Detailed procedures for monoclonal antibody production are described in Harlow and Lane, *Using Antibodies: A Laboratory Manual*, CSHL, New York, 1999.

Antigen: A compound, composition, or substance that can stimulate the production of antibodies or a T-cell response in an animal, including compositions that are injected or absorbed into an animal. An antigen reacts with the products of specific humoral or cellular immunity, including those induced by heterologous immunogens. In one embodiment, an antigen is a coronavirus antigen.

Binding or Stable Binding: An oligonucleotide binds or stably binds to a target nucleic acid if a sufficient amount of the oligonucleotide forms base pairs or is hybridized to its target nucleic acid, to permit detection of that binding. Binding can be detected by either physical or functional properties of the target:oligonucleotide complex. Binding between a target and an oligonucleotide can be detected by

any procedure known to one skilled in the art, including functional or physical binding assays. Binding can be detected functionally by determining whether binding has an observable effect upon a biosynthetic process such as expression of a gene, DNA replication, transcription, translation, and the like.

Physical methods of detecting the binding of complementary strands of DNA or RNA are well known in the art, and include such methods as DNase I or chemical footprinting, gel shift and affinity cleavage assays, Northern blotting, Southern blotting, dot blotting, and light absorption detection procedures. For example, a method which is widely used, because it is so simple and reliable, involves observing a change in light absorption of a solution containing an oligonucleotide (or an analog) and a target nucleic acid at 220 to 300 nm as the temperature is slowly increased. If the oligonucleotide or analog has bound to its target, there is a sudden increase in absorption at a characteristic temperature as the oligonucleotide (or analog) and target dissociate or melt.

The binding between an oligomer and its target nucleic acid is frequently characterized by the temperature (T_m) at which 50% of the oligomer is melted from its target. A higher T_m means a stronger or more stable complex relative to a complex with a lower T_m .

cDNA (complementary DNA): A piece of DNA lacking internal, non-coding segments (introns) and regulatory sequences that determine transcription. cDNA is synthesized in the laboratory by reverse transcription from messenger RNA extracted from cells.

Electrophoresis: Electrophoresis refers to the migration of charged solutes or particles in a liquid medium under the influence of an electric field. Electrophoretic separations are widely used for analysis of macromolecules. Of particular importance is the identification of proteins and nucleic acid sequences. Such separations can be based on differences in size and/or charge. Nucleotide sequences have a uniform charge and are therefore separated based on differences in size. Electrophoresis can be performed in an unsupported liquid medium (for example, capillary electrophoresis), but more commonly the liquid medium travels through a solid supporting medium. The most widely used supporting media are gels, for example, polyacrylamide and agarose gels.

Sieving gels (for example, agarose) impede the flow of molecules. The pore size of the gel determines the size of a molecule that can flow freely through the gel. The amount of time to travel through the gel increases as the size of the molecule increases. As a result, small molecules travel through the gel more quickly than large molecules and thus progress further from the sample application area than larger molecules, in a given time period. Such gels are used for size-based separations of nucleotide sequences.

Fragments of linear DNA migrate through agarose gels with a mobility that is inversely proportional to the log₁₀ of their molecular weight. By using gels with different concentrations of agarose, different sizes of DNA fragments can be resolved. Higher concentrations of agarose facilitate separation of small DNAs, while low agarose concentrations allow resolution of larger DNAs.

Hybridization: Oligonucleotides and their analogs hybridize by hydrogen bonding, which includes Watson-Crick, Hoogsteen or reversed Hoogsteen hydrogen bonding, between complementary bases. Generally, nucleic acid consists of nitrogenous bases that are either pyrimidines (cytosine (C), uracil (U), and thymine (T)) or purines (adenine (A) and guanine (G)). These nitrogenous bases form hydrogen bonds between a pyrimidine and a purine, and the bonding of the pyrimidine to the purine is referred to as "base pairing." More specifically, A will hydrogen bond to T or U, and G will bond to C. "Complementary" refers to the

base pairing that occurs between two distinct nucleic acid sequences or two distinct regions of the same nucleic acid sequence.

“Specifically hybridizable” and “specifically complementary” are terms that indicate a sufficient degree of complementarity such that stable and specific binding occurs between the oligonucleotide (or its analog) and the DNA or RNA target. The oligonucleotide or oligonucleotide analog need not be 100% complementary to its target sequence to be specifically hybridizable. An oligonucleotide or analog is specifically hybridizable when binding of the oligonucleotide or analog to the target DNA or RNA molecule interferes with the normal function of the target DNA or RNA, and there is a sufficient degree of complementarity to avoid non-specific binding of the oligonucleotide or analog to non-target sequences under conditions where specific binding is desired, for example under physiological conditions in the case of in vivo assays or systems. Such binding is referred to as specific hybridization.

Hybridization conditions resulting in particular degrees of stringency will vary depending upon the nature of the hybridization method of choice and the composition and length of the hybridizing nucleic acid sequences. Generally, the temperature of hybridization and the ionic strength (especially the Na⁺ and/or Mg⁺⁺ concentration) of the hybridization buffer will determine the stringency of hybridization, though wash times also influence stringency. Calculations regarding hybridization conditions required for attaining particular degrees of stringency are discussed by Sambrook et al. (ed.), *Molecular Cloning: A Laboratory Manual*, 2nd ed., vol. 1–3, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989, chapters 9 and 11; and Ausubel et al. *Short Protocols in Molecular Biology*, 4th ed., John Wiley & Sons, Inc., 1999.

For purposes of the present disclosure, “stringent conditions” encompass conditions under which hybridization will only occur if there is less than 25% mismatch between the hybridization molecule and the target sequence. “Stringent conditions” may be broken down into particular levels of stringency for more precise definition. Thus, as used herein, “moderate stringency” conditions are those under which molecules with more than 25% sequence mismatch will not hybridize; conditions of “medium stringency” are those under which molecules with more than 15% mismatch will not hybridize, and conditions of “high stringency” are those under which sequences with more than 10% mismatch will not hybridize. Conditions of “very high stringency” are those under which sequences with more than 6% mismatch will not hybridize.

Immune Stimulatory Composition: A term used herein to mean a composition useful for stimulating or eliciting a specific immune response (or immunogenic response) in a vertebrate. In some embodiments, the immunogenic response is protective or provides protective immunity, in that it enables the vertebrate animal to better resist infection with or disease progression from the organism against which the vaccine is directed.

Without wishing to be bound by a specific theory, it is believed that an immunogenic response may arise from the generation of an antibody specific to one or more of the epitopes provided in the immune stimulatory composition. Alternatively, the response may comprise a T-helper or cytotoxic cell-based response to one or more of the epitopes provided in the immune stimulatory composition. All three of these responses may originate from naïve or memory cells. One specific example of a type of immune stimulatory composition is a vaccine.

In some embodiments, an “effective amount” or “immune-stimulatory amount” of an immune stimulatory composition is an amount which, when administered to a

subject, is sufficient to engender a detectable immune response. Such a response may comprise, for instance, generation of an antibody specific to one or more of the epitopes provided in the immune stimulatory composition. Alternatively, the response may comprise a T-helper or CTL-based response to one or more of the epitopes provided in the immune stimulatory composition. All three of these responses may originate from naïve or memory cells. In other embodiments, a “protective effective amount” of an immune stimulatory composition is an amount which, when administered to a subject, is sufficient to confer protective immunity upon the subject.

Inhibiting or Treating a Disease: Inhibiting the full development of a disease or condition, for example, in a subject who is at risk for a disease such as SARS. “Treatment” refers to a therapeutic intervention that ameliorates a sign or symptom of a disease or pathological condition after it has begun to develop. As used herein, the term “ameliorating,” with reference to a disease, pathological condition or symptom, refers to any observable beneficial effect of the treatment. The beneficial effect can be evidenced, for example, by a delayed onset of clinical symptoms of the disease in a susceptible subject, a reduction in severity of some or all clinical symptoms of the disease, a slower progression of the disease, a reduction in the number of relapses of the disease, an improvement in the overall health or well-being of the subject, or by other parameters well known in the art that are specific to the particular disease.

Isolated: An “isolated” microorganism (such as a virus, bacterium, fungus, or protozoan) has been substantially separated or purified away from microorganisms of different types, strains, or species. Microorganisms can be isolated by a variety of techniques, including serial dilution and culturing.

An “isolated” biological component (such as a nucleic acid molecule, protein or organelle) has been substantially separated or purified away from other biological components in the cell of the organism in which the component naturally occurs, such as other chromosomal and extrachromosomal DNA and RNA, proteins, and organelles. Nucleic acids and proteins that have been “isolated” include nucleic acids and proteins purified by standard purification methods. The term also embraces nucleic acids and proteins prepared by recombinant expression in a host cell, as well as chemically synthesized nucleic acids or proteins, or fragments thereof.

Label: A detectable compound or composition that is conjugated directly or indirectly to another molecule to facilitate detection of that molecule. Specific, non-limiting examples of labels include fluorescent tags, enzymatic linkages, and radioactive isotopes.

Nucleic Acid Molecule: A polymeric form of nucleotides, which may include both sense and anti-sense strands of RNA, cDNA, genomic DNA, and synthetic forms and mixed polymers of the above. A nucleotide refers to a ribonucleotide, deoxynucleotide or a modified form of either type of nucleotide. A “nucleic acid molecule” as used herein is synonymous with “nucleic acid” and “polynucleotide.” A nucleic acid molecule is usually at least 10 bases in length, unless otherwise specified. The term includes single- and double-stranded forms of DNA. A polynucleotide may include either or both naturally occurring and modified nucleotides linked together by naturally occurring and/or non-naturally occurring nucleotide linkages.

Oligonucleotide: A nucleic acid molecule generally comprising a length of 300 bases or fewer. The term often refers to single-stranded deoxyribonucleotides, but it can refer as well to single- or double-stranded ribonucleotides, RNA: DNA hybrids and double-stranded DNAs, among others. The term “oligonucleotide” also includes oligonucleosides

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(that is, an oligonucleotide minus the phosphate) and any other organic base polymer. In some examples, oligonucleotides are about 10 to about 90 bases in length, for example, 12, 13, 14, 15, 16, 17, 18, 19 or 20 bases in length. Other oligonucleotides are about 25, about 30, about 35, about 40, about 45, about 50, about 55, about 60 bases, about 65 bases, about 70 bases, about 75 bases or about 80 bases in length. Oligonucleotides may be single-stranded, for example, for use as probes or primers, or may be double-stranded, for example, for use in the construction of a mutant gene. Oligonucleotides can be either sense or anti-sense oligonucleotides. An oligonucleotide can be modified as discussed above in reference to nucleic acid molecules. Oligonucleotides can be obtained from existing nucleic acid sources (for example, genomic or cDNA), but can also be synthetic (for example, produced by laboratory or in vitro oligonucleotide synthesis).

Open Reading Frame (ORF): A series of nucleotide triplets (codons) coding for amino acids without any internal termination codons. These sequences are usually translatable into a peptide/polypeptide/protein/polypeptide.

Operably Linked: A first nucleic acid sequence is operably linked with a second nucleic acid sequence when the first nucleic acid sequence is placed in a functional relationship with the second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Generally, operably linked DNA sequences are contiguous and, where necessary to join two protein coding regions, in the same reading frame. If introns are present, the operably linked DNA sequences may not be contiguous.

Pharmaceutically Acceptable Carriers: The pharmaceutically acceptable carriers useful in this disclosure are conventional. *Remington's Pharmaceutical Sciences*, by E. W. Martin, Mack Publishing Co., Easton, Pa., 15th Edition (1975), describes compositions and formulations suitable for pharmaceutical delivery of one or more therapeutic compounds or molecules, such as one or more SARS-CoV nucleic acid molecules, proteins or antibodies that bind these proteins, and additional pharmaceutical agents.

In general, the nature of the carrier will depend on the particular mode of administration being employed. For instance, parenteral formulations usually comprise injectable fluids that include pharmaceutically and physiologically acceptable fluids such as water, physiological saline, balanced salt solutions, aqueous dextrose, glycerol or the like as a vehicle. For solid compositions (for example, powder, pill, tablet, or capsule forms), conventional non-toxic solid carriers can include, for example, pharmaceutical grades of mannitol, lactose, starch, or magnesium stearate. In addition to biologically-neutral carriers, pharmaceutical compositions to be administered can contain minor amounts of non-toxic auxiliary substances, such as wetting or emulsifying agents, preservatives, and pH buffering agents and the like, for example sodium acetate or sorbitan monolaurate.

Polypeptide: A polymer in which the monomers are amino acid residues which are joined together through amide bonds. When the amino acids are alpha-amino acids, either the L-optical isomer or the D-optical isomer can be used, the L-isomers being preferred. The terms "polypeptide" or "protein" as used herein are intended to encompass any amino acid sequence and include modified sequences such as glycoproteins. The term "polypeptide" is specifically intended to cover naturally occurring proteins, as well as those which are recombinantly or synthetically produced.

Conservative amino acid substitutions are those substitutions that, when made, least interfere with the properties of the original protein, that is, the structure and especially the

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function of the protein is conserved and not significantly changed by such substitutions. Examples of conservative substitutions are shown below.

Original Residue	Conservative Substitutions
Ala	Ser
Arg	Lys
Asn	Gln, His
Asp	Glu
Cys	Ser
Gln	Asn
Glu	Asp
His	Asn; Gln
Ile	Leu, Val
Leu	Ile; Val
Lys	Arg; Gln; Glu
Met	Leu; Ile
Phe	Met; Leu; Tyr
Ser	Thr
Thr	Ser
Trp	Tyr
Tyr	Trp; Phe
Val	Ile; Leu

Conservative substitutions generally maintain (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain.

The substitutions which in general are expected to produce the greatest changes in protein properties will be non-conservative, for instance changes in which (a) a hydrophilic residue, for example, seryl or threonyl, is substituted for (or by) a hydrophobic residue, for example, leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, for example, lysyl, arginyl, or histadyl, is substituted for (or by) an electronegative residue, for example, glutamyl or aspartyl; or (d) a residue having a bulky side chain, for example, phenylalanine, is substituted for (or by) one not having a side chain, for example, glycine.

Probes and Primers: A probe comprises an isolated nucleic acid attached to a detectable label or other reporter molecule. Typical labels include radioactive isotopes, enzyme substrates, co-factors, ligands, chemiluminescent or fluorescent agents, haptens, and enzymes. Methods for labeling and guidance in the choice of labels appropriate for various purposes are discussed, for example, in Sambrook et al. (ed.), *Molecular Cloning: A Laboratory Manual*, 2nd ed., vol. 1-3, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989 and Ausubel et al. *Short Protocols in Molecular Biology*, 4th ed., John Wiley & Sons, Inc., 1999.

Primers are short nucleic acid molecules, for instance DNA oligonucleotides 10 nucleotides or more in length, for example that hybridize to contiguous complementary nucleotides or a sequence to be amplified. Longer DNA oligonucleotides may be about 15, 20, 25, 30 or 50 nucleotides or more in length. Primers can be annealed to a complementary target DNA strand by nucleic acid hybridization to form a hybrid between the primer and the target DNA strand, and then the primer extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification of a nucleic acid sequence, for example, by the PCR or other nucleic-acid amplification methods known in the art, as described above.

Methods for preparing and using nucleic acid probes and primers are described, for example, in Sambrook et al. (ed.), *Molecular Cloning: A Laboratory Manual*, 2nd ed., vol. 1-3, Cold Spring Harbor Laboratory Press, Cold Spring Harbor,

N.Y., 1989; Ausubel et al. *Short Protocols in Molecular Biology*, 4th ed., John Wiley & Sons, Inc., 1999; and Innis et al. *PCR Protocols, A Guide to Methods and Applications*, Academic Press, Inc., San Diego, Calif., 1990. Amplification primer pairs can be derived from a known sequence, for example, by using computer programs intended for that purpose such as Primer (Version 0.5, © 1991, Whitehead Institute for Biomedical Research, Cambridge, Mass.). One of ordinary skill in the art will appreciate that the specificity of a particular probe or primer increases with its length. Thus, in order to obtain greater specificity, probes and primers can be selected that comprise at least 20, 25, 30, 35, 40, 45, 50 or more consecutive nucleotides of a target nucleotide sequences.

Protein: A biological molecule, particularly a polypeptide, expressed by a gene and comprised of amino acids. A "polyprotein" is a protein that, after synthesis, is cleaved to produce several functionally distinct polypeptides.

Purified: The term "purified" does not require absolute purity; rather, it is intended as a relative term. Thus, for example, a purified protein preparation is one in which the subject protein is more pure than in its natural environment within a cell. Generally, a protein preparation is purified such that the protein represents at least 50% of the total protein content of the preparation.

Recombinant Nucleic Acid: A sequence that is not naturally occurring or has a sequence that is made by an artificial combination of two otherwise separated segments of sequence. This artificial combination is often accomplished by chemical synthesis or, more commonly, by the artificial manipulation of isolated segments of nucleic acids, for example, by genetic engineering techniques such as those described in Sambrook et al. (ed.), *Molecular Cloning: A Laboratory Manual*, 2nd ed., vol. 1-3, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989. The term recombinant includes nucleic acids that have been altered solely by addition, substitution, or deletion of a portion of the nucleic acid.

Sample: A portion, piece, or segment that is representative of a whole. This term encompasses any material, including for instance samples obtained from an animal, a plant, or the environment.

An "environmental sample" includes a sample obtained from inanimate objects or reservoirs within an indoor or outdoor environment. Environmental samples include, but are not limited to: soil, water, dust, and air samples; bulk samples, including building materials, furniture, and landfill contents; and other reservoir samples, such as animal refuse, harvested grains, and foodstuffs.

A "biological sample" is a sample obtained from a plant or animal subject. As used herein, biological samples include all samples useful for detection of viral infection in subjects, including, but not limited to: cells, tissues, and bodily fluids, such as blood; derivatives and fractions of blood (such as serum); extracted galls; biopsied or surgically removed tissue, including tissues that are, for example, unfixed, frozen, fixed in formalin and/or embedded in paraffin; tears; milk; skin scrapes; surface washings; urine; sputum; cerebrospinal fluid; prostate fluid; pus; bone marrow aspirates; BAL; saliva; cervical swabs; vaginal swabs; and oropharyngeal wash.

Sequence Identity: The similarity between two nucleic acid sequences, or two amino acid sequences, is expressed in terms of the similarity between the sequences, otherwise referred to as sequence identity. Sequence identity is frequently measured in terms of percentage identity (or similarity or homology); the higher the percentage, the more similar the two sequences are.

Methods of alignment of sequences for comparison are well known in the art. Various programs and alignment

algorithms are described in: Smith and Waterman (*Adv. Appl. Math.*, 2:482, 1981); Needleman and Wunsch (*J. Mol. Biol.*, 48:443, 1970); Pearson and Lipman (*Proc. Natl. Acad. Sci.*, 85:2444, 1988); Higgins and Sharp (*Gene*, 73:237-44, 1988); Higgins and Sharp (*CABIOS*, 5:151-53, 1989); Corpet et al. (*Nuc. Acids Res.*, 16:10881-90, 1988); Huang et al. (*Comp. Appls Biosci.*, 8:155-65, 1992); and Pearson et al. (*Meth. Mol. Biol.*, 24:307-31, 1994). Altschul et al. (*Nature Genet.*, 6:119-29, 1994) presents a detailed consideration of sequence alignment methods and homology calculations.

The alignment tools ALIGN (Myers and Miller, *CABIOS* 4:11-17, 1989) or LFASTA (Pearson and Lipman, 1988) may be used to perform sequence comparisons (Internet Program© 1996, W. R. Pearson and the University of Virginia, "fasta20u63" version 2.0u63, release date December 1996). ALIGN compares entire sequences against one another, while LFASTA compares regions of local similarity. These alignment tools and their respective tutorials are available on the Internet at the NCSA website. Alternatively, for comparisons of amino acid sequences of greater than about 30 amino acids, the "Blast 2 sequences" function can be employed using the default BLOSUM62 matrix set to default parameters, (gap existence cost of 11, and a per residue gap cost of 1). When aligning short peptides (fewer than around 30 amino acids), the alignment should be performed using the "Blast 2 sequences" function, employing the PAM30 matrix set to default parameters (open gap 9, extension gap 1 penalties). The BLAST sequence comparison system is available, for instance, from the NCBI web site; see also Altschul et al., *J. Mol. Biol.*, 215:403-10, 1990; Gish, and States, *Nature Genet.*, 3:266-72, 1993; Madden et al., *Meth. Enzymol.*, 266:131-41, 1996; Altschul et al., *Nucleic Acids Res.*, 25:3389-402, 1997; and Zhang and Madden, *Genome Res.*, 7:649-56, 1997.

Orthologs (equivalent to proteins of other species) of proteins are in some instances characterized by possession of greater than 75% sequence identity counted over the full-length alignment with the amino acid sequence of specific protein using ALIGN set to default parameters. Proteins with even greater similarity to a reference sequence will show increasing percentage identities when assessed by this method, such as at least 80%, at least 85%, at least 90%, at least 92%, at least 95%, or at least 98% sequence identity. In addition, sequence identity can be compared over the full length of one or both binding domains of the disclosed fusion proteins.

When significantly less than the entire sequence is being compared for sequence identity, homologous sequences will typically possess at least 80% sequence identity over short windows of 10-20, and may possess sequence identities of at least 85%, at least 90%, at least 95%, or at least 99% depending on their similarity to the reference sequence. Sequence identity over such short windows can be determined using LFASTA; methods are described at the NCSA website. One of skill in the art will appreciate that these sequence identity ranges are provided for guidance only; it is entirely possible that strongly significant homologs could be obtained that fall outside of the ranges provided. Similar homology concepts apply for nucleic acids as are described for protein.

An alternative indication that two nucleic acid molecules are closely related is that the two molecules hybridize to each other under stringent conditions. Representative hybridization conditions are discussed above.

Nucleic acid sequences that do not show a high degree of identity may nevertheless encode similar amino acid sequences, due to the degeneracy of the genetic code. It is understood that changes in nucleic acid sequence can be made using this degeneracy to produce multiple nucleic acid sequences that each encode substantially the same protein.

Specific Binding Agent: An agent that binds substantially only to a defined target. Thus a protein-specific binding agent binds substantially only the defined protein, or to a specific region within the protein. As used herein, a protein-specific binding agent includes antibodies and other agents that bind substantially to a specified polypeptide. The antibodies may be monoclonal or polyclonal antibodies that are specific for the polypeptide, as well as immunologically effective portions (“fragments”) thereof.

The determination that a particular agent binds substantially only to a specific polypeptide may readily be made by using or adapting routine procedures. One suitable in vitro assay makes use of the Western blotting procedure (described in many standard texts, including Harlow and Lane, *Using Antibodies: A Laboratory Manual*, CSHL, New York, 1999).

Transformed: A “transformed” cell is a cell into which has been introduced a nucleic acid molecule by molecular biology techniques. The term encompasses all techniques by which a nucleic acid molecule might be introduced into such a cell, including transfection with viral vectors, transformation with plasmid vectors, and introduction of naked DNA by electroporation, lipofection, and particle gun acceleration.

Vector: A nucleic acid molecule as introduced into a host cell, thereby producing a transformed host cell. A vector may include nucleic acid sequences that permit it to replicate in a host cell, such as an origin of replication. A vector may also include one or more selectable marker genes and other genetic elements known in the art.

Virus: Microscopic infectious organism that reproduces inside living cells. A virus typically consists essentially of a core of a single nucleic acid surrounded by a protein coat, and has the ability to replicate only inside a living cell. “Viral replication” is the production of additional virus by the occurrence of at least one viral life cycle. A virus may subvert the host cells’ normal functions, causing the cell to behave in a manner determined by the virus. For example, a viral infection may result in a cell producing a cytokine, or responding to a cytokine, when the uninfected cell does not normally do so.

“Coronaviruses” are large, enveloped, RNA viruses that cause respiratory and enteric diseases in humans and other animals. Coronavirus genomes are non-segmented, single-stranded, positive-sense RNA, approximately 27–31 kb in length. Genomes have a 5’ methylated cap and 3’ poly-A tail, and function directly as mRNA. Host cell entry occurs via endocytosis and membrane fusion, and replication occurs in the cytoplasm. Initially, the 5’ 20 kb of the positive-sense genome is translated to produce a viral polymerase, which then produces a full-length negative-sense strand used as a template to produce subgenomic mRNA as a “nested set” of transcripts. Assembly occurs by budding into the golgi apparatus, and particles are transported to the surface of the cell and released.

III. Overview of Several Embodiments

A newly isolated human coronavirus (SARS-CoV) is disclosed herein. The entire genomic nucleic acid sequence of this virus is also provided herein. Also disclosed are the nucleic acid sequences of the SARS-CoV ORFs, and the polypeptide sequences encoded by these ORFs. Pharmaceutical and immune stimulatory compositions are also disclosed that include one or more SARS-CoV viral nucleic acids, polypeptides encoded by these viral nucleic acids and antibodies that bind to a SARS-CoV polypeptide or SARS-CoV polypeptide fragment.

In one embodiment, a method is provided for detecting the presence of SARS-CoV in a sample. This method includes contacting the sample with a pair of nucleic acid

primers that hybridize to a SARS-CoV nucleic acid, wherein at least one primer is 5’-end labeled with a reporter dye, amplifying the SARS-CoV nucleic acid or a fragment thereof from the sample utilizing the pair of nucleic acid primers, electrophoresing the amplified products, and detecting the 5’-end labeled reporter dye, thereby detecting a SARS-CoV. In a specific, non-limiting example, the amplification utilizes RT-PCR. In a further specific example of the provided method, at least one of the nucleic acid primers that hybridize to a SARS-CoV nucleic acid includes a sequence as set forth in any one of SEQ ID NOs: 13–15.

In another example of the provided method, detecting the presence of SARS-CoV in a sample includes contacting the sample with a pair of nucleic acid primers that hybridize to a SARS-CoV nucleic acid, amplifying the SARS-CoV nucleic acid or a fragment thereof from the sample utilizing the pair of nucleic acid primers, adding to the amplified SARS-CoV nucleic acid or the fragment thereof a TaqMan SARS-CoV probe that hybridizes to the SARS-CoV nucleic acid, wherein the TaqMan SARS-CoV probe is labeled with a 5’-reporter dye and a 3’-quencher dye, performing one or more additional rounds of amplification, and detecting fluorescence of the 5’-reporter dye, thereby detecting a SARS-CoV. In a specific, non-limiting example, the amplification utilizes RT-PCR. In a further specific example of the provided method, at least one of the nucleic acid primers that hybridize to a SARS-CoV nucleic acid and/or the TaqMan SARS-CoV probe that hybridizes to the SARS-CoV nucleic acid includes a sequence as set forth in any one of SEQ ID NOs: 16–33.

In another embodiment, a method is provided for detecting a SARS-CoV in a biological sample that contains antibodies. This method includes contacting the biological sample with a SARS-CoV-specific antigen, wherein the antigen includes a SARS-CoV organism and determining whether a binding reaction occurs between the SARS-CoV-specific antigen and an antibody in the biological sample if such is present, thereby detecting SARS-CoV.

In a further embodiment, a method is provided for detecting a SARS-CoV in a biological sample that contains polypeptides and/or fragments thereof. This method includes contacting the biological sample with a SARS-CoV-specific antibody and determining whether a binding reaction occurs between the SARS-CoV-specific antibody and a SARS-CoV polypeptide or fragment thereof in the biological sample if such is present, thereby detecting SARS-CoV. In a specific, non-limiting example, determining whether a binding reaction occurs between the SARS-CoV-specific antibody and a SARS-CoV polypeptide or fragment thereof is carried out in situ or in a tissue sample. In a further specific example, determining whether a binding reaction occurs between the SARS-CoV-specific antibody and a SARS-CoV polypeptide or fragment thereof includes an immunohistochemical assay.

An additional embodiment includes a kit for detecting a SARS-CoV in a sample, including a pair of nucleic acid primers that hybridize under stringent conditions to a SARS-CoV nucleic acid, wherein one primer is 5’-end labeled with a reporter dye. In a specific, non-limiting example, at least one of the nucleic acid primers that hybridize to a SARS-CoV nucleic acid includes a sequence as set forth in any one of SEQ ID NOs: 13–15.

Another example of the provided kit includes a pair of nucleic acid primers that hybridize under high stringency conditions to a SARS-CoV nucleic acid and a TaqMan SARS-CoV probe that hybridizes to the SARS-CoV nucleic acid, wherein the TaqMan SARS-CoV probe is labeled with a 5’-reporter dye and a 3’-quencher dye. In a specific, non-limiting example, at least one of the nucleic acid primers that hybridize to a SARS-CoV nucleic acid and/or

the TaqMan SARS-CoV probe that hybridizes to the SARS-CoV nucleic acid includes a sequence as set forth in any one of SEQ ID NOs: 16–33.

Also disclosed herein is a composition including an isolated SARS-CoV organism. In one embodiment, the isolated SARS-CoV organism is an inactive isolated SARS-CoV organism. In another embodiment, the composition includes at least one component selected from the group consisting of pharmaceutically acceptable carriers, adjuvants and combinations of two or more thereof. In yet another embodiment, the composition is introduced into a subject, thereby eliciting an immune response against a SARS-CoV antigenic epitope in a subject.

IV. SARS-CoV Nucleotide and Amino Acid Sequences

The current disclosure provides an isolated SARS-CoV genome, isolated SARS-CoV polypeptides, and isolated nucleic acid molecules encoding the same. In one embodiment, the isolated SARS-CoV genome has a sequence as shown in SEQ ID NO: 1 or an equivalent thereof. Polynucleotides encoding a SARS-CoV polypeptide (encoded by an ORF from within the genome) are also provided, and are termed SARS-CoV nucleic acid molecules. These nucleic acid molecules include DNA, cDNA and RNA sequences which encode a SARS-CoV polypeptide. Specific, non-limiting examples of a SARS-CoV nucleic acid molecule encoding an ORF are nucleic acid 265 to nucleic acid 13,398 of SEQ ID NO: 1 (encoding SARS-CoV 1a, SEQ ID NO: 2), nucleic acid 13,398 to 21,482 of SEQ ID NO: 1 (encoding SARS-CoV 1b, SEQ ID NO: 3), nucleic acid 21,492 to 25,256 of SEQ ID NO: 1 (encoding SARS-CoV S, SEQ ID NO: 4), nucleic acid 25,268 to 26,089 of SEQ ID NO: 1 (encoding SARS-CoV X1, SEQ ID NO: 5), nucleic acid 25,689 to 26,150 of SEQ ID NO: 1 (encoding SARS-CoV X2, SEQ ID NO: 6), nucleic acid 26,117 to 26,344 of SEQ ID NO: 1 (encoding SARS-CoV E, SEQ ID NO: 7), nucleic acid 26,398 to 27,060 of SEQ ID NO: 1 (encoding SARS-CoV M, SEQ ID NO: 8), nucleic acid 27,074 to 27,262 of SEQ ID NO: 1 (encoding SARS-CoV X3, SEQ ID NO: 9), nucleic acid 27,273 to 27,638 of SEQ ID NO: 1 (encoding SARS-CoV X4, SEQ ID NO: 10), nucleic acid 27,864 to 28,115 of SEQ ID NO: 1 (encoding SARS-CoV X5, SEQ ID NO: 11), and nucleic acid 28,120 to 29,385 of SEQ ID NO: 1 (encoding SARS-CoV N, SEQ ID NO: 12).

Oligonucleotide primers and probes derived from the SARS-CoV genome (SEQ ID NO: 1) are also encompassed within the scope of the present disclosure. Such oligonucleotide primers and probes may comprise a sequence of at least about 15 consecutive nucleotides of the SARS-CoV nucleic acid sequence, such as at least about 20, 25, 30, 35, 40, 45, or 50 or more consecutive nucleotides. These primers and probes may be obtained from any region of the disclosed SARS-CoV genome (SEQ ID NO: 1), including particularly from any of the ORFs disclosed herein. Specific, non-limiting examples of oligonucleotide primers derived from the SARS-CoV genome (SEQ ID NO: 1) include: Cor-p-F2 (SEQ ID NO: 13), Cor-p-F3 (SEQ ID NO: 14), Cor-p-R1 (SEQ ID NO: 15), SARS1-F (SEQ ID NO: 16), SARS1-R (SEQ ID NO: 17), SARS2-F (SEQ ID NO: 19), SARS2-R (SEQ ID NO: 20), SARS3-F (SEQ ID NO: 22), SARS3-R (SEQ ID NO: 23), N3-F (SEQ ID NO: 25), N3-R (SEQ ID NO: 26), 3'NTR-F (SEQ ID NO: 28), 3'NTR-R (SEQ ID NO: 29), M-F (SEQ ID NO: 31), and M-R (SEQ ID NO: 32). Specific, non-limiting examples of oligonucleotide probes derived from the SARS-CoV genome (SEQ ID NO: 1) include: SARS1-P (SEQ ID NO: 18), SARS2-P (SEQ ID NO: 21), SARS3-P (SEQ ID NO: 24), N3-P (SEQ ID NO: 27), 3'NTR-P (SEQ ID NO: 30), and M-P (SEQ ID NO: 33).

Nucleic acid molecules encoding a SARS-CoV polypeptide can be operatively linked to regulatory sequences or

elements. Regulatory sequences or elements include, but are not limited to promoters, enhancers, transcription terminators, a start codon (for example, ATG), stop codons, and the like.

Additionally, nucleic acid molecules encoding a SARS-CoV polypeptide can be inserted into an expression vector. Specific, non-limiting examples of vectors include, plasmids, bacteriophages, cosmids, animal viruses and yeast artificial chromosomes (YACs) (Burke et al., *Science* 236: 806–12, 1987). Such vectors may then be introduced into a variety of hosts including somatic cells, and simple or complex organisms, such as bacteria, fungi (Timberlake and Marshall, *Science* 244:1313–17, 1989), invertebrates, plants (Gasser et al., *Plant Cell* 1:15–24, 1989), and animals (Pursel et al., *Science* 244:1281–88, 1989).

Transformation of a host cell with an expression vector carrying a nucleic acid molecule encoding a SARS-CoV polypeptide may be carried out by conventional techniques, as are well known to those skilled in the art. By way of example, where the host is prokaryotic, such as *E. coli*, competent cells that are capable of DNA uptake can be prepared from cells harvested after exponential growth phase and subsequently treated by the CaCl₂ method using procedures well known in the art. Alternatively, MgCl₂ or RbCl can be used. Transformation can also be performed after forming a protoplast of the host cell if desired, or by electroporation.

When the host is a eukaryote, methods of transfection of DNA, such as calcium phosphate coprecipitates, conventional mechanical procedures such as microinjection, electroporation, insertion of a plasmid encased in liposomes, or virus vectors, may be used. Eukaryotic cells can also be cotransformed with SARS-CoV nucleic acid molecules, and a second foreign DNA molecule encoding a selectable phenotype, such as the herpes simplex thymidine kinase gene. Another method is to use a eukaryotic viral vector, such as simian virus 40 or bovine papilloma virus, to transiently infect or transform eukaryotic cells and express the protein (see, for example, *Eukaryotic Viral Vectors*, Cold Spring Harbor Laboratory, Gluzman ed., 1982).

The SARS-CoV polypeptides of this disclosure include proteins encoded by any of the ORFs disclosed herein, and equivalents thereof. Specific, non-limiting examples of SARS-CoV proteins are provided in SEQ ID NOs: 2–12. Fusion proteins are also contemplated that include a heterologous amino acid sequence chemically linked to a SARS-CoV polypeptide. Exemplary heterologous sequences include short amino acid sequence tags (such as six histidine residues), as well a fusion of other proteins (such as c-myc or green fluorescent protein fusions). Epitopes of the SARS-CoV proteins, that are recognized by an antibody or that bind the major histocompatibility complex, and can be used to induce a SARS-CoV-specific immune response, are also encompassed by this disclosure.

Methods for expressing large amounts of protein from a cloned gene introduced into *E. coli* may be utilized for the purification and functional analysis of proteins. For example, fusion proteins consisting of amino terminal peptides encoded by a portion of the *E. coli* lacZ or trpE gene linked to SARS-CoV proteins may be used to prepare polyclonal and monoclonal antibodies against these proteins.

Intact native protein may also be produced in *E. coli* in large amounts for functional studies. Methods and plasmid vectors for producing fusion proteins and intact native proteins in bacteria are described by Sambrook et al. (ed.), *Molecular Cloning: A Laboratory Manual*, 2nd ed., vol. 1–3, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989. Such fusion proteins may be made in large amounts, are easy to purify, and can be used to elicit

antibody response. Native proteins can be produced in bacteria by placing a strong, regulated promoter and an efficient ribosome-binding site upstream of the cloned gene. If low levels of protein are produced, additional steps may be taken to increase protein production; if high levels of protein are produced, purification is relatively easy. Suitable methods are presented by Sambrook et al. (ed.), *Molecular Cloning: A Laboratory Manual*, 2nd ed., vol. 1-3, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989, and are well known in the art. Often, proteins expressed at high levels are found in insoluble inclusion bodies. Methods for extracting proteins from these aggregates are described by Sambrook et al. (ed.), *Molecular Cloning: A Laboratory Manual*, 2nd ed., vol. 1-3, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.

Isolation and purification of recombinantly expressed proteins may be carried out by conventional means including preparative chromatography and immunological separations. Additionally, the proteins can be chemically synthesized by any of a number of manual or automated methods of synthesis known in the art.

V. Specific Binding Agents

The disclosure provides specific binding agents that bind to SARS-CoV polypeptides disclosed herein. The binding agent may be useful for purifying and detecting the polypeptides, as well as for detection and diagnosis of SARS-CoV. Examples of the binding agents are a polyclonal or monoclonal antibody, and fragments thereof, that bind to any of the SARS-CoV polypeptides disclosed herein.

Monoclonal or polyclonal antibodies may be raised to recognize a SARS-CoV polypeptide described herein, or a fragment or variant thereof. Optimally, antibodies raised against these polypeptides would specifically detect the polypeptide with which the antibodies are generated. That is, antibodies raised against a specific SARS-CoV polypeptide will recognize and bind that polypeptide, and will not substantially recognize or bind to other polypeptides or antigens. The determination that an antibody specifically binds to a target polypeptide is made by any one of a number of standard immunoassay methods; for instance, the Western blotting technique (Sambrook et al. (ed.), *Molecular Cloning: A Laboratory Manual*, 2nd ed., vol. 1-3, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989).

Substantially pure SARS-CoV recombinant polypeptide antigens suitable for use as immunogen may be isolated from the transformed cells described above, using methods well known in the art. Monoclonal or polyclonal antibodies to the antigens may then be prepared.

Monoclonal antibodies to the polypeptides can be prepared from murine hybridomas according to the classic method of Kohler & Milstein (*Nature* 256:495-97, 1975), or a derivative method thereof. Briefly, a mouse is repetitively inoculated with a few micrograms of the selected protein immunogen (for example, a polypeptide comprising at least one SARS-CoV-specific epitope, a portion of a polypeptide comprising at least one SARS-CoV-specific epitope, or a synthetic peptide comprising at least one SARS-CoV-specific epitope) over a period of a few weeks. The mouse is then sacrificed, and the antibody-producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells destroyed by growth of the system on selective media comprising aminopterin (HAT media). The successfully fused cells are diluted and aliquots of the dilution placed in wells of a microtiter plate where growth of the culture is continued. Antibody-producing clones are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as ELISA, as

originally described by Engvall (*Meth. Enzymol.*, 70:419-39, 1980), or a derivative method thereof. Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Harlow and Lane, *Using Antibodies: A Laboratory Manual*, CSHL, New York, 1999.

Polyclonal antiserum containing antibodies can be prepared by immunizing suitable animals with a polypeptide comprising at least one SARS-CoV-specific epitope, a portion of a polypeptide comprising at least one SARS-CoV-specific epitope, or a synthetic peptide comprising at least one SARS-CoV-specific epitope, which can be unmodified or modified, to enhance immunogenicity.

Effective antibody production (whether monoclonal or polyclonal) is affected by many factors related both to the antigen and the host species. For example, small molecules tend to be less immunogenic than others and may require the use of carriers and adjuvant. Also, host animals vary in response to site of inoculations and dose, with either inadequate or excessive doses of antigen resulting in low titer antisera. Small doses (ng level) of antigen administered at multiple intradermal sites appear to be most reliable. An effective immunization protocol for rabbits can be found in Vaitukaitis et al. (*J. Clin. Endocrinol. Metab.*, 33:988-91, 1971).

Booster injections can be given at regular intervals, and antiserum harvested when the antibody titer thereof, as determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen, begins to fall. See, for example, Ouchterlony et al., *Handbook of Experimental Immunology*, Wier, D. (ed.), Chapter 19, Blackwell, 1973. A plateau concentration of antibody is usually in the range of 0.1 to 0.2 mg/ml of serum (about 12 μ M). Affinity of the antisera for the antigen is determined by preparing competitive binding curves, as described, for example, by Fisher (*Manual of Clinical Immunology*, Ch. 42, 1980).

Antibody fragments may be used in place of whole antibodies and may be readily expressed in prokaryotic host cells. Methods of making and using immunologically effective portions of monoclonal antibodies, also referred to as "antibody fragments," are well known and include those described in Better & Horowitz, *Methods Enzymol.* 178: 476-96, 1989; Glockshuber et al., *Biochemistry* 29:1362-67, 1990; and U.S. Pat. No. 5,648,237 (Expression of Functional Antibody Fragments); U.S. Pat. No. 4,946,778 (Single Polypeptide Chain Binding Molecules); and U.S. Pat. No. 5,455,030 (Immunotherapy Using Single Chain Polypeptide Binding Molecules), and references cited therein. Conditions whereby a polypeptide/binding agent complex can form, as well as assays for the detection of the formation of a polypeptide/binding agent complex and quantitation of binding affinities of the binding agent and polypeptide, are standard in the art. Such assays can include, but are not limited to, Western blotting, immunoprecipitation, immunofluorescence, immunocytochemistry, immunohistochemistry, fluorescence activated cell sorting (FACS), fluorescence in situ hybridization (FISH), immunomagnetic assays, ELISA, ELISPOT (Coligan et al., *Current Protocols in Immunology*, Wiley, NY, 1995), agglutination assays, flocculation assays, cell panning, and the like, as are well known to one of skill in the art.

Binding agents of this disclosure can be bound to a substrate (for example, beads, tubes, slides, plates, nitrocellulose sheets, and the like) or conjugated with a detectable moiety, or both bound and conjugated. The detectable moieties contemplated for the present disclosure can include, but are not limited to, an immunofluorescent moiety (for example, fluorescein, rhodamine), a radioactive moiety (for

example, ^{32}P , ^{125}I , ^{35}S), an enzyme moiety (for example, horseradish peroxidase, alkaline phosphatase), a colloidal gold moiety, and a biotin moiety. Such conjugation techniques are standard in the art (for example, see Harlow and Lane, *Using Antibodies: A Laboratory Manual*, CSHL, New York, 1999; Yang et al., *Nature*, 382:319–24, 1996).

VI. Detection and Diagnosis of SARS-CoV

A. Nucleic Acid Based Methods of Detection and Diagnosis

A major application of the SARS-CoV sequence information presented herein is in the area of detection and diagnostic testing for SARS-CoV infection. Methods for screening a subject to determine if the subject has been or is currently infected with SARS-CoV are disclosed herein.

One such method includes providing a sample, which sample includes a nucleic acid such as DNA or RNA, and providing an assay for detecting in the sample the presence of a SARS-CoV nucleic acid molecule. Suitable samples include all biological samples useful for detection of viral infection in subjects, including, but not limited to, cells, tissues (for example, lung and kidney), bodily fluids (for example, blood, serum, urine, saliva, sputum, and cerebrospinal fluid), bone marrow aspirates, BAL, and oropharyngeal wash. Additional suitable samples include all environmental samples useful for detection of viral presence in the environment, including, but not limited to, a sample obtained from inanimate objects or reservoirs within an indoor or outdoor environment. The detection in the sample of a SARS-CoV nucleic acid molecule may be performed by a number of methodologies, non-limiting examples of which are outlined below.

In one embodiment, detecting in the sample the presence of a SARS-CoV nucleic acid molecule includes the amplification of a SARS-CoV nucleic acid sequence (or a fragment thereof). Any nucleic acid amplification method can be used. In one specific, non-limiting example, PCR is used to amplify the SARS-CoV nucleic acid sequence(s). In another non-limiting example, RT-PCR can be used to amplify the SARS-CoV nucleic acid sequences. In an additional non-limiting example, transcription-mediated amplification can be used to amplify the SARS-CoV nucleic acid sequences.

In some embodiments, a pair of SARS-CoV-specific primers are utilized in the amplification reaction. One or both of the primers can be end-labeled (for example, radio-labeled, fluoresceinated, or biotinylated). In one specific, non-limiting example, at least one of the primers is 5'-end labeled with the reporter dye 6-carboxyfluorescein (6-FAM). The pair of primers includes an upstream primer (which binds 5' to the downstream primer) and a downstream primer (which binds 3' to the upstream primer). In one embodiment, either the upstream primer or the downstream primer is labeled. Specific, non-limiting examples of SARS-CoV-specific primers include, but are not limited to: Cor-p-F2 (SEQ ID NO: 13), Cor-p-F3 (SEQ ID NO: 14), Cor-p-R1 (SEQ ID NO: 15), SARS1-F (SEQ ID NO: 16), SARS1-R (SEQ ID NO: 17), SARS2-F (SEQ ID NO: 19), SARS2-R (SEQ ID NO: 20), SARS3-F (SEQ ID NO: 22), SARS3-R (SEQ ID NO: 23), N3-F (SEQ ID NO: 25), N3-R (SEQ ID NO: 26), 3'NTR-F (SEQ ID NO: 28), 3'NTR-R (SEQ ID NO: 29), M-F (SEQ ID NO: 31), and M-R (SEQ ID NO: 32). Additional primer pairs can be generated, for instance, to amplify any of the specific ORFs described herein, using well known primer design principles and methods.

In one specific, non-limiting example, electrophoresis is used to detect amplified SARS-CoV-specific sequences. Electrophoresis can be automated using many methods well known in the art. In one embodiment, a genetic analyzer is used, such as an ABI 3100 Prism Genetic Analyzer (PE

Applied Biosystems, Foster City, Calif.), wherein the bands are analyzed using GeneScan software (PE Applied Biosystems, Foster City, Calif.).

In another specific, non-limiting example, hybridization assays are used to detect amplified SARS-CoV-specific sequences using distinguishing oligonucleotide probes. Such probes include "TaqMan" probes. TaqMan probes consist of an oligonucleotide with a reporter at the 5'-end and a quencher at the 3'-end. In one specific, non-limiting example, the reporter is 6-FAM and the quencher is Black-hole Quencher (Biosearch Tech., Inc., Novato, Calif.). When the probe is intact, the proximity of the reporter to the quencher results in suppression of reporter fluorescence, primarily by fluorescence resonance energy transfer. If the target of interest is present, the TaqMan probe specifically hybridizes between the forward and reverse primer sites during the PCR annealing step. In the process of PCR elongation, the 5'-3' nucleolytic activity of the Taq DNA polymerase cleaves the hybridized probe between the reporter and the quencher. The probe fragments are then displaced from the target, and polymerization of the strand continues. Taq DNA polymerase does not cleave non-hybridized probe, and cleaves the hybridized probe only during polymerization. The 3'-end of the probe is blocked to prevent extension of the probe during PCR. The 5'-3' nuclease cleavage of the hybridized probe occurs in every cycle and does not interfere with the exponential accumulation of PCR product. Accumulation of PCR products is detected directly by monitoring the increase in fluorescence of the released reporter. The increase in fluorescence signal is detected only if the target sequence is complementary to the probe and is amplified during PCR. Therefore, non-specific amplification is not detected. SARS-CoV-specific TaqMan probes of the present disclosure include, but are not limited to: SARS1-P (SEQ ID NO: 18), SARS2-P (SEQ ID NO: 21), SARS3-P (SEQ ID NO: 24), N3-P (SEQ ID NO: 27), 3'NTR-P (SEQ ID NO: 30), and M-P (SEQ ID NO: 33), and hybridization assays include, but are not limited to, a real-time RT-PCR assay.

B. Protein Based Methods of Detection and Diagnosis

The present disclosure further provides methods of detecting a SARS-CoV antigen in a sample, and/or diagnosing SARS-CoV infection in a subject by detecting a SARS-CoV antigen. Examples of such methods comprise contacting the sample with a SARS-CoV-specific binding agent under conditions whereby an antigen/binding agent complex can form; and detecting formation of the complex, thereby detecting SARS-CoV antigen in a sample and/or diagnosing SARS-CoV infection in a subject. It is contemplated that at least certain antigens will be on an intact SARS-CoV virion, will be a SARS-CoV-encoded protein displayed on the surface of a SARS-CoV-infected cell expressing the antigen, or will be a fragment of the antigen. Contemplated samples subject to analysis by these methods can comprise any sample, such as a clinical sample, useful for detection of viral infection in a subject.

Methods for detecting antigens in a sample are discussed, for example, in Ausubel et al. *Short Protocols in Molecular Biology*, 4th ed., John Wiley & Sons, Inc., 1999. Enzyme immunoassays such as IFA, ELISA and immunoblotting can be readily adapted to accomplish the detection of SARS-CoV antigens according to the methods of this disclosure. An ELISA method effective for the detection of soluble SARS-CoV antigens is the direct competitive ELISA. This method is most useful when a specific SARS-CoV antibody and purified SARS-CoV antigen are available. Briefly: 1) coat a substrate (for example, a microtiter plate) with a sample suspected of containing a SARS-CoV antigen; 2) contact the bound SARS-CoV antigen with a SARS-CoV-specific antibody bound to a detectable moiety (for example,

horseradish peroxidase enzyme or alkaline phosphatase enzyme); 3) add purified inhibitor SARS-CoV antigen; 4) contact the above with the substrate for the enzyme; and 5) observe/measure inhibition of color change or fluorescence and quantitate antigen concentration (for example, using a microtiter plate reader).

An additional ELISA method effective for the detection of soluble SARS-CoV antigens is the antibody-sandwich ELISA. This method is frequently more sensitive in detecting antigen than the direct competitive ELISA method. Briefly: 1) coat a substrate (for example, a microtiter plate) with a SARS-CoV-specific antibody; 2) contact the bound SARS-CoV antibody with a sample suspected of containing a SARS-CoV antigen; 3) contact the above with SARS-CoV-specific antibody bound to a detectable moiety (for example, horseradish peroxidase enzyme or alkaline phosphatase enzyme); 4) contact the above with the substrate for the enzyme; and 5) observe/measure color change or fluorescence and quantitate antigen concentration (for example, using a microtiter plate reader).

An ELISA method effective for the detection of cell-surface SARS-CoV antigens is the direct cellular ELISA. Briefly, cells suspected of exhibiting a cell-surface SARS-CoV antigen are fixed (for example, using glutaraldehyde) and incubated with a SARS-CoV-specific antibody bound to a detectable moiety (for example, horseradish peroxidase enzyme or alkaline phosphatase enzyme). Following a wash to remove unbound antibody, substrate for the enzyme is added and color change or fluorescence is observed/measured.

The present disclosure further provides methods of detecting a SARS-CoV-reactive antibody in a sample, and/or diagnosing SARS-CoV infection in a subject by detecting a SARS-CoV-reactive antibody. Examples of such methods comprise contacting the sample with a SARS-CoV polypeptide of this disclosure under conditions whereby a polypeptide/antibody complex can form; and detecting formation of the complex, thereby detecting SARS-CoV antibody in a sample and/or diagnosing SARS-CoV infection in a subject. Contemplated samples subject to analysis by these methods can comprise any sample, such as a clinical sample, as described herein as being useful for detection of viral infection in a subject.

Methods for detecting antibodies in a sample are discussed, for example, in Ausubel et al. *Short Protocols in Molecular Biology*, 4th ed., John Wiley & Sons, Inc., 1999. Enzyme immunoassays such as IFA, ELISA and immunoblotting can be readily adapted to accomplish the detection of SARS-CoV antibodies according to the methods of this disclosure. An ELISA method effective for the detection of specific SARS-CoV antibodies is the indirect ELISA method. Briefly: 1) bind a SARS-CoV polypeptide to a substrate (for example, a microtiter plate); 2) contact the bound polypeptide with a sample suspected of containing SARS-CoV antibody; 3) contact the above with a secondary antibody bound to a detectable moiety which is reactive with the bound antibody (for example, horseradish peroxidase enzyme or alkaline phosphatase enzyme); 4) contact the above with the substrate for the enzyme; and 5) observe/measure color change or fluorescence.

Another immunologic technique that can be useful in the detection of SARS-CoV antibodies uses monoclonal antibodies for detection of antibodies specifically reactive with SARS-CoV polypeptides in a competitive inhibition assay. Briefly, a sample suspected of containing SARS-CoV antibodies is contacted with a SARS-CoV polypeptide of this disclosure which is bound to a substrate (for example, a microtiter plate). Excess sample is thoroughly washed away. A labeled (for example, enzyme-linked, fluorescent, radioactive, and the like) monoclonal antibody specific for the

SARS-CoV polypeptide is then contacted with any previously formed polypeptide-antibody complexes and the amount of monoclonal antibody binding is measured. The amount of inhibition of monoclonal antibody binding is measured relative to a control (no monoclonal antibody), allowing for detection and measurement of antibody in the sample. The degree of monoclonal antibody inhibition can be a very specific assay for detecting SARS-CoV. Monoclonal antibodies can also be used for direct detection of SARS-CoV in cells or tissue samples by, for example, IFA analysis according to standard methods.

As a further example, a micro-agglutination test can be used to detect the presence of SARS-CoV antibodies in a sample. Briefly, latex beads, red blood cells or other agglutinable particles are coated with a SARS-CoV polypeptide of this disclosure and mixed with a sample, such that antibodies in the sample that are specifically reactive with the antigen crosslink with the antigen, causing agglutination. The agglutinated polypeptide-antibody complexes form a precipitate, visible with the naked eye or measurable by spectrophotometer. In a modification of the above test, SARS-CoV-specific antibodies of this disclosure can be bound to the agglutinable particles and SARS-CoV antigen in the sample thereby detected.

VII. Pharmaceutical and Immune Stimulatory Compositions and Uses Thereof

Pharmaceutical compositions including SARS-CoV nucleic acid sequences, SARS-CoV polypeptides, or antibodies that bind these polypeptides, are also encompassed by the present disclosure. These pharmaceutical compositions include a therapeutically effective amount of one or more SARS-CoV polypeptides, one or more nucleic acid molecules encoding a SARS-CoV polypeptide, or an antibody that binds a SARS-CoV polypeptide, in conjunction with a pharmaceutically acceptable carrier.

Disclosed herein are substances suitable for use as immune stimulatory compositions for the inhibition or treatment of SARS. Particular immune stimulatory compositions are directed against SARS-CoV, and include antigens obtained from SARS-CoV. In one embodiment, an immune stimulatory composition contains attenuated SARS-CoV. Methods of viral attenuation are well known in the art, and include, but are not limited to, high serial passage (for example, in susceptible host cells under specific environmental conditions to select for attenuated virions), exposure to a mutagenic agent (for example, a chemical mutagen or radiation), genetic engineering using recombinant DNA technology (for example, using gene replacement or gene knockout to disable one or more viral genes), or some combination thereof.

In another embodiment, the immune stimulatory composition contains inactivated SARS-CoV. Methods of viral inactivation are well known in the art, and include, but are not limited to, heat and chemicals (for example, formalin, β -propiolactone, and ethylenimines).

In yet another embodiment, the immune stimulatory composition contains a nucleic acid vector that includes SARS-CoV nucleic acid molecules described herein, or that includes a nucleic acid sequence encoding an immunogenic polypeptide or polypeptide fragment of SARS-CoV or derived from SARS-CoV, such as a polypeptide that encodes a surface protein of SARS-CoV.

In a further embodiment, the immune stimulatory composition contains a SARS-CoV subunit, such as glycoprotein, major capsid protein, or other gene products found to elicit humoral and/or cell mediated immune responses.

The provided immune stimulatory SARS-CoV polypeptides, constructs or vectors encoding such polypeptides, are combined with a pharmaceutically acceptable carrier or

vehicle for administration as an immune stimulatory composition to human or animal subjects. In some embodiments, more than one immune stimulatory SARS-CoV polypeptide may be combined to form a single preparation.

The immunogenic formulations may be conveniently presented in unit dosage form and prepared using conventional pharmaceutical techniques. Such techniques include the step of bringing into association the active ingredient and the pharmaceutical carrier(s) or excipient(s). In general, the formulations are prepared by uniformly and intimately bringing into association the active ingredient with liquid carriers. Formulations suitable for parenteral administration include aqueous and non-aqueous sterile injection solutions which may contain anti-oxidants, buffers, bacteriostats and solutes which render the formulation isotonic with the blood of the intended recipient; and aqueous and non-aqueous sterile suspensions which may include suspending agents and thickening agents. The formulations may be presented in unit-dose or multi-dose containers, for example, sealed ampules and vials, and may be stored in a freeze-dried (lyophilized) condition requiring only the addition of a sterile liquid carrier, for example, water for injections, immediately prior to use. Extemporaneous injection solutions and suspensions may be prepared from sterile powders, granules and tablets commonly used by one of ordinary skill in the art.

In certain embodiments, unit dosage formulations are those containing a dose or unit, or an appropriate fraction thereof, of the administered ingredient. It should be understood that in addition to the ingredients particularly mentioned above, formulations encompassed herein may include other agents commonly used by one of ordinary skill in the art.

The compositions provided herein, including those for use as immune stimulatory compositions, may be administered through different routes, such as oral, including buccal and sublingual, rectal, parenteral, aerosol, nasal, intramuscular, subcutaneous, intradermal, and topical. They may be administered in different forms, including but not limited to solutions, emulsions and suspensions, microspheres, particles, microparticles, nanoparticles, and liposomes.

The volume of administration will vary depending on the route of administration. By way of example, intramuscular injections may range from about 0.1 ml to about 1.0 ml. Those of ordinary skill in the art will know appropriate volumes for different routes of administration.

A relatively recent development in the field of immune stimulatory compounds (for example, vaccines) is the direct injection of nucleic acid molecules encoding peptide antigens (broadly described in Janeway & Travers, *Immunobiology: The Immune System In Health and Disease*, page 13.25, Garland Publishing, Inc., New York, 1997; and McDonnell & Askari, *N. Engl. J. Med.* 334:42-45, 1996). Vectors that include nucleic acid molecules described herein, or that include a nucleic acid sequence encoding an immunogenic SARS-CoV polypeptide may be utilized in such DNA vaccination methods.

Thus, the term "immune stimulatory composition" as used herein also includes nucleic acid vaccines in which a nucleic acid molecule encoding a SARS-CoV polypeptide is administered to a subject in a pharmaceutical composition. For genetic immunization, suitable delivery methods known to those skilled in the art include direct injection of plasmid DNA into muscles (Wolff et al., *Hum. Mol. Genet.* 1:363, 1992), delivery of DNA complexed with specific protein carriers (Wu et al., *J. Biol. Chem.* 264:16985, 1989), coprecipitation of DNA with calcium phosphate (Benvenisty and Reshef, *Proc. Natl. Acad. Sci.* 83:9551, 1986), encapsulation of DNA in liposomes (Kaneda et al., *Science* 243:375, 1989), particle bombardment (Tang et al., *Nature*

356:152, 1992; Eisenbraun et al., *DNA Cell Biol.* 12:791, 1993), and in vivo infection using cloned retroviral vectors (Seeger et al., *Proc. Natl. Acad. Sci.* 81:5849, 1984). Similarly, nucleic acid vaccine preparations can be administered via viral carrier.

The amount of immunostimulatory compound in each dose of an immune stimulatory composition is selected as an amount that induces an immunostimulatory or immunoprotective response without significant, adverse side effects. Such amount will vary depending upon which specific immunogen is employed and how it is presented. Initial injections may range from about 1 µg to about 1 mg, with some embodiments having a range of about 10 µg to about 800 µg, and still other embodiments a range of from about 25 µg to about 500 µg. Following an initial administration of the immune stimulatory composition, subjects may receive one or several booster administrations, adequately spaced. Booster administrations may range from about 1 µg to about 1 mg, with other embodiments having a range of about 10 µg to about 750 µg, and still others a range of about 50 µg to about 500 µg. Periodic boosters at intervals of 1-5 years, for instance three years, may be desirable to maintain the desired levels of protective immunity.

It is also contemplated that the provided immunostimulatory molecules and compositions can be administered to a subject indirectly, by first stimulating a cell in vitro, which stimulated cell is thereafter administered to the subject to elicit an immune response. Additionally, the pharmaceutical or immune stimulatory compositions or methods of treatment may be administered in combination with other therapeutic treatments.

VIII. Kits

Also provided herein are kits useful in the detection and/or diagnosis of SARS-CoV. This includes kits for use with nucleic acid and protein detection methods, such as those disclosed herein.

The SARS-CoV-specific oligonucleotide primers and probes described herein can be supplied in the form of a kit for use in detection of SARS-CoV. In such a kit, an appropriate amount of one or more of the oligonucleotides is provided in one or more containers, or held on a substrate. An oligonucleotide primer or probe can be provided in an aqueous solution or as a freeze-dried or lyophilized powder, for instance. The container(s) in which the oligonucleotide(s) are supplied can be any conventional container that is capable of holding the supplied form, for instance, microfuge tubes, ampoules, or bottles. In some applications, pairs of primers are provided in pre-measured single use amounts in individual (typically disposable) tubes or equivalent containers. With such an arrangement, the sample to be tested for the presence of a SARS-CoV nucleic acid can be added to the individual tubes and amplification carried out directly.

The amount of each oligonucleotide supplied in the kit can be any appropriate amount, and can depend on the market to which the product is directed. For instance, if the kit is adapted for research or clinical use, the amount of each oligonucleotide primer provided would likely be an amount sufficient to prime several PCR amplification reactions. General guidelines for determining appropriate amounts can be found, for example, in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 2001; Ausubel et al. (eds.), *Short Protocols in Molecular Biology*, John Wiley and Sons, New York, N.Y., 1999; and Innis et al., *PCR Applications, Protocols for Functional Genomics*, Academic Press, Inc., San Diego, Calif., 1999. A kit can include more than two primers, in order to facilitate the amplification of a larger number of SARS-CoV nucleotide sequences.

In some embodiments, kits also include one or more reagents necessary to carry out in vitro amplification reactions, including DNA sample preparation reagents, appropriate buffers (for example, polymerase buffer), salts (for example, magnesium chloride), and deoxyribonucleotides (dNTPs).

Kits can include either labeled or unlabeled oligonucleotide primers and/or probes for use in detection of SARS-CoV nucleotide sequences. The appropriate sequences for such a probe will be any sequence that falls between the annealing sites of the two provided oligonucleotide primers, such that the sequence that the probe is complementary to is amplified during the amplification reaction.

One or more control sequences for use in the amplification reactions also can be supplied in the kit. In other particular embodiments, the kit includes equipment, reagents, and instructions for extracting and/or purifying nucleotides from a sample.

Kits for the detection of SARS-CoV antigen include for instance at least one SARS-CoV antigen-specific binding agent (for example, a polyclonal or monoclonal antibody or antibody fragment). The kits may also include means for detecting antigen:specific binding agent complexes, for instance the specific binding agent may be detectably labeled. If the specific binding agent is not labeled, it may be detected by second antibodies or protein A, for example, which may also be provided in some kits in one or more separate containers. Such techniques are well known.

Another example of an assay kit provided herein is a recombinant SARS-CoV-specific polypeptide (or fragment thereof) as an antigen and an enzyme-conjugated anti-human antibody as a second antibody. Examples of such kits also can include one or more enzymatic substrates. Such kits can be used to test if a sample from a subject contains antibodies against a SARS-CoV-specific protein.

The subject matter of the present disclosure is further illustrated by the following non-limiting Examples.

Example 1

Isolation and Characterization of SARS-CoV

Virus Isolation and Ultrastructural Characterization

This example describes the original isolation and characterization of a new human coronavirus from patients with SARS.

A variety of clinical specimens (blood, serum, material from oropharyngeal swabs or washings, material from nasopharyngeal swabs, and tissues of major organs collected at autopsy) from patients meeting the case definition of SARS were sent to the Centers for Disease Control and Prevention (CDC) as part of the etiologic investigation of SARS. These samples were inoculated onto a number of continuous cell lines, including Vero E6, NCI-H292, MDCK, LLC-MK2, and B95-8 cells, and into suckling ICR mice by the intracranial and intraperitoneal routes. All cultures were observed daily for CPE. Maintenance medium was replenished at day seven, and cultures were terminated fourteen days after inoculation. Any cultures exhibiting identifiable CPE were subjected to several procedures to identify the cause of the effect. Suckling mice were observed daily for fourteen days, and any sick or dead mice were further tested by preparing a brain suspension that was filtered and subcultured. Mice that remained well after fourteen days were killed, and their test results were recorded as negative.

Two cell lines, Vero E6 cells and NCI-H292 cells, inoculated with oropharyngeal specimens from Patient 16 (a 46 year old male physician with an epidemiologic link to a hospital with multiple SARS patients) initially showed CPE (Table 1)

TABLE 1

Specimens from patients with SARS that were positive for SARS-CoV by one or more methods*.								
Patient No.	Exposure and Setting	Age/Sex	Findings on Chest Radiograph	Hospitalization	Serologic Results	Specimen	Isolation	RT-PCR
1	Singapore, hospital	53 yr/F	Pneumonia	Yes	+	Nasal, oropharyngeal swabs	-	Not done
2†	Hong Kong, hotel	36 yr/F	Pneumonia	Yes	+	Nasal, swab	-	Not done
3	Hong Kong, hotel	22 yr/M	Pneumonia	Yes	+	Swab	-	-
4†	Hong Kong, hotel	39 yr/M	Pneumonia	Yes	+	Nasal, pharyngeal swab	-	-
5	Hong Kong, hotel	49 Yr/M	Pneumonia	Yes	Not done	Sputum	+	+
6‡	Hong Kong, hotel	46 yr/M	Pneumonia	Yes	+	Kidney, lung, bronchoalveolar lavage	+§	+
7	Vietnam, hospital	Adult/unknown	Pneumonia	Yes	-	Oropharyngeal wash	+	+
8	Vietnam, hospital	Adult/unknown	Pneumonia	Yes	-	Oropharyngeal wash	-	+
9	Vietnam, hospital	Adult/unknown	Pneumonia	Yes	-	Oropharyngeal wash	-	+
10	Vietnam, hospital	Adult/unknown	Pneumonia	Yes	-	Oropharyngeal wash	-	+
11	Vietnam, hospital	Adult/unknown	Pneumonia	Yes	-	Oropharyngeal wash	-	+

TABLE 1-continued

Specimens from patients with SARS that were positive for SARS-CoV by one or more methods*.								
Patient No.	Exposure and Setting	Age/Sex	Findings on Chest Radiograph	Hospitalization	Serologic Results	Specimen	Isolation	RT-PCR
12	Vietnam, hospital	Adult/unknown	Pneumonia	Yes	-	Oropharyngeal wash	-	+
13	Vietnam, hospital	Adult/unknown	Pneumonia	Yes	-	Oropharyngeal wash	+	+
14	Vietnam, hospital	Adult/unknown	Pneumonia	Yes	-	Oropharyngeal wash	-	+
15	Vietnam, hospital	Adult/unknown	Pneumonia	Yes	-	Oropharyngeal wash	-	+
16	Vietnam, hospital	46 yr/M	Pneumonia	Yes	+	Nasal, oropharyngeal swabs	+¶	+
17	Canada, family	43 yr/M	Pneumonia	Yes	Not done	Lung, bone marrow	-	
18	Taiwan, family	51 yr/F	Pneumonia	Yes	-	Sputum	-	+
19	Hong Kong, hotel	Adult/F	Pneumonia	Yes	+	Oropharyngeal wash	-	+

*Plus signs denote positive results, and minus signs negative results. The serologic and RT-PCR assays were not necessarily performed on samples obtained at the same time.

†This was a late specimen, antibody positive at first sample.

‡Travel included China, Hong Kong (hotel), and Hanoi (the patient was the index patient in the French Hospital).

§Isolation was from the kidney only.

¶Isolation was from the oropharyngeal only.

The CPE in the Vero E6 cells was first noted on the fifth day post-inoculation; it was focal, with cell rounding and a refractive appearance in the affected cells that was soon followed by cell detachment (FIG. 1A). The CPE spread quickly to involve the entire cell monolayer within 24 to 48 hours. Subculture of material after preparation of a master seed stock (used for subsequent antigen production) resulted in the rapid appearance of CPE, as noted above, and in complete destruction of the monolayer in the inoculated flasks within 48 hours. Similar CPE was also noted in four additional cultures: three cultures of respiratory specimens (two oropharyngeal washes and one sputum specimen) and one culture of a suspension of kidney tissue obtained at autopsy. In these specimens, the initial CPE was observed between day two and day four and, as noted above, the CPE rapidly progressed to involve the entire cell monolayer.

Tissue culture samples showing CPE were prepared for electron-microscopical examination. Negative-stain electron-microscopical specimens were prepared by drying culture supernatant, mixed 1:1 with 2.5% paraformaldehyde, onto Formvarcarbon-coated grids and staining with 2% methylamine tungstate. Thin-section electron-microscopical specimens were prepared by fixing a washed cell pellet with 2.5% glutaraldehyde and embedding the cell pellet in epoxy resin. In addition, a master seed stock was prepared from the remaining culture supernatant and cells by freeze-thawing the culture flask, clarifying the thawed contents by centrifugation at 1000×g, and dispensing the supernatant into aliquots stored in gas phase over liquid nitrogen. The master seed stock was subcultured into 850-cm² roller bottles of Vero E6 cells for the preparation of formalin-fixed positive control cells for immunohistochemical analysis, mixed with normal Vero E6 cells, and gamma-irradiated for preparation of spot slides for IFA tests or extracted with detergent and gamma-irradiated for use as an ELISA antigen for antibody tests.

Examination of CPE-positive Vero E6 cells by thin-section electron microscopy revealed characteristic coronavirus particles within the cisternae of the rough endoplasmic reticulum and in vesicles (FIG. 2A) (Becker et al., *J.*

Virol. 1:1019–27, 1967; Oshiro et al. *J. Gen. Virol.* 12:161–8, 1971). Extracellular particles were found in large clusters and adhering to the surface of the plasma membrane. Negative-stain electron microscopy identified coronavirus particles, 80 to 140 nm in diameter, with 20- to 40-nm complex surface projections surrounding the periphery (FIG. 2B). Hemagglutinin esterase-type glycoprotein projections were not seen.

The isolation and growth of a human-derived coronavirus in Vero E6 cells were unexpected. The previously known human coronaviruses are notably fastidious, preferring select cell lines, organ culture, or suckling mice for propagation. The only human or animal coronavirus which has been shown to grow in Vero E6 cells is PEDV, and it requires the addition of trypsin to culture medium for growth in the cells. Moreover, PEDV adapted to growth in Vero E6 cells results in a strikingly different CPE, with cytoplasmic vacuoles and the formation of large syncytia. Syncytial cells were only observed occasionally in monolayers of Vero E6 cells infected with the SARS-CoV; they clearly do not represent the dominant CPE.

Reverse Transcription-Polymerase Chain Reaction and Sequencing

For RT-PCR assays, cell-culture supernatants were placed in lysis buffer. RNA extracts were prepared from 100 µl of each specimen (or culture supernatant) with the automated NucliSens extraction system (bioMérieux, Durham, N.C.). Initially, degenerate, inosine-containing primers IN-2 (+) 5'GGGTTGGGACTA TCCTAAGTGTGA3' (SEQ ID NO: 34) and IN-4 (-) 5'TAACACACAACICCATCA TCA3' (SEQ ID NO: 35) were designed to anneal to sites encoding conserved amino acid motifs that were identified on the basis of alignments of available coronavirus ORF1a, ORF1b, S, HE, M, and N gene sequences. Additional, SARS-specific, primers Cor-p-F2 (+) 5'CTAACATGCT-TAGGATAATGG3' (SEQ ID NO: 13), Cor-p-F3 (+) 5'GCCTCTCTTGTCTTGCTCGC3' (SEQ ID NO: 14), and Cor-p-R1 (-) 5'CAGGTAAGCGTAAACTCATC3 (SEQ ID NO: 15) were designed as sequences were gener-

ated from RT-PCR products amplified with the degenerate primers. These SARS-specific primers were used to test patient specimens for SARS (see below). Primers used for specific amplification of human metapneumovirus have been described by Falsey et al. (*J. Infect. Dis.* 87:785–90, 2003).

For RT-PCR products of less than 3 kb, cDNA was synthesized in a 20 μ l reaction mixture containing 500 ng of RNA, 200 U of Superscript™ II reverse transcriptase (Invitrogen Life Technologies, Carlsbad, Calif.), 40 U of RNasin (Promega Corp., Madison, Wis.), 100 mM each dNTP (Roche Molecular Biochemicals, Indianapolis, Ind.), 4 μ l of 5 \times reaction buffer (Invitrogen Life Technologies, Carlsbad, Calif.), and 200 pmol of the reverse primer. The reaction mixture, except for the reverse transcriptase, was heated to 70° C. for 2 minutes, cooled to 4° C. for 5 minutes and then heated to 42° C. in a thermocycler. The mixture was held at 42° C. for 4 minutes, and then the reverse transcriptase was added, and the reactions were incubated at 42° C. for 45 minutes. Two microliters of the cDNA reaction was used in a 50 μ l PCR reaction containing 67 mM Tris-HCl (pH 8.8), 1 mM each primer, 17 mM ammonium sulfate, 6 mM EDTA, 2 mM MgCl₂, 200 mM each dNTP, and 2.5 U of Taq DNA polymerase (Roche Molecular Biochemicals, Indianapolis, Ind.). The thermocycler program for the PCR consisted of 40 cycles of denaturation at 95° C. for 30 seconds, annealing at 42° C. for 30 seconds, and extension at 65° C. for 30 seconds. For SARS-CoV-specific primers, the annealing temperature was increased to 55° C.

For amplification of fragments longer than 3 kb, regions of the genome between sections of known sequence were amplified by means of a long RT-PCR protocol and SARS-CoV-specific primers. First-strand cDNA synthesis was performed at 42° C. or 50° C. using Superscript™ II RNase H reverse transcriptase (Invitrogen Life Technologies, Carlsbad, Calif.) according to the manufacturer's instructions with minor modifications. Coronavirus-specific primers (500 ng) and SARS-CoV RNA (350 ng) were combined with the PCR Nucleotide Mix (Roche Molecular Biochemicals, Indianapolis, Ind.), heated for 1 minute at 94° C., and cooled to 4° C. in a thermocycler. The 5 \times first-strand buffer, dithiothreitol (Invitrogen Life Technologies, Carlsbad, Calif.), and Protector RNase Inhibitor (Roche Molecular Biochemicals, Indianapolis, Ind.) were added, and the samples were incubated at 42° C. or 50° C. for 2 minutes. After reverse transcriptase (200 U) was added, the samples were incubated at 42° C. or 50° C. for 1.5 to 2 hours. Samples were inactivated at 70° C. for 15 minutes and subsequently treated with 2 U of RNase H (Roche Molecular Biochemicals, Indianapolis, Ind.) at 37° C. for 30 minutes. Long RT-PCR amplification of 5- to 8-kb fragments was performed using Taq Plus Precision (Stratagene, La Jolla, Calif.) and AmpliWax PCR Gem 100 beads (Applied Biosystems; Foster City, Calif.) for "hot start" PCR with the following thermocycling parameters: denaturation at 94° C. for 1 minute followed by 35 cycles of 94° C. for 30 seconds, 55° C. for 30 seconds, an increase of 0.4 degrees per second up to 72° C., and 72° C. for 7 to 10 minutes, with a final extension at 72° C. for 10 minutes. RT-PCR products were separated by electrophoresis on 0.9% agarose TAE gels and purified by use of a QIAquick Gel Extraction Kit (Qiagen, Inc., Santa Clarita, Calif.).

In all cases, the RT-PCR products were gel-isolated and purified for sequencing by means of a QIAquick Gel Extraction kit (Qiagen, Inc., Santa Clarita, Calif.). Both strands were sequenced by automated methods, using fluorescent dideoxy-chain terminators (Applied Biosystems; Foster City, Calif.).

The sequence of the leader was obtained from the sub-genomic mRNA coding for the N gene and from the 5'

terminus of genomic RNA. The 5' rapid amplification of cDNA ends (RACE) technique (Harcourt et al., *Virology* 271:334–49, 2000) was used with reverse primers specific for the N gene or for the 5' untranslated region. RACE products were either sequenced directly or were cloned into a plasmid vector before sequencing. A primer that was specific for the leader of SARS-CoV was used to amplify the region between the 5'-terminus of the genome and known sequences in the rep gene. The 3'-terminus of the genome was amplified for sequencing by use of an oligo-(dT) primer and primers specific for the N gene.

Once the complete SARS-CoV genomic sequence had been determined, it was confirmed by sequencing a series of independently amplified RT-PCR products spanning the entire genome. Positive- and negative-sense sequencing primers, at intervals of approximately 300 nt, were used to generate a confirmatory sequence with an average redundancy of 9.1. The confirmatory sequence was identical to the original sequence. The genomic sequence (SEQ ID NO: 1) was published in the GenBank sequence database (Accession No. AY278741) on Apr. 21, 2003.

Sequence Analysis

Predicted amino acid sequences were compared with those from reference viruses representing each species for which complete genomic sequence information was available: group 1 representatives included human coronavirus 229E (GenBank Accession No. AF304460), porcine epidemic diarrhea virus (GenBank Accession No. AF353511), and transmissible gastroenteritis virus (GenBank Accession No. AF271965); group 2 representatives included bovine coronavirus (GenBank Accession No. AF220295) and mouse hepatitis virus (GenBank Accession No. AF201929); group 3 was represented by infectious bronchitis virus (GenBank Accession No. M95169). Sequences for representative strains of other coronavirus species for which partial sequence information was available were included for some of the structural protein comparisons: group 1 representative strains included canine coronavirus (GenBank Accession No. D13096), feline coronavirus (GenBank Accession No. AY204704), and porcine respiratory coronavirus (GenBank Accession No. Z24675); and group 2 representatives included three strains of human coronavirus OC43 (GenBank Accession Nos. M76373, L14643 and M93390), porcine hemagglutinating encephalomyelitis virus (GenBank Accession No. AY078417), and rat coronavirus (GenBank Accession No. AF207551).

Partial nucleotide sequences of the polymerase gene were aligned with published coronavirus sequences, using CLUSTAL W for Unix (version 1.7; Thompson et al., *Nucleic Acids Res.* 22:4673–80, 1994). Phylogenetic trees were computed by maximum parsimony, distance, and maximum likelihood-based criteria analysis with PAUP (version 4.0.d10; Swofford ed., *Phylogenetic Analysis using Parsimony and other Methods*, Sinauer Associates, Sunderland, Mass.). When compared with other human and animal coronaviruses, the nucleotide and deduced amino acid sequence from this region had similarity scores ranging from 0.56 to 0.63 and from 0.57 to 0.74, respectively. The highest sequence similarity was obtained with group II coronaviruses. The maximum-parsimony tree obtained from the nucleotide-sequence alignment is shown in FIG. 3. Bootstrap analyses of the internal nodes at the internal branches of the tree provided strong evidence that the SARS-CoV is genetically distinct from other known coronaviruses.

Microarray analyses (using a long oligonucleotide DNA microarray with array elements derived from highly conserved regions within viral families) of samples from infected and uninfected cell cultures gave a positive signal for a group of eight oligonucleotides derived from two virus

families: Coronaviridae and Astroviridae (Wang et al., *PNAS* 99:15687–92, 2002). All of the astroviruses and two of the coronavirus oligonucleotides share a consensus sequence motif that maps to the extreme 3'-end of astroviruses and two members of the coronavirus family: avian infectious bron-

chitis and turkey coronavirus (Jonassen et al., *J. Gen. Virol.* 79:715–8, 1998). Results were consistent with the identity of the isolate as a coronavirus.

Additional sequence alignments and neighbor-joining trees were generated by using ClustalX (Thompson et al., *Nucleic Acids Res.* 25:4876–82, 1997), version 1.83, with the Gonnet protein comparison matrix. The resulting trees were adjusted for final output by using treeool version 2.0.1. Uncorrected pairwise distances were calculated from the aligned sequences by using the Distances program from the Wisconsin Sequence Analysis Package, version 10.2 (Accelrys, Burlington, Mass.). Distances were converted to percent identity by subtracting from 100. The amino acid sequences for three well-defined enzymatic proteins encoded by the rep gene and the four major structural proteins of SARS-CoV were compared with those from representative viruses for each of the species of coronavirus for which complete genomic sequence information was available (FIG. 4, Table 2). The topologies of the resulting phylograms are remarkably similar (FIG. 4). For each protein analyzed, the species formed monophyletic clusters consistent with the established taxonomic groups. In all cases, SARS-CoV sequences segregated into a fourth, well-resolved branch. These clusters were supported by bootstrap values above 90% (1000 replicates). Consistent with pairwise comparisons between the previously characterized coronavirus species (Table 2), there was greater sequence conservation in the enzymatic proteins (3CL^{pro}, polymerase (POL), and helicase (HEL)) than among the structural proteins (S, E, M, and N). These results indicate that SARS-CoV is not closely related to any of the previously characterized coronaviruses and forms a distinct group within the genus Coronavirus.

TABLE 2

Pairwise amino acid identities of coronavirus proteins.								
Group	Virus	3CLPRO	POL	HEL	S	E	M	N
Pairwise Amino Acid Identity (Percent)								
G1	HCoV-229E	40.1	58.8	59.7	23.9	22.7	28.8	23.0
	PEDV	44.4	59.5	61.7	21.7	17.6	31.8	22.6
	TGEV	44.0	59.4	61.2	20.6	22.4	30.0	25.6
G2	BCoV	48.8	66.3	68.3	27.1	20.0	39.7	31.9
	MHV	49.2	66.5	67.3	26.5	21.1	39.0	33.0
G3	IBV	41.3	62.5	58.6	21.8	18.4	27.2	24.0
Predicted Protein Length (aa)								
	SARS-CoV	306	932	601	1255	76	221	422
	CoV Range	302–307	923–940	506–600	1173–1452	76–108	225–262	377–454

Example 2

Detection of SARS-CoV in a Subject

This example demonstrates the detection of SARS-CoV in patient specimens using SARS-CoV-specific primers.

The SARS-specific primers Cor-p-F2 (SEQ ID NO: 13), Cor-p-F3 (SEQ ID NO: 14) and Cor-p-R1 (SEQ ID NO: 15) were used to test patient specimens for SARS. One primer for each set was 5'-end-labeled with 6-FAM to facilitate GeneScan analysis. One-step amplification reactions were performed with the Access RT-PCR System (Promega, Madison, Wis.) as described by Falsey et al., *J. Infect. Dis.*

87:785–90, 2003. Positive and negative RT-PCR controls, containing standardized viral RNA extracts, and nuclease-free water were included in each run. Amplified 6-FAM-labeled products were analyzed by capillary electrophoresis on an ABI 3100 Prism Genetic Analyzer with GeneScan software (version 3.1.2; Applied Biosystems; Foster City, Calif.). Specimens were considered positive for SARS-CoV if the amplification products were within one nucleotide of the expected product size (368 nucleotides for Cor-p-F2 or Cor-p-R1 and 348 nucleotides for Cor-p-F3 or Cor-p-R1) for both specific primer sets, as confirmed by a second PCR reaction from another aliquot of RNA extract in a separate laboratory. Where DNA yield was sufficient, the amplified products were also sequenced. Additionally, as described above, microarray-based detection of SARS-CoV in patient specimens was carried out (Wang et al., *PNAS* 99:15687–92, 2002 and Bohlander et al., *Genomics* 13:1322–24, 1992).

Example 3

Immunohistochemical and Histopathological Analysis, and Electron-Microscopical Analysis of Bronchoalveolar Lavage Fluid

This example illustrates immunohistochemical, histopathological and electron-microscopical analysis of Vero E6 cells infected with the SARS-CoV and tissue samples from SARS patients.

Formalin-fixed, paraffin-embedded Vero E6 cells infected with the SARS-CoV and tissues obtained from patients with SARS were stained with hematoxylin and eosin and various immunohistochemical stains. Immunohistochemical assays were based on a method described previously for hantavirus (Zaki et al., *Amer. J. Pathol.* 146:552–79, 1995). Briefly, 4- μ m sections were deparaffinized, rehydrated, and digested in Proteinase K for 15 minutes. Slides were then incubated for 60 minutes at room temperature with monoclonal anti-

bodies, polyclonal antiserum or ascitic fluids derived from animal species with reactivities to various known coronaviruses, and with a convalescent-phase serum specimen from a patient with SARS.

Optimal dilutions of the primary antibodies were determined by titration experiments with coronavirus-infected cells from patients with SARS and with noninfected cells or, when available, with concentrations recommended by the manufacturers. After sequential application of the appropriate biotinylated link antibody, avidin-alkaline phosphatase complex, and naphthol-fast red substrate, sections were counterstained in Mayer's hematoxylin and mounted with aqueous mounting medium. The following antibody and tissue controls were used: serum specimens from nonin-

ected animals, various coronavirus-infected cell cultures and animal tissues, noninfected cell cultures, and normal human and animal tissues. Tissues from patients were also tested by immunohistochemical assays for various other viral and bacterial pulmonary pathogens. In addition, a BAL specimen was available from one patient for thin-section electron-microscopical evaluation.

Lung tissues were obtained from the autopsy of three patients and by open lung biopsy of one patient, 14–19 days following onset of SARS symptoms. Confirmatory laboratory evidence of infection with coronavirus was available for two patients (patients 6 and 17) and included PCR amplification of coronavirus nucleic acids from tissues, viral isolation from BAL fluid or detection of serum antibodies reactive with coronavirus (Table 1). For two patients, no samples were available for molecular, cell culture, or serological analysis; however, both patients met the CDC definition for probable SARS cases and had strong epidemiologic links with laboratory-confirmed SARS cases. Histopathologic evaluation of lung tissues of the four patients showed diffuse alveolar damage at various levels of progression and severity. Changes included hyaline membrane formation, interstitial mononuclear inflammatory infiltrates, and desquamation of pneumocytes in alveolar spaces (FIG. 5A). Other findings identified in some patients included focal intraalveolar hemorrhage, necrotic inflammatory debris in small airways, and organizing pneumonia. Multinucleated syncytial cells were identified in the intraalveolar spaces of two patients who died 14 and 17 days, respectively, after onset of illness. These cells contained abundant vacuolated cytoplasm with cleaved and convoluted nuclei. No obvious intranuclear or intracytoplasmic viral inclusions were identified (FIG. 5B), and electron-microscopical examination of a limited number of these syncytial cells revealed no coronavirus particles. No definitive immunostaining was identified in tissues from SARS patients with the use of a battery of immunohistochemical stains reactive with coronaviruses from antigenic groups I, II, and III. In addition, no staining of patient tissues was identified with the use of immunohistochemical stains for influenzaviruses A and B, adenoviruses, Hendra and Nipah viruses, human metapneumovirus, respiratory syncytial virus, measles virus, *Mycoplasma pneumoniae*, and *Chlamydia pneumoniae*.

Evaluation of Vero E6 cells infected with coronavirus isolated from a patient with SARS revealed viral CPE that included occasional multinucleated syncytial cells but no obvious viral inclusions (FIG. 5C). Immunohistochemical assays with various antibodies reactive with coronaviruses from antigenic group I, including HCoV-229E, FIPV and TGEV, and with an immune serum specimen from a patient with SARS, demonstrated strong cytoplasmic and membranous staining of infected cells (FIG. 5C and Table 3); however, cross-reactivity with the same immune human serum sample and FIPV antigen was not observed. No staining was identified with any of several monoclonal or polyclonal antibodies reactive with coronaviruses in antigenic group II (HCoV-OC43, BCoV and MHV) or group III (TCoV and IBV-Avian). Electron microscopical examination of a BAL fluid from one patient revealed many coronavirus-infected cells (FIGS. 6A–B).

TABLE 3

Immunohistochemical reactivities of various polyclonal group I anti-coronavirus reference antiserum samples with a coronavirus isolated from a patient with SARS and with selected antigenic group I coronaviruses.

Antiserum	Immunohistochemical reactivity of antiserum with coronavirus-infected culture cells		
	SARS-CoV (Vero E6)	HCoV-229E (mouse 3T3-hAPN)	FIPV-1 (BHK-fAPN)
Convalescent-phase SARS (patient 3)	+	+	–
Guinea pig anti-HCoV-229E	+	+	–
Rabbit anti-HCoV-229E	+	+	+
Feline anti-FIPV-1	+	+	+
Porcine anti-TGEV	+	–	+

Example 4

SARS-CoV Serologic Analysis

This example illustrates representative methods of performing serological analysis of SARS-CoV.

Spot slides were prepared by applying 15 μ l of the suspension of gamma-irradiated mixed infected and noninfected cells onto 12-well Teflon-coated slides. Slides were allowed to air dry before being fixed in acetone. Slides were then stored at -70° C. until used for IFA tests (Wulff and Lange, *Bull. WHO* 52:429–36, 1975). An ELISA antigen was prepared by detergent extraction and subsequent gamma irradiation of infected Vero E6 cells (Ksiazek et al., *J. Infect. Dis.* 179 (suppl. 1):S191–8, 1999). The optimal dilution (1:1000) for the use of this antigen was determined by checkerboard titration against SARS patient serum from the convalescent phase; a control antigen, similarly prepared from uninfected Vero E6 cells, was used to control for specific reactivity of tested sera. The conjugates used were goat antihuman IgG, IgA, and IgM conjugated to fluorescein isothiocyanate and horseradish peroxidase (Kirkegaard and Perry, Gaithersburg, Md.), for the IFA test and ELISA, respectively. Specificity and cross-reactivity of a variety of serum samples to the newly identified virus were evaluated by using the tests described herein. For this evaluation, serum from SARS patients in Singapore, Bangkok and Hong Kong was used, along with serum from healthy blood donors from the CDC serum bank and from persons infected with known human coronavirus (human coronaviruses OC43 and 229E) (samples provided by E. Walsh and A. Falsey, University of Rochester School of Medicine and Dentistry, Rochester, N.Y.).

Spot slides with infected cells reacted with serum from patients with probable SARS in the convalescent phase (FIG. 1B). Screening of a panel of serum from patients with suspected SARS from Hong Kong, Singapore as well as the United States showed a high level of specific reaction with infected cells, and conversion from negative to positive reactivity or diagnostic rises in the IFA test by a factor of four. Similarly, tests of these same serum samples with the ELISA antigen showed high specific signal in the convalescent-phase samples and conversion from negative to positive antibody reactivity or diagnostic increases in titer (Table 4).

TABLE 4

Results of serological testing with both IFA assay and ELISA in SARS patients tested against the newly isolated human coronavirus.				
Source	Serum No.	Days After Onset	ELISA Titer*	IFA Titer*
Hong Kong	1.1	4	<100	<25
Hong Kong	1.2	13	≧6400	1600
Hong Kong	2.1	11	400	100
Hong Kong	2.2	16	1600	200
Hong Kong	3.1	7	<100	<25
Hong Kong	3.2	17	≧6400	800
Hong Kong	4.1	8	<100	<25
Hong Kong	4.2	13	1600	50
Hong Kong	5.1	10	100	<25
Hong Kong	5.2	17	≧6400	1600
Hong Kong	6.1	12	1600	200
Hong Kong	6.2	20	≧6400	6400
Hong Kong	7.1	17	400	50
Hong Kong	7.2	24	≧6400	3200
Hong Kong	8.1	3	<100	<25
Hong Kong	8.2	15	≧6400	200
Hong Kong	9.1	5	<100	<25
(Hanoi)				
Hong Kong	9.2	11	≧6400	1600
Bangkok	1.1	2	<100	<25
Bangkok	1.2	4	<100	<25
Bangkok	1.3	7	<100	<25
Bangkok	1.4	15	1600	200
United States	1.1	2	<100	<25
United States	1.2	6	400	50
United States	1.3	13	≧6400	800
Singapore	1.1	2	100	<25
Singapore	1.2	11	≧6400	800
Singapore	2.1	6	100	<25
Singapore	2.2	25	≧6400	400
Singapore	3.1	6	100	<25
Singapore	3.2	14	≧6400	400
Singapore	4.1	5	100	<25
Singapore	4.2	16	1600	400

*Reciprocal of dilution

Information from the limited numbers of samples tested suggests that antibody is first detectable by IFA assay and ELISA between one and two weeks after the onset of symptoms in the patient. IFA testing and ELISA of a panel of 384 randomly selected serum samples (from U.S. blood donors) were negative for antibodies to the new coronavirus, with the exception of one specimen that had minimal reactivity on ELISA. A panel of paired human serum samples with diagnostic increases (by a factor of four or more) in antibody (with very high titers to the homologous viral antigen in the convalescent-phase serum) to the two known human coronaviruses, OC43 (13 pairs) and 229E (14 pairs), showed no reactivity in either acute- or convalescent-phase serum with the newly isolated coronavirus by either the IFA test or the ELISA.

Example 5

Poly(A)⁺ RNA Isolation and Northern Hybridization

This example illustrates a representative method of Northern hybridization to detect SARS-CoV messages in Vero E6 cells.

Total RNA from infected or uninfected Vero E6 cells was isolated with Trizol reagent (Invitrogen Life Technologies, Carlsbad, Calif.) used according to the manufacturer's recommendations. Poly(A)⁺ RNA was isolated from total RNA by use of the Oligotex Direct mRNA Kit (Qiagen, Inc., Santa Clarita, Calif.), following the instructions for the batch protocol, followed by ethanol precipitation. RNA isolated from 1 cm² of cells was separated by electrophoresis on a

0.9% agarose gel containing 3.7% formaldehyde, followed by partial alkaline hydrolysis (Ausubel et al. eds. *Current Protocols in Molecular Biology*, vol. 1, John Wiley & Sons, Inc., NY, N.Y., Ch. 4.9, 1996). RNA was transferred to a nylon membrane (Roche Molecular Biochemicals, Indianapolis, Ind.) by vacuum blotting (Bio-Rad, Hercules, Calif.) and fixed by UV cross-linking. The DNA template for probe synthesis was generated by RT-PCR amplification of SARS-CoV nt 29,083 to 29,608 (SEQ ID NO: 1), by using a reverse primer containing a T7 RNA polymerase promoter to facilitate generation of a negative-sense riboprobe. In vitro transcription of the digoxigenin-labeled riboprobe, hybridization, and detection of the bands were carried out with the digoxigenin system by using manufacturer's recommended procedures (Roche Molecular Biochemicals, Indianapolis, Ind.). Signals were visualized by chemiluminescence and detected with x-ray film.

Example 6

SARS-CoV Genome Organization

This example illustrates the genomic organization of the SARS-CoV genome, including the location of SARS-CoV ORFs.

The genome of SARS-CoV is a 29,727-nucleotide, polyadenylated RNA, and 41% of the residues are G or C (range for published coronavirus complete genome sequences, 37% to 42%). The genomic organization is typical of coronaviruses, having the characteristic gene order [5'-replicase (rep), spike (S), envelope (E), membrane (M), nucleocapsid (N)-3'] and short untranslated regions at both termini (FIG. 7A, Table 5). The SARS-CoV rep gene, which comprises approximately two-thirds of the genome, encodes two polyproteins (encoded by ORF1a and ORF1b) that undergo co-translational proteolytic processing. There are four ORFs downstream of rep that encode the structural proteins, S, E, M, and N, which are common to all known coronaviruses. The hemagglutinin-esterase gene, which is present between ORF1b and S in group 2 and some group 3 coronaviruses (Lai and Holmes, in *Fields Virology*, eds. Knipe and Howley, Lippincott Williams and Wilkins, New York, 4th edition, 2001, Ch. 35), was not found in SARS-CoV.

Coronaviruses also encode a number of non-structural proteins that are located between S and E, between M and N, or downstream of N. These non-structural proteins, which vary widely among the different coronavirus species, are of unknown function and are dispensable for virus replication (Lai and Holmes, in *Fields Virology*, eds. Knipe and Howley, Lippincott Williams and Wilkins, New York, 4th edition, 2001, Ch. 35). The genome of SARS-CoV contains ORFs for five non-structural proteins of greater than 50 amino acids (FIG. 7B, Table 5). Two overlapping ORFs encoding proteins of 274 and 154 amino acids (termed X1 (SEQ ID NO: 5) and X2 (SEQ ID NO: 6), respectively) are located between S (SEQ ID NO: 4) and E (SEQ ID NO: 7). Three additional non-structural genes, X3 (SEQ ID NO: 9), X4 (SEQ ID NO: 10), and X5 (SEQ ID NO: 11) (encoding proteins of 63, 122, and 84 amino acids, respectively), are located between M (SEQ ID NO: 8) and N (SEQ ID NO: 12). In addition to the five ORFs encoding the non-structural proteins described above, there are also two smaller ORFs between M and N, encoding proteins of less than 50 amino acids. Searches of the GenBank database (BLAST and FastA) indicated that there is no significant sequence similarity between these non-structural proteins of SARS-CoV and any other proteins.

The coronavirus rep gene products are translated from genomic RNA, but the remaining viral proteins are translated from subgenomic mRNAs that form a 3'-coterminal nested set, each with a 5'-end derived from the genomic 5'-leader sequence. The coronavirus subgenomic mRNAs are synthesized through a discontinuous transcription process, the mechanism of which has not been unequivocally established (Lai and Holmes, in *Fields Virology*, eds. Knipe and Howley, Lippincott Williams and Wilkins, New York, 4th edition, 2001, Ch. 35; Sawicki and Sawicki, *Adv. Exp. Med. Biol.* 440:215–19, 1998). The SARS-CoV leader sequence was mapped by comparing the sequence of 5'-RACE products synthesized from the N gene mRNA with those synthesized from genomic RNA. A sequence, AAAC-GAAC (nucleotides 65–72 of SEQ ID NO: 1), was identified immediately upstream of the site where the N gene mRNA and genomic sequences diverged. This sequence was also present upstream of ORF1a and immediately upstream of five other ORFs (Table 5), suggesting that it functions as the conserved core of the transcriptional regulatory sequence (TRS).

In addition to the site at the 5'-terminus of the genome, the TRS conserved core sequence appears six times in the remainder of the genome. The positions of the TRS in the genome of SARS-CoV predict that subgenomic mRNAs of 8.3, 4.5, 3.4, 2.5, 2.0, and 1.7 kb, not including the poly(A) tail, should be produced (FIGS. 7A–B, Table 5). At least five subgenomic mRNAs were detected by Northern hybridization of RNA from SARS-CoV-infected cells, using a probe derived from the 3'-untranslated region (FIG. 7C). The calculated sizes of the five predominant bands correspond to the sizes of five of the predicted subgenomic mRNAs of SARS-CoV; the possibility that other, low-abundance mRNAs are present cannot be excluded. By analogy with other coronaviruses (Lai and Holmes, in *Fields Virology*, eds. Knipe and Howley, Lippincott Williams and Wilkins, New York, 4th edition, 2001, Ch. 35), the 8.3-kb and 1.7-kb subgenomic mRNAs are monocistronic, directing translation of S and N, respectively, whereas multiple proteins are translated from the 4.5-kb (X1, X2, and E), 3.4-kb (M and X3), and 2.5-kb (X4 and X5) mRNAs. A consensus TRS is not found directly upstream of the ORF encoding the predicted E protein, and a monocistronic mRNA that would be predicted to code for E could not be clearly identified by Northern blot analysis. It is possible that the 3.6-kb band contains more than one mRNA species or that the monocistronic mRNA for E is a low-abundance message.

TABLE 5

ORF	Genome Location			Predicted Size	
	TRS ^a	ORF Start	ORF End	Protein (aa)	mRNA (nt) ^b
1a	72	265	13,398	4,378	29,727
1b		13,398	21,482	2,695	
S	21,491	21,492	25,256	1,255	8,308 ^c
X1	25,265	25,268	26,089	274	4,534 ^c
X2		25,689	26,150	154	
E		26,117	26,344	76	
M	26,353	26,398	27,060	221	3,446 ^c
X3		27,074	27,262	63	
X4	27,272	27,273	27,638	122	2,527 ^c

TABLE 5-continued

ORF	Genome Location			Predicted Size	
	TRS ^a	ORF Start	ORF End	Protein (aa)	mRNA (nt) ^b
X5	27,778	27,864	28,115	84	2,021 ^d
N	28,111	28,120	29,385	422	1,688 ^c

^aThe location is the 3'-most nucleotide in the consensus TRS, AAAC-GAAC.

^bNot including poly(A). Predicted size is based on the position of the conserved TRS.

^cCorresponding mRNA detected by Northern blot analysis (FIG. 7C)

^dNo mRNA corresponding to utilization of this consensus TRS was detected by Northern blot analysis (FIG. 7C)

Example 7

Real-Time RT-PCR Assay for SARS-CoV Detection

This example demonstrates the use of SARS-CoV-specific primers and probes in a real-time RT-PCR assay to detect SARS-CoV in patient specimens.

A variant of the real-time format, based on TaqMan probe hydrolysis technology (Applied Biosystems, Foster City, Calif.), was used to analyze a total of 340 clinical specimens collected from 246 persons with confirmed or suspected SARS-CoV infection. Specimens included oro- and nasopharyngeal swabs (dry and in viral transport media), sputa, nasal aspirates and washes, BAL, and lung tissue specimens collected at autopsy.

Nucleic Acid Extraction

SARS-CoV nucleic acids were recovered from clinical specimens using the automated NucliSens extraction system (bioMérieux, Durham, N.C.). Following manufacturer's instructions, specimens received in NucliSens lysis buffer were incubated at 37° C. for 30 min with intermittent mixing, and 50 µL of silica suspension, provided in the extraction kit, was added and mixed. The contents of the tube were then transferred to a nucleic acid extraction cartridge and processed on an extractor workstation. Approximately 40–50 µL of total nucleic acid eluate was recovered into nuclease-free vials and either tested immediately or stored at –70° C.

Primers and Probes

Multiple primer and probe sets were designed from the SARS-CoV polymerase 1b (nucleic acid 13,398 to 21,482 of SEQ ID NO: 1) and nucleocapsid gene (nucleic acid 28,120 to 29,385 of SEQ ID NO: 1) sequences by using Primer Express software version 1.5 or 2.0.0 (Applied Biosystems, Foster City, Calif.) with the following default settings: primer melting temperature (T_M) set at 60° C.; probe T_M set at 10° C. greater than the primers at approximately 70° C.; and no guanidine residues permitted at the 5' probe termini. All primers and probes were synthesized by standard phosphoramidite chemistry techniques. TaqMan probes were labeled at the 5'-end with the reporter 6-FAM and at the 3'-end with the quencher Blackhole Quencher 1 (Biosearch Technologies, Inc., Novato, Calif.). Optimal primer and probe concentrations were determined by cross-titration of serial twofold dilutions of each primer against a constant amount of purified SARS-CoV RNA. Primer and probe concentrations that gave the highest amplification efficiencies were selected for further study (Table 6).

TABLE 6

Primers and probes used for real-time RT-PCR assays ^a			Genomic Region
Assay ID	Primer/probe	Sequence	
<u>Primary diagnostic assay</u>			
SARS1	F	CATGTTGGCGGCTCACTATAT (SEQ ID NO: 16)	RNA Pol
	R	GACACTATTAGCATAAGCAGTTGTAGCA (SEQ ID NO: 17)	
	P	TTAAACCAGGTGGAACATCATCCGGTG (SEQ ID NO: 18)	
SARS2	F	GGAGCCTTGAATACACCCAAAG (SEQ ID NO: 19)	Nucleocapsid
	R	GCACGGTGGCAGCATTG (SEQ ID NO: 20)	
SARS3	P	CCACATTGGCACCCGCAATCC (SEQ ID NO: 21)	Nucleocapsid
	F	CAAACATTGGCCGCAAATT (SEQ ID NO: 22)	
	R	CAATGCGTGACATTCCAAAGA (SEQ ID NO: 23)	
	P	CACAATTTGCTCCAAGTGCCTCTGCA (SEQ ID NO: 24)	
<u>To confirm positive results</u>			
N3	F	GAAGTACCATCTGGGGCTGAG (SEQ ID NO: 25)	Nucleocapsid
	R	CCGAAGAGCTACCCGACG (SEQ ID NO: 26)	
	P	CTCTTTCATTTTGCCGTCACCACCAC (SEQ ID NO: 27)	
3'-NTR	F	AGCTCTCCCTAGCATTATTCAGT (SEQ ID NO: 28)	3'-NTR
	R	CACCACATTTTCATCGAGGC (SEQ ID NO: 29)	
M	P	TACCTCGATCGTACTCCGCGT (SEQ ID NO: 30)	M protein
	F	TGTAGGCACTGATTCAGGTTTTG (SEQ ID NO: 31)	
	R	CGGCGTGGTCTGTATTTAATTTA (SEQ ID NO: 32)	
	P	CTGCATACAACCGCTACCGTATTGAA (SEQ ID NO: 33)	

^aRT-PCR, reverse transcription-polymerase chain reaction; F, forward primer; R, reverse primer; P, probe; NTR, nontranslated region.

Real-Time RT-PCR Assay

The real-time RT-PCR assay was performed by using the Real-Time One-Step RT-PCR Master Mix (Applied Biosystems, Foster City, Calif.). Each 25- μ L reaction mixture contained 12.5 μ L of 2 \times Master Mix, 0.625 μ L of the 40 \times MultiScribe and RNase Inhibitor mix, 0.25 μ L of 10 μ M probe, 0.25 μ L each of 50 μ M forward and reverse primers, 6.125 μ L of nuclease-free water, and 5 μ L of nucleic acid extract. Amplification was carried out in 96-well plates on an iCycler iQ Real-Time Detection System (Bio-Rad, Hercules, Calif.). Thermocycling conditions consisted of 30 minutes at 48 $^{\circ}$ C. for reverse transcription, 10 minutes at 95 $^{\circ}$ C. for activation of the AmpliTaq Gold DNA polymerase, and 45 cycles of 15 seconds at 95 $^{\circ}$ C. and 1 minute at 60 $^{\circ}$ C. Each run included one SARS-CoV genomic template control and at least two no-template controls for the extraction (to check for contamination during sample processing) and one no-template control for the PCR-amplification step. As a control for PCR inhibitors, and to monitor nucleic acid extraction efficiency, each sample was tested by real-time RT-PCR for the presence of the human ribonuclease (RNase) P gene (GenBank Accession No. NM_006413) by using the fol-

lowing primers and probe: forward primer 5'-AGATTTG-GACCTGCGAGCG-3' (SEQ ID NO: 36); reverse primer 5'-GAGCGGCTGTCTCCACAAGT-3' (SEQ ID NO: 37); probe 5'-TTCTGACC TGAAGGCTCTGCGCG-3' (SEQ ID NO: 38). The assay reaction was performed identically to that described above except that primer concentrations used were 30 μ M each. Fluorescence measurements were taken and the threshold cycle (C_T) value for each sample was calculated by determining the point at which fluorescence exceeded a threshold limit set at the mean plus 10 standard deviations above the baseline. A test result was considered positive if two or more of the SARS genomic targets showed positive results ($C_T \leq 45$ cycles) and all positive and negative control reactions gave expected values.

While this disclosure has been described with an emphasis upon preferred embodiments, it will be obvious to those of ordinary skill in the art that variations and equivalents of the preferred embodiments may be used and it is intended that the disclosure may be practiced otherwise than as specifically described herein. Accordingly, this disclosure includes all modifications encompassed within the spirit and scope of the disclosure as defined by the claims below.

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 Ser Leu Pro Val Leu Gln Val Arg Asp Val Leu Val Arg Gly Phe Gly
 20 25 30
 Asp Ser Val Glu Glu Ala Leu Ser Glu Ala Arg Glu His Leu Lys Asn
 35 40 45
 Gly Thr Cys Gly Leu Val Glu Leu Glu Lys Gly Val Leu Pro Gln Leu
 50 55 60
 Glu Gln Pro Tyr Val Phe Ile Lys Arg Ser Asp Ala Leu Ser Thr Asn
 65 70 75 80
 His Gly His Lys Val Val Glu Leu Val Ala Glu Met Asp Gly Ile Gln
 85 90 95
 Tyr Gly Arg Ser Gly Ile Thr Leu Gly Val Leu Val Pro His Val Gly
 100 105 110
 Glu Thr Pro Ile Ala Tyr Arg Asn Val Leu Leu Arg Lys Asn Gly Asn
 115 120 125
 Lys Gly Ala Gly Gly His Ser Tyr Gly Ile Asp Leu Lys Ser Tyr Asp
 130 135 140
 Leu Gly Asp Glu Leu Gly Thr Asp Pro Ile Glu Asp Tyr Glu Gln Asn
 145 150 155 160
 Trp Asn Thr Lys His Gly Ser Gly Ala Leu Arg Glu Leu Thr Arg Glu
 165 170 175
 Leu Asn Gly Gly Ala Val Thr Arg Tyr Val Asp Asn Asn Phe Cys Gly
 180 185 190
 Pro Asp Gly Tyr Pro Leu Asp Cys Ile Lys Asp Phe Leu Ala Arg Ala
 195 200 205
 Gly Lys Ser Met Cys Thr Leu Ser Glu Gln Leu Asp Tyr Ile Glu Ser
 210 215 220
 Lys Arg Gly Val Tyr Cys Cys Arg Asp His Glu His Glu Ile Ala Trp
 225 230 235 240
 Phe Thr Glu Arg Ser Asp Lys Ser Tyr Glu His Gln Thr Pro Phe Glu
 245 250 255
 Ile Lys Ser Ala Lys Lys Phe Asp Thr Phe Lys Gly Glu Cys Pro Lys
 260 265 270
 Phe Val Phe Pro Leu Asn Ser Lys Val Lys Val Ile Gln Pro Arg Val
 275 280 285
 Glu Lys Lys Lys Thr Glu Gly Phe Met Gly Arg Ile Arg Ser Val Tyr
 290 295 300
 Pro Val Ala Ser Pro Gln Glu Cys Asn Asn Met His Leu Ser Thr Leu
 305 310 315 320
 Met Lys Cys Asn His Cys Asp Glu Val Ser Trp Gln Thr Cys Asp Phe
 325 330 335
 Leu Lys Ala Thr Cys Glu His Cys Gly Thr Glu Asn Leu Val Ile Glu
 340 345 350

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Gly	Pro	Thr	Thr	Cys	Gly	Tyr	Leu	Pro	Thr	Asn	Ala	Val	Val	Lys	Met
		355					360					365			
Pro	Cys	Pro	Ala	Cys	Gln	Asp	Pro	Glu	Ile	Gly	Pro	Glu	His	Ser	Val
	370					375					380				
Ala	Asp	Tyr	His	Asn	His	Ser	Asn	Ile	Glu	Thr	Arg	Leu	Arg	Lys	Gly
385				390						395					400
Gly	Arg	Thr	Arg	Cys	Phe	Gly	Gly	Cys	Val	Phe	Ala	Tyr	Val	Gly	Cys
				405					410					415	
Tyr	Asn	Lys	Arg	Ala	Tyr	Trp	Val	Pro	Arg	Ala	Ser	Ala	Asp	Ile	Gly
			420					425					430		
Ser	Gly	His	Thr	Gly	Ile	Thr	Gly	Asp	Asn	Val	Glu	Thr	Leu	Asn	Glu
		435					440					445			
Asp	Leu	Leu	Glu	Ile	Leu	Ser	Arg	Glu	Arg	Val	Asn	Ile	Asn	Ile	Val
	450					455					460				
Gly	Asp	Phe	His	Leu	Asn	Glu	Glu	Val	Ala	Ile	Ile	Leu	Ala	Ser	Phe
465					470					475					480
Ser	Ala	Ser	Thr	Ser	Ala	Phe	Ile	Asp	Thr	Ile	Lys	Ser	Leu	Asp	Tyr
				485					490					495	
Lys	Ser	Phe	Lys	Thr	Ile	Val	Glu	Ser	Cys	Gly	Asn	Tyr	Lys	Val	Thr
			500					505					510		
Lys	Gly	Lys	Pro	Val	Lys	Gly	Ala	Trp	Asn	Ile	Gly	Gln	Gln	Arg	Ser
		515					520					525			
Val	Leu	Thr	Pro	Leu	Cys	Gly	Phe	Pro	Ser	Gln	Ala	Ala	Gly	Val	Ile
	530					535					540				
Arg	Ser	Ile	Phe	Ala	Arg	Thr	Leu	Asp	Ala	Ala	Asn	His	Ser	Ile	Pro
545					550					555					560
Asp	Leu	Gln	Arg	Ala	Ala	Val	Thr	Ile	Leu	Asp	Gly	Ile	Ser	Glu	Gln
				565					570					575	
Ser	Leu	Arg	Leu	Val	Asp	Ala	Met	Val	Tyr	Thr	Ser	Asp	Leu	Leu	Thr
		580						585					590		
Asn	Ser	Val	Ile	Ile	Met	Ala	Tyr	Val	Thr	Gly	Gly	Leu	Val	Gln	Gln
		595					600					605			
Thr	Ser	Gln	Trp	Leu	Ser	Asn	Leu	Leu	Gly	Thr	Thr	Val	Glu	Lys	Leu
	610					615					620				
Arg	Pro	Ile	Phe	Glu	Trp	Ile	Glu	Ala	Lys	Leu	Ser	Ala	Gly	Val	Glu
625					630					635					640
Phe	Leu	Lys	Asp	Ala	Trp	Glu	Ile	Leu	Lys	Phe	Leu	Ile	Thr	Gly	Val
				645					650					655	
Phe	Asp	Ile	Val	Lys	Gly	Gln	Ile	Gln	Val	Ala	Ser	Asp	Asn	Ile	Lys
			660					665					670		
Asp	Cys	Val	Lys	Cys	Phe	Ile	Asp	Val	Val	Asn	Lys	Ala	Leu	Glu	Met
		675					680					685			
Cys	Ile	Asp	Gln	Val	Thr	Ile	Ala	Gly	Ala	Lys	Leu	Arg	Ser	Leu	Asn
	690					695					700				
Leu	Gly	Glu	Val	Phe	Ile	Ala	Gln	Ser	Lys	Gly	Leu	Tyr	Arg	Gln	Cys
705					710					715					720
Ile	Arg	Gly	Lys	Glu	Gln	Leu	Gln	Leu	Leu	Met	Pro	Leu	Lys	Ala	Pro
				725					730					735	
Lys	Glu	Val	Thr	Phe	Leu	Glu	Gly	Asp	Ser	His	Asp	Thr	Val	Leu	Thr
			740					745					750		
Ser	Glu	Glu	Val	Val	Leu	Lys	Asn	Gly	Glu	Leu	Glu	Ala	Leu	Glu	Thr
		755					760					765			
Pro	Val	Asp	Ser	Phe	Thr	Asn	Gly	Ala	Ile	Val	Gly	Thr	Pro	Val	Cys

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770		775		780											
Val	Asn	Gly	Leu	Met	Leu	Leu	Glu	Ile	Lys	Asp	Lys	Glu	Gln	Tyr	Cys
785					790					795					800
Ala	Leu	Ser	Pro	Gly	Leu	Leu	Ala	Thr	Asn	Asn	Val	Phe	Arg	Leu	Lys
				805					810						815
Gly	Gly	Ala	Pro	Ile	Lys	Gly	Val	Thr	Phe	Gly	Glu	Asp	Thr	Val	Trp
			820					825						830	
Glu	Val	Gln	Gly	Tyr	Lys	Asn	Val	Arg	Ile	Thr	Phe	Glu	Leu	Asp	Glu
		835					840						845		
Arg	Val	Asp	Lys	Val	Leu	Asn	Glu	Lys	Cys	Ser	Val	Tyr	Thr	Val	Glu
	850					855						860			
Ser	Gly	Thr	Glu	Val	Thr	Glu	Phe	Ala	Cys	Val	Val	Ala	Glu	Ala	Val
865					870					875					880
Val	Lys	Thr	Leu	Gln	Pro	Val	Ser	Asp	Leu	Leu	Thr	Asn	Met	Gly	Ile
				885					890						895
Asp	Leu	Asp	Glu	Trp	Ser	Val	Ala	Thr	Phe	Tyr	Leu	Phe	Asp	Asp	Ala
			900					905						910	
Gly	Glu	Glu	Asn	Phe	Ser	Ser	Arg	Met	Tyr	Cys	Ser	Phe	Tyr	Pro	Pro
			915					920					925		
Asp	Glu	Glu	Glu	Glu	Asp	Asp	Ala	Glu	Cys	Glu	Glu	Glu	Glu	Ile	Asp
	930					935							940		
Glu	Thr	Cys	Glu	His	Glu	Tyr	Gly	Thr	Glu	Asp	Asp	Tyr	Gln	Gly	Leu
945					950					955					960
Pro	Leu	Glu	Phe	Gly	Ala	Ser	Ala	Glu	Thr	Val	Arg	Val	Glu	Glu	Glu
				965					970						975
Glu	Glu	Glu	Asp	Trp	Leu	Asp	Asp	Thr	Thr	Glu	Gln	Ser	Glu	Ile	Glu
			980						985					990	
Pro	Glu	Pro	Glu	Pro	Thr	Pro	Glu	Glu	Pro	Val	Asn	Gln	Phe	Thr	Gly
			995					1000						1005	
Tyr	Leu	Lys	Leu	Thr	Asp	Asn	Val	Ala	Ile	Lys	Cys	Val	Asp	Ile	
	1010					1015						1020			
Val	Lys	Glu	Ala	Gln	Ser	Ala	Asn	Pro	Met	Val	Ile	Val	Asn	Ala	
	1025					1030						1035			
Ala	Asn	Ile	His	Leu	Lys	His	Gly	Gly	Gly	Val	Ala	Gly	Ala	Leu	
	1040					1045						1050			
Asn	Lys	Ala	Thr	Asn	Gly	Ala	Met	Gln	Lys	Glu	Ser	Asp	Asp	Tyr	
	1055					1060						1065			
Ile	Lys	Leu	Asn	Gly	Pro	Leu	Thr	Val	Gly	Gly	Ser	Cys	Leu	Leu	
	1070					1075						1080			
Ser	Gly	His	Asn	Leu	Ala	Lys	Lys	Cys	Leu	His	Val	Val	Gly	Pro	
	1085					1090						1095			
Asn	Leu	Asn	Ala	Gly	Glu	Asp	Ile	Gln	Leu	Leu	Lys	Ala	Ala	Tyr	
	1100					1105						1110			
Glu	Asn	Phe	Asn	Ser	Gln	Asp	Ile	Leu	Leu	Ala	Pro	Leu	Leu	Ser	
	1115					1120						1125			
Ala	Gly	Ile	Phe	Gly	Ala	Lys	Pro	Leu	Gln	Ser	Leu	Gln	Val	Cys	
	1130					1135						1140			
Val	Gln	Thr	Val	Arg	Thr	Gln	Val	Tyr	Ile	Ala	Val	Asn	Asp	Lys	
	1145					1150						1155			
Ala	Leu	Tyr	Glu	Gln	Val	Val	Met	Asp	Tyr	Leu	Asp	Asn	Leu	Lys	
	1160					1165						1170			
Pro	Arg	Val	Glu	Ala	Pro	Lys	Gln	Glu	Glu	Pro	Pro	Asn	Thr	Glu	
	1175					1180						1185			

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Asp	Ser	Lys	Thr	Glu	Glu	Lys	Ser	Val	Val	Gln	Lys	Pro	Val	Asp
1190						1195					1200			
Val	Lys	Pro	Lys	Ile	Lys	Ala	Cys	Ile	Asp	Glu	Val	Thr	Thr	Thr
1205						1210					1215			
Leu	Glu	Glu	Thr	Lys	Phe	Leu	Thr	Asn	Lys	Leu	Leu	Leu	Phe	Ala
1220						1225					1230			
Asp	Ile	Asn	Gly	Lys	Leu	Tyr	His	Asp	Ser	Gln	Asn	Met	Leu	Arg
1235						1240					1245			
Gly	Glu	Asp	Met	Ser	Phe	Leu	Glu	Lys	Asp	Ala	Pro	Tyr	Met	Val
1250						1255					1260			
Gly	Asp	Val	Ile	Thr	Ser	Gly	Asp	Ile	Thr	Cys	Val	Val	Ile	Pro
1265						1270					1275			
Ser	Lys	Lys	Ala	Gly	Gly	Thr	Thr	Glu	Met	Leu	Ser	Arg	Ala	Leu
1280						1285					1290			
Lys	Lys	Val	Pro	Val	Asp	Glu	Tyr	Ile	Thr	Thr	Tyr	Pro	Gly	Gln
1295						1300					1305			
Gly	Cys	Ala	Gly	Tyr	Thr	Leu	Glu	Glu	Ala	Lys	Thr	Ala	Leu	Lys
1310						1315					1320			
Lys	Cys	Lys	Ser	Ala	Phe	Tyr	Val	Leu	Pro	Ser	Glu	Ala	Pro	Asn
1325						1330					1335			
Ala	Lys	Glu	Glu	Ile	Leu	Gly	Thr	Val	Ser	Trp	Asn	Leu	Arg	Glu
1340						1345					1350			
Met	Leu	Ala	His	Ala	Glu	Glu	Thr	Arg	Lys	Leu	Met	Pro	Ile	Cys
1355						1360					1365			
Met	Asp	Val	Arg	Ala	Ile	Met	Ala	Thr	Ile	Gln	Arg	Lys	Tyr	Lys
1370						1375					1380			
Gly	Ile	Lys	Ile	Gln	Glu	Gly	Ile	Val	Asp	Tyr	Gly	Val	Arg	Phe
1385						1390					1395			
Phe	Phe	Tyr	Thr	Ser	Lys	Glu	Pro	Val	Ala	Ser	Ile	Ile	Thr	Lys
1400						1405					1410			
Leu	Asn	Ser	Leu	Asn	Glu	Pro	Leu	Val	Thr	Met	Pro	Ile	Gly	Tyr
1415						1420					1425			
Val	Thr	His	Gly	Phe	Asn	Leu	Glu	Glu	Ala	Ala	Arg	Cys	Met	Arg
1430						1435					1440			
Ser	Leu	Lys	Ala	Pro	Ala	Val	Val	Ser	Val	Ser	Ser	Pro	Asp	Ala
1445						1450					1455			
Val	Thr	Thr	Tyr	Asn	Gly	Tyr	Leu	Thr	Ser	Ser	Ser	Lys	Thr	Ser
1460						1465					1470			
Glu	Glu	His	Phe	Val	Glu	Thr	Val	Ser	Leu	Ala	Gly	Ser	Tyr	Arg
1475						1480					1485			
Asp	Trp	Ser	Tyr	Ser	Gly	Gln	Arg	Thr	Glu	Leu	Gly	Val	Glu	Phe
1490						1495					1500			
Leu	Lys	Arg	Gly	Asp	Lys	Ile	Val	Tyr	His	Thr	Leu	Glu	Ser	Pro
1505						1510					1515			
Val	Glu	Phe	His	Leu	Asp	Gly	Glu	Val	Leu	Ser	Leu	Asp	Lys	Leu
1520						1525					1530			
Lys	Ser	Leu	Leu	Ser	Leu	Arg	Glu	Val	Lys	Thr	Ile	Lys	Val	Phe
1535						1540					1545			
Thr	Thr	Val	Asp	Asn	Thr	Asn	Leu	His	Thr	Gln	Leu	Val	Asp	Met
1550						1555					1560			
Ser	Met	Thr	Tyr	Gly	Gln	Gln	Phe	Gly	Pro	Thr	Tyr	Leu	Asp	Gly
1565						1570					1575			

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Ala	Asp	Val	Thr	Lys	Ile	Lys	Pro	His	Val	Asn	His	Glu	Gly	Lys
1580						1585					1590			
Thr	Phe	Phe	Val	Leu	Pro	Ser	Asp	Asp	Thr	Leu	Arg	Ser	Glu	Ala
1595						1600					1605			
Phe	Glu	Tyr	Tyr	His	Thr	Leu	Asp	Glu	Ser	Phe	Leu	Gly	Arg	Tyr
1610						1615					1620			
Met	Ser	Ala	Leu	Asn	His	Thr	Lys	Lys	Trp	Lys	Phe	Pro	Gln	Val
1625						1630					1635			
Gly	Gly	Leu	Thr	Ser	Ile	Lys	Trp	Ala	Asp	Asn	Asn	Cys	Tyr	Leu
1640						1645					1650			
Ser	Ser	Val	Leu	Leu	Ala	Leu	Gln	Gln	Leu	Glu	Val	Lys	Phe	Asn
1655						1660					1665			
Ala	Pro	Ala	Leu	Gln	Glu	Ala	Tyr	Tyr	Arg	Ala	Arg	Ala	Gly	Asp
1670						1675					1680			
Ala	Ala	Asn	Phe	Cys	Ala	Leu	Ile	Leu	Ala	Tyr	Ser	Asn	Lys	Thr
1685						1690					1695			
Val	Gly	Glu	Leu	Gly	Asp	Val	Arg	Glu	Thr	Met	Thr	His	Leu	Leu
1700						1705					1710			
Gln	His	Ala	Asn	Leu	Glu	Ser	Ala	Lys	Arg	Val	Leu	Asn	Val	Val
1715						1720					1725			
Cys	Lys	His	Cys	Gly	Gln	Lys	Thr	Thr	Thr	Leu	Thr	Gly	Val	Glu
1730						1735					1740			
Ala	Val	Met	Tyr	Met	Gly	Thr	Leu	Ser	Tyr	Asp	Asn	Leu	Lys	Thr
1745						1750					1755			
Gly	Val	Ser	Ile	Pro	Cys	Val	Cys	Gly	Arg	Asp	Ala	Thr	Gln	Tyr
1760						1765					1770			
Leu	Val	Gln	Gln	Glu	Ser	Ser	Phe	Val	Met	Met	Ser	Ala	Pro	Pro
1775						1780					1785			
Ala	Glu	Tyr	Lys	Leu	Gln	Gln	Gly	Thr	Phe	Leu	Cys	Ala	Asn	Glu
1790						1795					1800			
Tyr	Thr	Gly	Asn	Tyr	Gln	Cys	Gly	His	Tyr	Thr	His	Ile	Thr	Ala
1805						1810					1815			
Lys	Glu	Thr	Leu	Tyr	Arg	Ile	Asp	Gly	Ala	His	Leu	Thr	Lys	Met
1820						1825					1830			
Ser	Glu	Tyr	Lys	Gly	Pro	Val	Thr	Asp	Val	Phe	Tyr	Lys	Glu	Thr
1835						1840					1845			
Ser	Tyr	Thr	Thr	Thr	Ile	Lys	Pro	Val	Ser	Tyr	Lys	Leu	Asp	Gly
1850						1855					1860			
Val	Thr	Tyr	Thr	Glu	Ile	Glu	Pro	Lys	Leu	Asp	Gly	Tyr	Tyr	Lys
1865						1870					1875			
Lys	Asp	Asn	Ala	Tyr	Tyr	Thr	Glu	Gln	Pro	Ile	Asp	Leu	Val	Pro
1880						1885					1890			
Thr	Gln	Pro	Leu	Pro	Asn	Ala	Ser	Phe	Asp	Asn	Phe	Lys	Leu	Thr
1895						1900					1905			
Cys	Ser	Asn	Thr	Lys	Phe	Ala	Asp	Asp	Leu	Asn	Gln	Met	Thr	Gly
1910						1915					1920			
Phe	Thr	Lys	Pro	Ala	Ser	Arg	Glu	Leu	Ser	Val	Thr	Phe	Phe	Pro
1925						1930					1935			
Asp	Leu	Asn	Gly	Asp	Val	Val	Ala	Ile	Asp	Tyr	Arg	His	Tyr	Ser
1940						1945					1950			
Ala	Ser	Phe	Lys	Lys	Gly	Ala	Lys	Leu	Leu	His	Lys	Pro	Ile	Val
1955						1960					1965			
Trp	His	Ile	Asn	Gln	Ala	Thr	Thr	Lys	Thr	Thr	Phe	Lys	Pro	Asn

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1970	1975	1980
Thr Trp Cys Leu Arg Cys Leu 1985	Trp Ser Thr Lys 1990	Pro Val Asp Thr 1995
Ser Asn Ser Phe Glu Val Leu 2000	Ala Val Glu Asp 2005	Thr Gln Gly Met 2010
Asp Asn Leu Ala Cys Glu Ser 2015	Gln Gln Pro Thr 2020	Ser Glu Glu Val 2025
Val Glu Asn Pro Thr Ile Gln 2030	Lys Glu Val Ile 2035	Glu Cys Asp Val 2040
Lys Thr Thr Glu Val Val Gly 2045	Asn Val Ile Leu 2050	Lys Pro Ser Asp 2055
Glu Gly Val Lys Val Thr Gln 2060	Glu Leu Gly His 2065	Glu Asp Leu Met 2070
Ala Ala Tyr Val Glu Asn Thr 2075	Ser Ile Thr Ile 2080	Lys Lys Pro Asn 2085
Glu Leu Ser Leu Ala Leu Gly 2090	Leu Lys Thr Ile 2095	Ala Thr His Gly 2100
Ile Ala Ala Ile Asn Ser Val 2105	Pro Trp Ser Lys 2110	Ile Leu Ala Tyr 2115
Val Lys Pro Phe Leu Gly Gln 2120	Ala Ala Ile Thr 2125	Thr Ser Asn Cys 2130
Ala Lys Arg Leu Ala Gln Arg 2135	Val Phe Asn Asn 2140	Tyr Met Pro Tyr 2145
Val Phe Thr Leu Leu Phe Gln 2150	Leu Cys Thr Phe 2155	Thr Lys Ser Thr 2160
Asn Ser Arg Ile Arg Ala Ser 2165	Leu Pro Thr Thr 2170	Ile Ala Lys Asn 2175
Ser Val Lys Ser Val Ala Lys 2180	Leu Cys Leu Asp 2185	Ala Gly Ile Asn 2190
Tyr Val Lys Ser Pro Lys Phe 2195	Ser Lys Leu Phe 2200	Thr Ile Ala Met 2205
Trp Leu Leu Leu Leu Ser Ile 2210	Cys Leu Gly Ser 2215	Leu Ile Cys Val 2220
Thr Ala Ala Phe Gly Val Leu 2225	Leu Ser Asn Phe 2230	Gly Ala Pro Ser 2235
Tyr Cys Asn Gly Val Arg Glu 2240	Leu Tyr Leu Asn 2245	Ser Ser Asn Val 2250
Thr Thr Met Asp Phe Cys Glu 2255	Gly Ser Phe Pro 2260	Cys Ser Ile Cys 2265
Leu Ser Gly Leu Asp Ser Leu 2270	Asp Ser Tyr Pro 2275	Ala Leu Glu Thr 2280
Ile Gln Val Thr Ile Ser Ser 2285	Tyr Lys Leu Asp 2290	Leu Thr Ile Leu 2295
Gly Leu Ala Ala Glu Trp Val 2300	Leu Ala Tyr Met 2305	Leu Phe Thr Lys 2310
Phe Phe Tyr Leu Leu Gly Leu 2315	Ser Ala Ile Met 2320	Gln Val Phe Phe 2325
Gly Tyr Phe Ala Ser His Phe 2330	Ile Ser Asn Ser 2335	Trp Leu Met Trp 2340
Phe Ile Ile Ser Ile Val Gln 2345	Met Ala Pro Val 2350	Ser Ala Met Val 2355
Arg Met Tyr Ile Phe Phe Ala 2360	Ser Phe Tyr Tyr 2365	Ile Trp Lys Ser 2370

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Tyr	Val	His	Ile	Met	Asp	Gly	Cys	Thr	Ser	Ser	Thr	Cys	Met	Met
2375						2380					2385			
Cys	Tyr	Lys	Arg	Asn	Arg	Ala	Thr	Arg	Val	Glu	Cys	Thr	Thr	Ile
2390						2395					2400			
Val	Asn	Gly	Met	Lys	Arg	Ser	Phe	Tyr	Val	Tyr	Ala	Asn	Gly	Gly
2405						2410					2415			
Arg	Gly	Phe	Cys	Lys	Thr	His	Asn	Trp	Asn	Cys	Leu	Asn	Cys	Asp
2420						2425					2430			
Thr	Phe	Cys	Thr	Gly	Ser	Thr	Phe	Ile	Ser	Asp	Glu	Val	Ala	Arg
2435						2440					2445			
Asp	Leu	Ser	Leu	Gln	Phe	Lys	Arg	Pro	Ile	Asn	Pro	Thr	Asp	Gln
2450						2455					2460			
Ser	Ser	Tyr	Ile	Val	Asp	Ser	Val	Ala	Val	Lys	Asn	Gly	Ala	Leu
2465						2470					2475			
His	Leu	Tyr	Phe	Asp	Lys	Ala	Gly	Gln	Lys	Thr	Tyr	Glu	Arg	His
2480						2485					2490			
Pro	Leu	Ser	His	Phe	Val	Asn	Leu	Asp	Asn	Leu	Arg	Ala	Asn	Asn
2495						2500					2505			
Thr	Lys	Gly	Ser	Leu	Pro	Ile	Asn	Val	Ile	Val	Phe	Asp	Gly	Lys
2510						2515					2520			
Ser	Lys	Cys	Asp	Glu	Ser	Ala	Ser	Lys	Ser	Ala	Ser	Val	Tyr	Tyr
2525						2530					2535			
Ser	Gln	Leu	Met	Cys	Gln	Pro	Ile	Leu	Leu	Leu	Asp	Gln	Val	Leu
2540						2545					2550			
Val	Ser	Asp	Val	Gly	Asp	Ser	Thr	Glu	Val	Ser	Val	Lys	Met	Phe
2555						2560					2565			
Asp	Ala	Tyr	Val	Asp	Thr	Phe	Ser	Ala	Thr	Phe	Ser	Val	Pro	Met
2570						2575					2580			
Glu	Lys	Leu	Lys	Ala	Leu	Val	Ala	Thr	Ala	His	Ser	Glu	Leu	Ala
2585						2590					2595			
Lys	Gly	Val	Ala	Leu	Asp	Gly	Val	Leu	Ser	Thr	Phe	Val	Ser	Ala
2600						2605					2610			
Ala	Arg	Gln	Gly	Val	Val	Asp	Thr	Asp	Val	Asp	Thr	Lys	Asp	Val
2615						2620					2625			
Ile	Glu	Cys	Leu	Lys	Leu	Ser	His	His	Ser	Asp	Leu	Glu	Val	Thr
2630						2635					2640			
Gly	Asp	Ser	Cys	Asn	Asn	Phe	Met	Leu	Thr	Tyr	Asn	Lys	Val	Glu
2645						2650					2655			
Asn	Met	Thr	Pro	Arg	Asp	Leu	Gly	Ala	Cys	Ile	Asp	Cys	Asn	Ala
2660						2665					2670			
Arg	His	Ile	Asn	Ala	Gln	Val	Ala	Lys	Ser	His	Asn	Val	Ser	Leu
2675						2680					2685			
Ile	Trp	Asn	Val	Lys	Asp	Tyr	Met	Ser	Leu	Ser	Glu	Gln	Leu	Arg
2690						2695					2700			
Lys	Gln	Ile	Arg	Ser	Ala	Ala	Lys	Lys	Asn	Asn	Ile	Pro	Phe	Arg
2705						2710					2715			
Leu	Thr	Cys	Ala	Thr	Thr	Arg	Gln	Val	Val	Asn	Val	Ile	Thr	Thr
2720						2725					2730			
Lys	Ile	Ser	Leu	Lys	Gly	Gly	Lys	Ile	Val	Ser	Thr	Cys	Phe	Lys
2735						2740					2745			
Leu	Met	Leu	Lys	Ala	Thr	Leu	Leu	Cys	Val	Leu	Ala	Ala	Leu	Val
2750						2755					2760			

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Cys	Tyr	Ile	Val	Met	Pro	Val	His	Thr	Leu	Ser	Ile	His	Asp	Gly
2765						2770					2775			
Tyr	Thr	Asn	Glu	Ile	Ile	Gly	Tyr	Lys	Ala	Ile	Gln	Asp	Gly	Val
2780						2785					2790			
Thr	Arg	Asp	Ile	Ile	Ser	Thr	Asp	Asp	Cys	Phe	Ala	Asn	Lys	His
2795						2800					2805			
Ala	Gly	Phe	Asp	Ala	Trp	Phe	Ser	Gln	Arg	Gly	Gly	Ser	Tyr	Lys
2810						2815					2820			
Asn	Asp	Lys	Ser	Cys	Pro	Val	Val	Ala	Ala	Ile	Ile	Thr	Arg	Glu
2825						2830					2835			
Ile	Gly	Phe	Ile	Val	Pro	Gly	Leu	Pro	Gly	Thr	Val	Leu	Arg	Ala
2840						2845					2850			
Ile	Asn	Gly	Asp	Phe	Leu	His	Phe	Leu	Pro	Arg	Val	Phe	Ser	Ala
2855						2860					2865			
Val	Gly	Asn	Ile	Cys	Tyr	Thr	Pro	Ser	Lys	Leu	Ile	Glu	Tyr	Ser
2870						2875					2880			
Asp	Phe	Ala	Thr	Ser	Ala	Cys	Val	Leu	Ala	Ala	Glu	Cys	Thr	Ile
2885						2890					2895			
Phe	Lys	Asp	Ala	Met	Gly	Lys	Pro	Val	Pro	Tyr	Cys	Tyr	Asp	Thr
2900						2905					2910			
Asn	Leu	Leu	Glu	Gly	Ser	Ile	Ser	Tyr	Ser	Glu	Leu	Arg	Pro	Asp
2915						2920					2925			
Thr	Arg	Tyr	Val	Leu	Met	Asp	Gly	Ser	Ile	Ile	Gln	Phe	Pro	Asn
2930						2935					2940			
Thr	Tyr	Leu	Glu	Gly	Ser	Val	Arg	Val	Val	Thr	Thr	Phe	Asp	Ala
2945						2950					2955			
Glu	Tyr	Cys	Arg	His	Gly	Thr	Cys	Glu	Arg	Ser	Glu	Val	Gly	Ile
2960						2965					2970			
Cys	Leu	Ser	Thr	Ser	Gly	Arg	Trp	Val	Leu	Asn	Asn	Glu	His	Tyr
2975						2980					2985			
Arg	Ala	Leu	Ser	Gly	Val	Phe	Cys	Gly	Val	Asp	Ala	Met	Asn	Leu
2990						2995					3000			
Ile	Ala	Asn	Ile	Phe	Thr	Pro	Leu	Val	Gln	Pro	Val	Gly	Ala	Leu
3005						3010					3015			
Asp	Val	Ser	Ala	Ser	Val	Val	Ala	Gly	Gly	Ile	Ile	Ala	Ile	Leu
3020						3025					3030			
Val	Thr	Cys	Ala	Ala	Tyr	Tyr	Phe	Met	Lys	Phe	Arg	Arg	Val	Phe
3035						3040					3045			
Gly	Glu	Tyr	Asn	His	Val	Val	Ala	Ala	Asn	Ala	Leu	Leu	Phe	Leu
3050						3055					3060			
Met	Ser	Phe	Thr	Ile	Leu	Cys	Leu	Val	Pro	Ala	Tyr	Ser	Phe	Leu
3065						3070					3075			
Pro	Gly	Val	Tyr	Ser	Val	Phe	Tyr	Leu	Tyr	Leu	Thr	Phe	Tyr	Phe
3080						3085					3090			
Thr	Asn	Asp	Val	Ser	Phe	Leu	Ala	His	Leu	Gln	Trp	Phe	Ala	Met
3095						3100					3105			
Phe	Ser	Pro	Ile	Val	Pro	Phe	Trp	Ile	Thr	Ala	Ile	Tyr	Val	Phe
3110						3115					3120			
Cys	Ile	Ser	Leu	Lys	His	Cys	His	Trp	Phe	Phe	Asn	Asn	Tyr	Leu
3125						3130					3135			
Arg	Lys	Arg	Val	Met	Phe	Asn	Gly	Val	Thr	Phe	Ser	Thr	Phe	Glu
3140						3145					3150			
Glu	Ala	Ala	Leu	Cys	Thr	Phe	Leu	Leu	Asn	Lys	Glu	Met	Tyr	Leu

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3155						3160								3165
Lys	Leu	Arg	Ser	Glu	Thr	Leu	Leu	Pro	Leu	Thr	Gln	Tyr	Asn	Arg
3170						3175					3180			
Tyr	Leu	Ala	Leu	Tyr	Asn	Lys	Tyr	Lys	Tyr	Phe	Ser	Gly	Ala	Leu
3185						3190					3195			
Asp	Thr	Thr	Ser	Tyr	Arg	Glu	Ala	Ala	Cys	Cys	His	Leu	Ala	Lys
3200						3205					3210			
Ala	Leu	Asn	Asp	Phe	Ser	Asn	Ser	Gly	Ala	Asp	Val	Leu	Tyr	Gln
3215						3220					3225			
Pro	Pro	Gln	Thr	Ser	Ile	Thr	Ser	Ala	Val	Leu	Gln	Ser	Gly	Phe
3230						3235					3240			
Arg	Lys	Met	Ala	Phe	Pro	Ser	Gly	Lys	Val	Glu	Gly	Cys	Met	Val
3245						3250					3255			
Gln	Val	Thr	Cys	Gly	Thr	Thr	Thr	Leu	Asn	Gly	Leu	Trp	Leu	Asp
3260						3265					3270			
Asp	Thr	Val	Tyr	Cys	Pro	Arg	His	Val	Ile	Cys	Thr	Ala	Glu	Asp
3275						3280					3285			
Met	Leu	Asn	Pro	Asn	Tyr	Glu	Asp	Leu	Leu	Ile	Arg	Lys	Ser	Asn
3290						3295					3300			
His	Ser	Phe	Leu	Val	Gln	Ala	Gly	Asn	Val	Gln	Leu	Arg	Val	Ile
3305						3310					3315			
Gly	His	Ser	Met	Gln	Asn	Cys	Leu	Leu	Arg	Leu	Lys	Val	Asp	Thr
3320						3325					3330			
Ser	Asn	Pro	Lys	Thr	Pro	Lys	Tyr	Lys	Phe	Val	Arg	Ile	Gln	Pro
3335						3340					3345			
Gly	Gln	Thr	Phe	Ser	Val	Leu	Ala	Cys	Tyr	Asn	Gly	Ser	Pro	Ser
3350						3355					3360			
Gly	Val	Tyr	Gln	Cys	Ala	Met	Arg	Pro	Asn	His	Thr	Ile	Lys	Gly
3365						3370					3375			
Ser	Phe	Leu	Asn	Gly	Ser	Cys	Gly	Ser	Val	Gly	Phe	Asn	Ile	Asp
3380						3385					3390			
Tyr	Asp	Cys	Val	Ser	Phe	Cys	Tyr	Met	His	His	Met	Glu	Leu	Pro
3395						3400					3405			
Thr	Gly	Val	His	Ala	Gly	Thr	Asp	Leu	Glu	Gly	Lys	Phe	Tyr	Gly
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Pro	Phe	Val	Asp	Arg	Gln	Thr	Ala	Gln	Ala	Ala	Gly	Thr	Asp	Thr
3425						3430					3435			
Thr	Ile	Thr	Leu	Asn	Val	Leu	Ala	Trp	Leu	Tyr	Ala	Ala	Val	Ile
3440						3445					3450			
Asn	Gly	Asp	Arg	Trp	Phe	Leu	Asn	Arg	Phe	Thr	Thr	Thr	Leu	Asn
3455						3460					3465			
Asp	Phe	Asn	Leu	Val	Ala	Met	Lys	Tyr	Asn	Tyr	Glu	Pro	Leu	Thr
3470						3475					3480			
Gln	Asp	His	Val	Asp	Ile	Leu	Gly	Pro	Leu	Ser	Ala	Gln	Thr	Gly
3485						3490					3495			
Ile	Ala	Val	Leu	Asp	Met	Cys	Ala	Ala	Leu	Lys	Glu	Leu	Leu	Gln
3500						3505					3510			
Asn	Gly	Met	Asn	Gly	Arg	Thr	Ile	Leu	Gly	Ser	Thr	Ile	Leu	Glu
3515						3520					3525			
Asp	Glu	Phe	Thr	Pro	Phe	Asp	Val	Val	Arg	Gln	Cys	Ser	Gly	Val
3530						3535					3540			
Thr	Phe	Gln	Gly	Lys	Phe	Lys	Lys	Ile	Val	Lys	Gly	Thr	His	His
3545						3550					3555			

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Trp	Met	Leu	Leu	Thr	Phe	Leu	Thr	Ser	Leu	Leu	Ile	Leu	Val	Gln
3560						3565					3570			
Ser	Thr	Gln	Trp	Ser	Leu	Phe	Phe	Phe	Val	Tyr	Glu	Asn	Ala	Phe
3575					3580						3585			
Leu	Pro	Phe	Thr	Leu	Gly	Ile	Met	Ala	Ile	Ala	Ala	Cys	Ala	Met
3590					3595						3600			
Leu	Leu	Val	Lys	His	Lys	His	Ala	Phe	Leu	Cys	Leu	Phe	Leu	Leu
3605					3610						3615			
Pro	Ser	Leu	Ala	Thr	Val	Ala	Tyr	Phe	Asn	Met	Val	Tyr	Met	Pro
3620					3625						3630			
Ala	Ser	Trp	Val	Met	Arg	Ile	Met	Thr	Trp	Leu	Glu	Leu	Ala	Asp
3635					3640						3645			
Thr	Ser	Leu	Ser	Gly	Tyr	Arg	Leu	Lys	Asp	Cys	Val	Met	Tyr	Ala
3650					3655						3660			
Ser	Ala	Leu	Val	Leu	Leu	Ile	Leu	Met	Thr	Ala	Arg	Thr	Val	Tyr
3665					3670						3675			
Asp	Asp	Ala	Ala	Arg	Arg	Val	Trp	Thr	Leu	Met	Asn	Val	Ile	Thr
3680					3685						3690			
Leu	Val	Tyr	Lys	Val	Tyr	Tyr	Gly	Asn	Ala	Leu	Asp	Gln	Ala	Ile
3695					3700						3705			
Ser	Met	Trp	Ala	Leu	Val	Ile	Ser	Val	Thr	Ser	Asn	Tyr	Ser	Gly
3710					3715						3720			
Val	Val	Thr	Thr	Ile	Met	Phe	Leu	Ala	Arg	Ala	Ile	Val	Phe	Val
3725					3730						3735			
Cys	Val	Glu	Tyr	Tyr	Pro	Leu	Leu	Phe	Ile	Thr	Gly	Asn	Thr	Leu
3740					3745						3750			
Gln	Cys	Ile	Met	Leu	Val	Tyr	Cys	Phe	Leu	Gly	Tyr	Cys	Cys	Cys
3755					3760						3765			
Cys	Tyr	Phe	Gly	Leu	Phe	Cys	Leu	Leu	Asn	Arg	Tyr	Phe	Arg	Leu
3770					3775						3780			
Thr	Leu	Gly	Val	Tyr	Asp	Tyr	Leu	Val	Ser	Thr	Gln	Glu	Phe	Arg
3785					3790						3795			
Tyr	Met	Asn	Ser	Gln	Gly	Leu	Leu	Pro	Pro	Lys	Ser	Ser	Ile	Asp
3800					3805						3810			
Ala	Phe	Lys	Leu	Asn	Ile	Lys	Leu	Leu	Gly	Ile	Gly	Gly	Lys	Pro
3815					3820						3825			
Cys	Ile	Lys	Val	Ala	Thr	Val	Gln	Ser	Lys	Met	Ser	Asp	Val	Lys
3830					3835						3840			
Cys	Thr	Ser	Val	Val	Leu	Leu	Ser	Val	Leu	Gln	Gln	Leu	Arg	Val
3845					3850						3855			
Glu	Ser	Ser	Ser	Lys	Leu	Trp	Ala	Gln	Cys	Val	Gln	Leu	His	Asn
3860					3865						3870			
Asp	Ile	Leu	Leu	Ala	Lys	Asp	Thr	Thr	Glu	Ala	Phe	Glu	Lys	Met
3875					3880						3885			
Val	Ser	Leu	Leu	Ser	Val	Leu	Leu	Ser	Met	Gln	Gly	Ala	Val	Asp
3890					3895						3900			
Ile	Asn	Arg	Leu	Cys	Glu	Glu	Met	Leu	Asp	Asn	Arg	Ala	Thr	Leu
3905					3910						3915			
Gln	Ala	Ile	Ala	Ser	Glu	Phe	Ser	Ser	Leu	Pro	Ser	Tyr	Ala	Ala
3920					3925						3930			
Tyr	Ala	Thr	Ala	Gln	Glu	Ala	Tyr	Glu	Gln	Ala	Val	Ala	Asn	Gly
3935					3940						3945			

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Asp	Ser	Glu	Val	Val	Leu	Lys	Lys	Leu	Lys	Lys	Ser	Leu	Asn	Val
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Ala	Lys	Ser	Glu	Phe	Asp	Arg	Asp	Ala	Ala	Met	Gln	Arg	Lys	Leu
3965						3970					3975			
Glu	Lys	Met	Ala	Asp	Gln	Ala	Met	Thr	Gln	Met	Tyr	Lys	Gln	Ala
3980						3985					3990			
Arg	Ser	Glu	Asp	Lys	Arg	Ala	Lys	Val	Thr	Ser	Ala	Met	Gln	Thr
3995						4000					4005			
Met	Leu	Phe	Thr	Met	Leu	Arg	Lys	Leu	Asp	Asn	Asp	Ala	Leu	Asn
4010						4015					4020			
Asn	Ile	Ile	Asn	Asn	Ala	Arg	Asp	Gly	Cys	Val	Pro	Leu	Asn	Ile
4025						4030					4035			
Ile	Pro	Leu	Thr	Thr	Ala	Ala	Lys	Leu	Met	Val	Val	Val	Pro	Asp
4040						4045					4050			
Tyr	Gly	Thr	Tyr	Lys	Asn	Thr	Cys	Asp	Gly	Asn	Thr	Phe	Thr	Tyr
4055						4060					4065			
Ala	Ser	Ala	Leu	Trp	Glu	Ile	Gln	Gln	Val	Val	Asp	Ala	Asp	Ser
4070						4075					4080			
Lys	Ile	Val	Gln	Leu	Ser	Glu	Ile	Asn	Met	Asp	Asn	Ser	Pro	Asn
4085						4090					4095			
Leu	Ala	Trp	Pro	Leu	Ile	Val	Thr	Ala	Leu	Arg	Ala	Asn	Ser	Ala
4100						4105					4110			
Val	Lys	Leu	Gln	Asn	Asn	Glu	Leu	Ser	Pro	Val	Ala	Leu	Arg	Gln
4115						4120					4125			
Met	Ser	Cys	Ala	Ala	Gly	Thr	Thr	Gln	Thr	Ala	Cys	Thr	Asp	Asp
4130						4135					4140			
Asn	Ala	Leu	Ala	Tyr	Tyr	Asn	Asn	Ser	Lys	Gly	Gly	Arg	Phe	Val
4145						4150					4155			
Leu	Ala	Leu	Leu	Ser	Asp	His	Gln	Asp	Leu	Lys	Trp	Ala	Arg	Phe
4160						4165					4170			
Pro	Lys	Ser	Asp	Gly	Thr	Gly	Thr	Ile	Tyr	Thr	Glu	Leu	Glu	Pro
4175						4180					4185			
Pro	Cys	Arg	Phe	Val	Thr	Asp	Thr	Pro	Lys	Gly	Pro	Lys	Val	Lys
4190						4195					4200			
Tyr	Leu	Tyr	Phe	Ile	Lys	Gly	Leu	Asn	Asn	Leu	Asn	Arg	Gly	Met
4205						4210					4215			
Val	Leu	Gly	Ser	Leu	Ala	Ala	Thr	Val	Arg	Leu	Gln	Ala	Gly	Asn
4220						4225					4230			
Ala	Thr	Glu	Val	Pro	Ala	Asn	Ser	Thr	Val	Leu	Ser	Phe	Cys	Ala
4235						4240					4245			
Phe	Ala	Val	Asp	Pro	Ala	Lys	Ala	Tyr	Lys	Asp	Tyr	Leu	Ala	Ser
4250						4255					4260			
Gly	Gly	Gln	Pro	Ile	Thr	Asn	Cys	Val	Lys	Met	Leu	Cys	Thr	His
4265						4270					4275			
Thr	Gly	Thr	Gly	Gln	Ala	Ile	Thr	Val	Thr	Pro	Glu	Ala	Asn	Met
4280						4285					4290			
Asp	Gln	Glu	Ser	Phe	Gly	Gly	Ala	Ser	Cys	Cys	Leu	Tyr	Cys	Arg
4295						4300					4305			
Cys	His	Ile	Asp	His	Pro	Asn	Pro	Lys	Gly	Phe	Cys	Asp	Leu	Lys
4310						4315					4320			
Gly	Lys	Tyr	Val	Gln	Ile	Pro	Thr	Thr	Cys	Ala	Asn	Asp	Pro	Val
4325						4330					4335			
Gly	Phe	Thr	Leu	Arg	Asn	Thr	Val	Cys	Thr	Val	Cys	Gly	Met	Trp

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4340 4345 4350

Lys Gly Tyr Gly Cys Ser Cys Asp Gln Leu Arg Glu Pro Leu Met
4355 4360 4365

Gln Ser Ala Asp Ala Ser Thr Phe Leu Asn Gly Phe Ala Val
4370 4375 4380

<210> SEQ ID NO 3
<211> LENGTH: 2695
<212> TYPE: PRT
<213> ORGANISM: Coronavirus

<400> SEQUENCE: 3

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Thr Ser Thr Asp Val Val Tyr Arg Ala Phe Asp Ile Tyr Asn Glu Lys
20 25 30

Val Ala Gly Phe Ala Lys Phe Leu Lys Thr Asn Cys Cys Arg Phe Gln
35 40 45

Glu Lys Asp Glu Glu Gly Asn Leu Leu Asp Ser Tyr Phe Val Val Lys
50 55 60

Arg His Thr Met Ser Asn Tyr Gln His Glu Glu Thr Ile Tyr Asn Leu
65 70 75 80

Val Lys Asp Cys Pro Ala Val Ala Val His Asp Phe Phe Lys Phe Arg
85 90 95

Val Asp Gly Asp Met Val Pro His Ile Ser Arg Gln Arg Leu Thr Lys
100 105 110

Tyr Thr Met Ala Asp Leu Val Tyr Ala Leu Arg His Phe Asp Glu Gly
115 120 125

Asn Cys Asp Thr Leu Lys Glu Ile Leu Val Thr Tyr Asn Cys Cys Asp
130 135 140

Asp Asp Tyr Phe Asn Lys Lys Asp Trp Tyr Asp Phe Val Glu Asn Pro
145 150 155 160

Asp Ile Leu Arg Val Tyr Ala Asn Leu Gly Glu Arg Val Arg Gln Ser
165 170 175

Leu Leu Lys Thr Val Gln Phe Cys Asp Ala Met Arg Asp Ala Gly Ile
180 185 190

Val Gly Val Leu Thr Leu Asp Asn Gln Asp Leu Asn Gly Asn Trp Tyr
195 200 205

Asp Phe Gly Asp Phe Val Gln Val Ala Pro Gly Cys Gly Val Pro Ile
210 215 220

Val Asp Ser Tyr Tyr Ser Leu Leu Met Pro Ile Leu Thr Leu Thr Arg
225 230 235 240

Ala Leu Ala Ala Glu Ser His Met Asp Ala Asp Leu Ala Lys Pro Leu
245 250 255

Ile Lys Trp Asp Leu Leu Lys Tyr Asp Phe Thr Glu Glu Arg Leu Cys
260 265 270

Leu Phe Asp Arg Tyr Phe Lys Tyr Trp Asp Gln Thr Tyr His Pro Asn
275 280 285

Cys Ile Asn Cys Leu Asp Asp Arg Cys Ile Leu His Cys Ala Asn Phe
290 295 300

Asn Val Leu Phe Ser Thr Val Phe Pro Pro Thr Ser Phe Gly Pro Leu
305 310 315 320

Val Arg Lys Ile Phe Val Asp Gly Val Pro Phe Val Val Ser Thr Gly
325 330 335

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Tyr	His	Phe	Arg	Glu	Leu	Gly	Val	Val	His	Asn	Gln	Asp	Val	Asn	Leu
			340						345					350	
His	Ser	Ser	Arg	Leu	Ser	Phe	Lys	Glu	Leu	Leu	Val	Tyr	Ala	Ala	Asp
			355				360					365			
Pro	Ala	Met	His	Ala	Ala	Ser	Gly	Asn	Leu	Leu	Leu	Asp	Lys	Arg	Thr
			370				375					380			
Thr	Cys	Phe	Ser	Val	Ala	Ala	Leu	Thr	Asn	Asn	Val	Ala	Phe	Gln	Thr
385					390					395					400
Val	Lys	Pro	Gly	Asn	Phe	Asn	Lys	Asp	Phe	Tyr	Asp	Phe	Ala	Val	Ser
				405					410					415	
Lys	Gly	Phe	Phe	Lys	Glu	Gly	Ser	Ser	Val	Glu	Leu	Lys	His	Phe	Phe
			420					425					430		
Phe	Ala	Gln	Asp	Gly	Asn	Ala	Ala	Ile	Ser	Asp	Tyr	Asp	Tyr	Tyr	Arg
			435				440					445			
Tyr	Asn	Leu	Pro	Thr	Met	Cys	Asp	Ile	Arg	Gln	Leu	Leu	Phe	Val	Val
			450			455					460				
Glu	Val	Val	Asp	Lys	Tyr	Phe	Asp	Cys	Tyr	Asp	Gly	Gly	Cys	Ile	Asn
465					470					475					480
Ala	Asn	Gln	Val	Ile	Val	Asn	Asn	Leu	Asp	Lys	Ser	Ala	Gly	Phe	Pro
				485					490					495	
Phe	Asn	Lys	Trp	Gly	Lys	Ala	Arg	Leu	Tyr	Tyr	Asp	Ser	Met	Ser	Tyr
			500					505					510		
Glu	Asp	Gln	Asp	Ala	Leu	Phe	Ala	Tyr	Thr	Lys	Arg	Asn	Val	Ile	Pro
			515				520					525			
Thr	Ile	Thr	Gln	Met	Asn	Leu	Lys	Tyr	Ala	Ile	Ser	Ala	Lys	Asn	Arg
	530				535						540				
Ala	Arg	Thr	Val	Ala	Gly	Val	Ser	Ile	Cys	Ser	Thr	Met	Thr	Asn	Arg
545					550					555					560
Gln	Phe	His	Gln	Lys	Leu	Leu	Lys	Ser	Ile	Ala	Ala	Thr	Arg	Gly	Ala
				565					570					575	
Thr	Val	Val	Ile	Gly	Thr	Ser	Lys	Phe	Tyr	Gly	Gly	Trp	His	Asn	Met
			580					585					590		
Leu	Lys	Thr	Val	Tyr	Ser	Asp	Val	Glu	Thr	Pro	His	Leu	Met	Gly	Trp
			595				600					605			
Asp	Tyr	Pro	Lys	Cys	Asp	Arg	Ala	Met	Pro	Asn	Met	Leu	Arg	Ile	Met
	610					615					620				
Ala	Ser	Leu	Val	Leu	Ala	Arg	Lys	His	Asn	Thr	Cys	Cys	Asn	Leu	Ser
625					630					635					640
His	Arg	Phe	Tyr	Arg	Leu	Ala	Asn	Glu	Cys	Ala	Gln	Val	Leu	Ser	Glu
				645					650					655	
Met	Val	Met	Cys	Gly	Gly	Ser	Leu	Tyr	Val	Lys	Pro	Gly	Gly	Thr	Ser
			660					665						670	
Ser	Gly	Asp	Ala	Thr	Thr	Ala	Tyr	Ala	Asn	Ser	Val	Phe	Asn	Ile	Cys
		675					680					685			
Gln	Ala	Val	Thr	Ala	Asn	Val	Asn	Ala	Leu	Leu	Ser	Thr	Asp	Gly	Asn
	690					695					700				
Lys	Ile	Ala	Asp	Lys	Tyr	Val	Arg	Asn	Leu	Gln	His	Arg	Leu	Tyr	Glu
705					710					715					720
Cys	Leu	Tyr	Arg	Asn	Arg	Asp	Val	Asp	His	Glu	Phe	Val	Asp	Glu	Phe
				725					730					735	
Tyr	Ala	Tyr	Leu	Arg	Lys	His	Phe	Ser	Met	Met	Ile	Leu	Ser	Asp	Asp
			740					745					750		
Ala	Val	Val	Cys	Tyr	Asn	Ser	Asn	Tyr	Ala	Ala	Gln	Gly	Leu	Val	Ala

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755					760					765					
Ser	Ile	Lys	Asn	Phe	Lys	Ala	Val	Leu	Tyr	Tyr	Gln	Asn	Asn	Val	Phe
770					775						780				
Met	Ser	Glu	Ala	Lys	Cys	Trp	Thr	Glu	Thr	Asp	Leu	Thr	Lys	Gly	Pro
785					790					795					800
His	Glu	Phe	Cys	Ser	Gln	His	Thr	Met	Leu	Val	Lys	Gln	Gly	Asp	Asp
				805					810					815	
Tyr	Val	Tyr	Leu	Pro	Tyr	Pro	Asp	Pro	Ser	Arg	Ile	Leu	Gly	Ala	Gly
			820						825					830	
Cys	Phe	Val	Asp	Asp	Ile	Val	Lys	Thr	Asp	Gly	Thr	Leu	Met	Ile	Glu
			835						840					845	
Arg	Phe	Val	Ser	Leu	Ala	Ile	Asp	Ala	Tyr	Pro	Leu	Thr	Lys	His	Pro
Asn	Gln	Glu	Tyr	Ala	Asp	Val	Phe	His	Leu	Tyr	Leu	Gln	Tyr	Ile	Arg
865					870					875					880
Lys	Leu	His	Asp	Glu	Leu	Thr	Gly	His	Met	Leu	Asp	Met	Tyr	Ser	Val
				885					890					895	
Met	Leu	Thr	Asn	Asp	Asn	Thr	Ser	Arg	Tyr	Trp	Glu	Pro	Glu	Phe	Tyr
				900					905					910	
Glu	Ala	Met	Tyr	Thr	Pro	His	Thr	Val	Leu	Gln	Ala	Val	Gly	Ala	Cys
				915					920					925	
Val	Leu	Cys	Asn	Ser	Gln	Thr	Ser	Leu	Arg	Cys	Gly	Ala	Cys	Ile	Arg
				930					935					940	
Arg	Pro	Phe	Leu	Cys	Cys	Lys	Cys	Cys	Tyr	Asp	His	Val	Ile	Ser	Thr
945					950					955					960
Ser	His	Lys	Leu	Val	Leu	Ser	Val	Asn	Pro	Tyr	Val	Cys	Asn	Ala	Pro
				965					970					975	
Gly	Cys	Asp	Val	Thr	Asp	Val	Thr	Gln	Leu	Tyr	Leu	Gly	Gly	Met	Ser
				980					985					990	
Tyr	Tyr	Cys	Lys	Ser	His	Lys	Pro	Pro	Ile	Ser	Phe	Pro	Leu	Cys	Ala
				995					1000					1005	
Asn	Gly	Gln	Val	Phe	Gly	Leu	Tyr	Lys	Asn	Thr	Cys	Val	Gly	Ser	
Asp	Asn	Val	Thr	Asp	Phe	Asn	Ala	Ile	Ala	Thr	Cys	Asp	Trp	Thr	
Asn	Ala	Gly	Asp	Tyr	Ile	Leu	Ala	Asn	Thr	Cys	Thr	Glu	Arg	Leu	
Lys	Leu	Phe	Ala	Ala	Glu	Thr	Leu	Lys	Ala	Thr	Glu	Glu	Thr	Phe	
Lys	Leu	Ser	Tyr	Gly	Ile	Ala	Thr	Val	Arg	Glu	Val	Leu	Ser	Asp	
Arg	Glu	Leu	His	Leu	Ser	Trp	Glu	Val	Gly	Lys	Pro	Arg	Pro	Pro	
Leu	Asn	Arg	Asn	Tyr	Val	Phe	Thr	Gly	Tyr	Arg	Val	Thr	Lys	Asn	
Ser	Lys	Val	Gln	Ile	Gly	Glu	Tyr	Thr	Phe	Glu	Lys	Gly	Asp	Tyr	
Gly	Asp	Ala	Val	Val	Tyr	Arg	Gly	Thr	Thr	Thr	Tyr	Lys	Leu	Asn	
Val	Gly	Asp	Tyr	Phe	Val	Leu	Thr	Ser	His	Thr	Val	Met	Pro	Leu	
Ser	Ala	Pro	Thr	Leu	Val	Pro	Gln	Glu	His	Tyr	Val	Arg	Ile	Thr	

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Gly	Leu	Tyr	Pro	Thr	Leu	Asn	Ile	Ser	Asp	Glu	Phe	Ser	Ser	Asn
1175						1180					1185			
Val	Ala	Asn	Tyr	Gln	Lys	Val	Gly	Met	Gln	Lys	Tyr	Ser	Thr	Leu
1190						1195					1200			
Gln	Gly	Pro	Pro	Gly	Thr	Gly	Lys	Ser	His	Phe	Ala	Ile	Gly	Leu
1205						1210					1215			
Ala	Leu	Tyr	Tyr	Pro	Ser	Ala	Arg	Ile	Val	Tyr	Thr	Ala	Cys	Ser
1220						1225					1230			
His	Ala	Ala	Val	Asp	Ala	Leu	Cys	Glu	Lys	Ala	Leu	Lys	Tyr	Leu
1235						1240					1245			
Pro	Ile	Asp	Lys	Cys	Ser	Arg	Ile	Ile	Pro	Ala	Arg	Ala	Arg	Val
1250						1255					1260			
Glu	Cys	Phe	Asp	Lys	Phe	Lys	Val	Asn	Ser	Thr	Leu	Glu	Gln	Tyr
1265						1270					1275			
Val	Phe	Cys	Thr	Val	Asn	Ala	Leu	Pro	Glu	Thr	Thr	Ala	Asp	Ile
1280						1285					1290			
Val	Val	Phe	Asp	Glu	Ile	Ser	Met	Ala	Thr	Asn	Tyr	Asp	Leu	Ser
1295						1300					1305			
Val	Val	Asn	Ala	Arg	Leu	Arg	Ala	Lys	His	Tyr	Val	Tyr	Ile	Gly
1310						1315					1320			
Asp	Pro	Ala	Gln	Leu	Pro	Ala	Pro	Arg	Thr	Leu	Leu	Thr	Lys	Gly
1325						1330					1335			
Thr	Leu	Glu	Pro	Glu	Tyr	Phe	Asn	Ser	Val	Cys	Arg	Leu	Met	Lys
1340						1345					1350			
Thr	Ile	Gly	Pro	Asp	Met	Phe	Leu	Gly	Thr	Cys	Arg	Arg	Cys	Pro
1355						1360					1365			
Ala	Glu	Ile	Val	Asp	Thr	Val	Ser	Ala	Leu	Val	Tyr	Asp	Asn	Lys
1370						1375					1380			
Leu	Lys	Ala	His	Lys	Asp	Lys	Ser	Ala	Gln	Cys	Phe	Lys	Met	Phe
1385						1390					1395			
Tyr	Lys	Gly	Val	Ile	Thr	His	Asp	Val	Ser	Ser	Ala	Ile	Asn	Arg
1400						1405					1410			
Pro	Gln	Ile	Gly	Val	Val	Arg	Glu	Phe	Leu	Thr	Arg	Asn	Pro	Ala
1415						1420					1425			
Trp	Arg	Lys	Ala	Val	Phe	Ile	Ser	Pro	Tyr	Asn	Ser	Gln	Asn	Ala
1430						1435					1440			
Val	Ala	Ser	Lys	Ile	Leu	Gly	Leu	Pro	Thr	Gln	Thr	Val	Asp	Ser
1445						1450					1455			
Ser	Gln	Gly	Ser	Glu	Tyr	Asp	Tyr	Val	Ile	Phe	Thr	Gln	Thr	Thr
1460						1465					1470			
Glu	Thr	Ala	His	Ser	Cys	Asn	Val	Asn	Arg	Phe	Asn	Val	Ala	Ile
1475						1480					1485			
Thr	Arg	Ala	Lys	Ile	Gly	Ile	Leu	Cys	Ile	Met	Ser	Asp	Arg	Asp
1490						1495					1500			
Leu	Tyr	Asp	Lys	Leu	Gln	Phe	Thr	Ser	Leu	Glu	Ile	Pro	Arg	Arg
1505						1510					1515			
Asn	Val	Ala	Thr	Leu	Gln	Ala	Glu	Asn	Val	Thr	Gly	Leu	Phe	Lys
1520						1525					1530			
Asp	Cys	Ser	Lys	Ile	Ile	Thr	Gly	Leu	His	Pro	Thr	Gln	Ala	Pro
1535						1540					1545			
Thr	His	Leu	Ser	Val	Asp	Ile	Lys	Phe	Lys	Thr	Glu	Gly	Leu	Cys
1550						1555					1560			

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Val 1565	Asp	Ile	Pro	Gly	Ile	Pro	Lys	Asp	Met	Thr	Tyr	Arg	Arg	Leu
						1570					1575			
Ile	Ser	Met	Met	Gly	Phe	Lys	Met	Asn	Tyr	Gln	Val	Asn	Gly	Tyr
	1580					1585					1590			
Pro	Asn	Met	Phe	Ile	Thr	Arg	Glu	Glu	Ala	Ile	Arg	His	Val	Arg
	1595					1600					1605			
Ala	Trp	Ile	Gly	Phe	Asp	Val	Glu	Gly	Cys	His	Ala	Thr	Arg	Asp
	1610					1615					1620			
Ala	Val	Gly	Thr	Asn	Leu	Pro	Leu	Gln	Leu	Gly	Phe	Ser	Thr	Gly
	1625					1630					1635			
Val	Asn	Leu	Val	Ala	Val	Pro	Thr	Gly	Tyr	Val	Asp	Thr	Glu	Asn
	1640					1645					1650			
Asn	Thr	Glu	Phe	Thr	Arg	Val	Asn	Ala	Lys	Pro	Pro	Pro	Gly	Asp
	1655					1660					1665			
Gln	Phe	Lys	His	Leu	Ile	Pro	Leu	Met	Tyr	Lys	Gly	Leu	Pro	Trp
	1670					1675					1680			
Asn	Val	Val	Arg	Ile	Lys	Ile	Val	Gln	Met	Leu	Ser	Asp	Thr	Leu
	1685					1690					1695			
Lys	Gly	Leu	Ser	Asp	Arg	Val	Val	Phe	Val	Leu	Trp	Ala	His	Gly
	1700					1705					1710			
Phe	Glu	Leu	Thr	Ser	Met	Lys	Tyr	Phe	Val	Lys	Ile	Gly	Pro	Glu
	1715					1720					1725			
Arg	Thr	Cys	Cys	Leu	Cys	Asp	Lys	Arg	Ala	Thr	Cys	Phe	Ser	Thr
	1730					1735					1740			
Ser	Ser	Asp	Thr	Tyr	Ala	Cys	Trp	Asn	His	Ser	Val	Gly	Phe	Asp
	1745					1750					1755			
Tyr	Val	Tyr	Asn	Pro	Phe	Met	Ile	Asp	Val	Gln	Gln	Trp	Gly	Phe
	1760					1765					1770			
Thr	Gly	Asn	Leu	Gln	Ser	Asn	His	Asp	Gln	His	Cys	Gln	Val	His
	1775					1780					1785			
Gly	Asn	Ala	His	Val	Ala	Ser	Cys	Asp	Ala	Ile	Met	Thr	Arg	Cys
	1790					1795					1800			
Leu	Ala	Val	His	Glu	Cys	Phe	Val	Lys	Arg	Val	Asp	Trp	Ser	Val
	1805					1810					1815			
Glu	Tyr	Pro	Ile	Ile	Gly	Asp	Glu	Leu	Arg	Val	Asn	Ser	Ala	Cys
	1820					1825					1830			
Arg	Lys	Val	Gln	His	Met	Val	Val	Lys	Ser	Ala	Leu	Leu	Ala	Asp
	1835					1840					1845			
Lys	Phe	Pro	Val	Leu	His	Asp	Ile	Gly	Asn	Pro	Lys	Ala	Ile	Lys
	1850					1855					1860			
Cys	Val	Pro	Gln	Ala	Glu	Val	Glu	Trp	Lys	Phe	Tyr	Asp	Ala	Gln
	1865					1870					1875			
Pro	Cys	Ser	Asp	Lys	Ala	Tyr	Lys	Ile	Glu	Glu	Leu	Phe	Tyr	Ser
	1880					1885					1890			
Tyr	Ala	Thr	His	His	Asp	Lys	Phe	Thr	Asp	Gly	Val	Cys	Leu	Phe
	1895					1900					1905			
Trp	Asn	Cys	Asn	Val	Asp	Arg	Tyr	Pro	Ala	Asn	Ala	Ile	Val	Cys
	1910					1915					1920			
Arg	Phe	Asp	Thr	Arg	Val	Leu	Ser	Asn	Leu	Asn	Leu	Pro	Gly	Cys
	1925					1930					1935			
Asp	Gly	Gly	Ser	Leu	Tyr	Val	Asn	Lys	His	Ala	Phe	His	Thr	Pro
	1940					1945					1950			
Ala	Phe	Asp	Lys	Ser	Ala	Phe	Thr	Asn	Leu	Lys	Gln	Leu	Pro	Phe

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1955	1960	1965
Phe Tyr Tyr Ser Asp Ser Pro 1970	Cys Glu Ser His Gly 1975	Lys Gln Val 1980
Val Ser Asp Ile Asp Tyr Val 1985	Pro Leu Lys Ser Ala 1990	Thr Cys Ile 1995
Thr Arg Cys Asn Leu Gly Gly 2000	Ala Val Cys Arg His 2005	His Ala Asn 2010
Glu Tyr Arg Gln Tyr Leu Asp 2015	Ala Tyr Asn Met Met 2020	Ile Ser Ala 2025
Gly Phe Ser Leu Trp Ile Tyr 2030	Lys Gln Phe Asp Thr 2035	Tyr Asn Leu 2040
Trp Asn Thr Phe Thr Arg Leu 2045	Gln Ser Leu Glu Asn 2050	Val Ala Tyr 2055
Asn Val Val Asn Lys Gly His 2060	Phe Asp Gly His Ala 2065	Gly Glu Ala 2070
Pro Val Ser Ile Ile Asn Asn 2075	Ala Val Tyr Thr Lys 2080	Val Asp Gly 2085
Ile Asp Val Glu Ile Phe Glu 2090	Asn Lys Thr Thr Leu 2095	Pro Val Asn 2100
Val Ala Phe Glu Leu Trp Ala 2105	Lys Arg Asn Ile Lys 2110	Pro Val Pro 2115
Glu Ile Lys Ile Leu Asn Asn 2120	Leu Gly Val Asp Ile 2125	Ala Ala Asn 2130
Thr Val Ile Trp Asp Tyr Lys 2135	Arg Glu Ala Pro Ala 2140	His Val Ser 2145
Thr Ile Gly Val Cys Thr Met 2150	Thr Asp Ile Ala Lys 2155	Lys Pro Thr 2160
Glu Ser Ala Cys Ser Ser Leu 2165	Thr Val Leu Phe Asp 2170	Gly Arg Val 2175
Glu Gly Gln Val Asp Leu Phe 2180	Arg Asn Ala Arg Asn 2185	Gly Val Leu 2190
Ile Thr Glu Gly Ser Val Lys 2195	Gly Leu Thr Pro Ser 2200	Lys Gly Pro 2205
Ala Gln Ala Ser Val Asn Gly 2210	Val Thr Leu Ile Gly 2215	Glu Ser Val 2220
Lys Thr Gln Phe Asn Tyr Phe 2225	Lys Lys Val Asp Gly 2230	Ile Ile Gln 2235
Gln Leu Pro Glu Thr Tyr Phe 2240	Thr Gln Ser Arg Asp 2245	Leu Glu Asp 2250
Phe Lys Pro Arg Ser Gln Met 2255	Glu Thr Asp Phe Leu 2260	Glu Leu Ala 2265
Met Asp Glu Phe Ile Gln Arg 2270	Tyr Lys Leu Glu Gly 2275	Tyr Ala Phe 2280
Glu His Ile Val Tyr Gly Asp 2285	Phe Ser His Gly Gln 2290	Leu Gly Gly 2295
Leu His Leu Met Ile Gly Leu 2300	Ala Lys Arg Ser Gln 2305	Asp Ser Pro 2310
Leu Lys Leu Glu Asp Phe Ile 2315	Pro Met Asp Ser Thr 2320	Val Lys Asn 2325
Tyr Phe Ile Thr Asp Ala Gln 2330	Thr Gly Ser Ser Lys 2335	Cys Val Cys 2340
Ser Val Ile Asp Leu Leu Leu 2345	Asp Asp Phe Val Glu 2350	Ile Ile Lys 2355

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Ser Gln Asp Leu Ser Val Ile Ser Lys Val Val Lys Val Thr Ile
 2360 2365 2370
 Asp Tyr Ala Glu Ile Ser Phe Met Leu Trp Cys Lys Asp Gly His
 2375 2380 2385
 Val Glu Thr Phe Tyr Pro Lys Leu Gln Ala Ser Gln Ala Trp Gln
 2390 2395 2400
 Pro Gly Val Ala Met Pro Asn Leu Tyr Lys Met Gln Arg Met Leu
 2405 2410 2415
 Leu Glu Lys Cys Asp Leu Gln Asn Tyr Gly Glu Asn Ala Val Ile
 2420 2425 2430
 Pro Lys Gly Ile Met Met Asn Val Ala Lys Tyr Thr Gln Leu Cys
 2435 2440 2445
 Gln Tyr Leu Asn Thr Leu Thr Leu Ala Val Pro Tyr Asn Met Arg
 2450 2455 2460
 Val Ile His Phe Gly Ala Gly Ser Asp Lys Gly Val Ala Pro Gly
 2465 2470 2475
 Thr Ala Val Leu Arg Gln Trp Leu Pro Thr Gly Thr Leu Leu Val
 2480 2485 2490
 Asp Ser Asp Leu Asn Asp Phe Val Ser Asp Ala Asp Ser Thr Leu
 2495 2500 2505
 Ile Gly Asp Cys Ala Thr Val His Thr Ala Asn Lys Trp Asp Leu
 2510 2515 2520
 Ile Ile Ser Asp Met Tyr Asp Pro Arg Thr Lys His Val Thr Lys
 2525 2530 2535
 Glu Asn Asp Ser Lys Glu Gly Phe Phe Thr Tyr Leu Cys Gly Phe
 2540 2545 2550
 Ile Lys Gln Lys Leu Ala Leu Gly Gly Ser Ile Ala Val Lys Ile
 2555 2560 2565
 Thr Glu His Ser Trp Asn Ala Asp Leu Tyr Lys Leu Met Gly His
 2570 2575 2580
 Phe Ser Trp Trp Thr Ala Phe Val Thr Asn Val Asn Ala Ser Ser
 2585 2590 2595
 Ser Glu Ala Phe Leu Ile Gly Ala Asn Tyr Leu Gly Lys Pro Lys
 2600 2605 2610
 Glu Gln Ile Asp Gly Tyr Thr Met His Ala Asn Tyr Ile Phe Trp
 2615 2620 2625
 Arg Asn Thr Asn Pro Ile Gln Leu Ser Ser Tyr Ser Leu Phe Asp
 2630 2635 2640
 Met Ser Lys Phe Pro Leu Lys Leu Arg Gly Thr Ala Val Met Ser
 2645 2650 2655
 Leu Lys Glu Asn Gln Ile Asn Asp Met Ile Tyr Ser Leu Leu Glu
 2660 2665 2670
 Lys Gly Arg Leu Ile Ile Arg Glu Asn Asn Arg Val Val Val Ser
 2675 2680 2685
 Ser Asp Ile Leu Val Asn Asn
 2690 2695

<210> SEQ ID NO 4

<211> LENGTH: 1255

<212> TYPE: PRT

<213> ORGANISM: Coronavirus

<400> SEQUENCE: 4

Met Phe Ile Phe Leu Leu Phe Leu Thr Leu Thr Ser Gly Ser Asp Leu

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1	5	10	15
Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln	20	25	30
His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg	35	40	45
Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser	50	55	60
Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val	65	70	80
Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn	85	90	95
Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln	100	105	110
Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys	115	120	125
Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met	130	135	140
Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn Ala Phe Asn Cys Thr	145	150	155
Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp Val Ser Glu Lys Ser	165	170	175
Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe Lys Asn Lys Asp Gly	180	185	190
Phe Leu Tyr Val Tyr Lys Gly Tyr Gln Pro Ile Asp Val Val Arg Asp	195	200	205
Leu Pro Ser Gly Phe Asn Thr Leu Lys Pro Ile Phe Lys Leu Pro Leu	210	215	220
Gly Ile Asn Ile Thr Asn Phe Arg Ala Ile Leu Thr Ala Phe Ser Pro	225	230	235
Ala Gln Asp Ile Trp Gly Thr Ser Ala Ala Ala Tyr Phe Val Gly Tyr	245	250	255
Leu Lys Pro Thr Thr Phe Met Leu Lys Tyr Asp Glu Asn Gly Thr Ile	260	265	270
Thr Asp Ala Val Asp Cys Ser Gln Asn Pro Leu Ala Glu Leu Lys Cys	275	280	285
Ser Val Lys Ser Phe Glu Ile Asp Lys Gly Ile Tyr Gln Thr Ser Asn	290	295	300
Phe Arg Val Val Pro Ser Gly Asp Val Val Arg Phe Pro Asn Ile Thr	305	310	315
Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Lys Phe Pro Ser	325	330	335
Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala Asp Tyr	340	345	350
Ser Val Leu Tyr Asn Ser Thr Phe Phe Ser Thr Phe Lys Cys Tyr Gly	355	360	365
Val Ser Ala Thr Lys Leu Asn Asp Leu Cys Phe Ser Asn Val Tyr Ala	370	375	380
Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg Gln Ile Ala Pro Gly	385	390	395
Gln Thr Gly Val Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe	405	410	415
Met Gly Cys Val Leu Ala Trp Asn Thr Arg Asn Ile Asp Ala Thr Ser	420	425	430

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Thr Gly Asn Tyr Asn Tyr Lys Tyr Arg Tyr Leu Arg His Gly Lys Leu
 435 440 445
 Arg Pro Phe Glu Arg Asp Ile Ser Asn Val Pro Phe Ser Pro Asp Gly
 450 455 460
 Lys Pro Cys Thr Pro Pro Ala Leu Asn Cys Tyr Trp Pro Leu Asn Asp
 465 470 475 480
 Tyr Gly Phe Tyr Thr Thr Thr Gly Ile Gly Tyr Gln Pro Tyr Arg Val
 485 490 495
 Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro Ala Thr Val Cys Gly
 500 505 510
 Pro Lys Leu Ser Thr Asp Leu Ile Lys Asn Gln Cys Val Asn Phe Asn
 515 520 525
 Phe Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Pro Ser Ser Lys Arg
 530 535 540
 Phe Gln Pro Phe Gln Gln Phe Gly Arg Asp Val Ser Asp Phe Thr Asp
 545 550 555 560
 Ser Val Arg Asp Pro Lys Thr Ser Glu Ile Leu Asp Ile Ser Pro Cys
 565 570 575
 Ser Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Ala Ser Ser
 580 585 590
 Glu Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Asp Val Ser Thr
 595 600 605
 Ala Ile His Ala Asp Gln Leu Thr Pro Ala Trp Arg Ile Tyr Ser Thr
 610 615 620
 Gly Asn Asn Val Phe Gln Thr Gln Ala Gly Cys Leu Ile Gly Ala Glu
 625 630 635 640
 His Val Asp Thr Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile
 645 650 655
 Cys Ala Ser Tyr His Thr Val Ser Leu Leu Arg Ser Thr Ser Gln Lys
 660 665 670
 Ser Ile Val Ala Tyr Thr Met Ser Leu Gly Ala Asp Ser Ser Ile Ala
 675 680 685
 Tyr Ser Asn Asn Thr Ile Ala Ile Pro Thr Asn Phe Ser Ile Ser Ile
 690 695 700
 Thr Thr Glu Val Met Pro Val Ser Met Ala Lys Thr Ser Val Asp Cys
 705 710 715 720
 Asn Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ala Asn Leu Leu Leu
 725 730 735
 Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Ser Gly Ile
 740 745 750
 Ala Ala Glu Gln Asp Arg Asn Thr Arg Glu Val Phe Ala Gln Val Lys
 755 760 765
 Gln Met Tyr Lys Thr Pro Thr Leu Lys Tyr Phe Gly Gly Phe Asn Phe
 770 775 780
 Ser Gln Ile Leu Pro Asp Pro Leu Lys Pro Thr Lys Arg Ser Phe Ile
 785 790 795 800
 Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly Phe Met
 805 810 815
 Lys Gln Tyr Gly Glu Cys Leu Gly Asp Ile Asn Ala Arg Asp Leu Ile
 820 825 830
 Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu Leu Thr
 835 840 845

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Asp Asp Met Ile Ala Ala Tyr Thr Ala Ala Leu Val Ser Gly Thr Ala
 850 855 860
 Thr Ala Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile Pro Phe
 865 870 875 880
 Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr Gln Asn
 885 890 895
 Val Leu Tyr Glu Asn Gln Lys Gln Ile Ala Asn Gln Phe Asn Lys Ala
 900 905 910
 Ile Ser Gln Ile Gln Glu Ser Leu Thr Thr Thr Ser Thr Ala Leu Gly
 915 920 925
 Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn Thr Leu
 930 935 940
 Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val Leu Asn
 945 950 955 960
 Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln Ile Asp
 965 970 975
 Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val Thr Gln
 980 985 990
 Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu Ala Ala
 995 1000 1005
 Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg Val Asp
 1010 1015 1020
 Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln Ala Ala
 1025 1030 1035
 Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro Ser Gln
 1040 1045 1050
 Glu Arg Asn Phe Thr Thr Ala Pro Ala Ile Cys His Glu Gly Lys
 1055 1060 1065
 Ala Tyr Phe Pro Arg Glu Gly Val Phe Val Phe Asn Gly Thr Ser
 1070 1075 1080
 Trp Phe Ile Thr Gln Arg Asn Phe Phe Ser Pro Gln Ile Ile Thr
 1085 1090 1095
 Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val Ile Gly
 1100 1105 1110
 Ile Ile Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu Leu Asp
 1115 1120 1125
 Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His Thr Ser
 1130 1135 1140
 Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala Ser Val
 1145 1150 1155
 Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val Ala Lys
 1160 1165 1170
 Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly Lys Tyr
 1175 1180 1185
 Glu Gln Tyr Ile Lys Trp Pro Trp Tyr Val Trp Leu Gly Phe Ile
 1190 1195 1200
 Ala Gly Leu Ile Ala Ile Val Met Val Thr Ile Leu Leu Cys Cys
 1205 1210 1215
 Met Thr Ser Cys Cys Ser Cys Leu Lys Gly Ala Cys Ser Cys Gly
 1220 1225 1230
 Ser Cys Cys Lys Phe Asp Glu Asp Asp Ser Glu Pro Val Leu Lys
 1235 1240 1245
 Gly Val Lys Leu His Tyr Thr

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1250 1255

<210> SEQ ID NO 5
 <211> LENGTH: 274
 <212> TYPE: PRT
 <213> ORGANISM: Coronavirus

<400> SEQUENCE: 5

Met Asp Leu Phe Met Arg Phe Phe Thr Leu Gly Ser Ile Thr Ala Gln
 1 5 10 15

Pro Val Lys Ile Asp Asn Ala Ser Pro Ala Ser Thr Val His Ala Thr
 20 25 30

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

Gly Val Ala Phe Leu Ala Val Phe Gln Ser Ala Thr Lys Ile Ile Ala
 50 55 60

Leu Asn Lys Arg Trp Gln Leu Ala Leu Tyr Lys Gly Phe Gln Phe Ile
 65 70 75 80

Cys Asn Leu Leu Leu Leu Phe Val Thr Ile Tyr Ser His Leu Leu Leu
 85 90 95

Val Ala Ala Gly Met Glu Ala Gln Phe Leu Tyr Leu Tyr Ala Leu Ile
 100 105 110

Tyr Phe Leu Gln Cys Ile Asn Ala Cys Arg Ile Ile Met Arg Cys Trp
 115 120 125

Leu Cys Trp Lys Cys Lys Ser Lys Asn Pro Leu Leu Tyr Asp Ala Asn
 130 135 140

Tyr Phe Val Cys Trp His Thr His Asn Tyr Asp Tyr Cys Ile Pro Tyr
 145 150 155 160

Asn Ser Val Thr Asp Thr Ile Val Val Thr Glu Gly Asp Gly Ile Ser
 165 170 175

Thr Pro Lys Leu Lys Glu Asp Tyr Gln Ile Gly Gly Tyr Ser Glu Asp
 180 185 190

Arg His Ser Gly Val Lys Asp Tyr Val Val Val His Gly Tyr Phe Thr
 195 200 205

Glu Val Tyr Tyr Gln Leu Glu Ser Thr Gln Ile Thr Thr Asp Thr Gly
 210 215 220

Ile Glu Asn Ala Thr Phe Phe Ile Phe Asn Lys Leu Val Lys Asp Pro
 225 230 235 240

Pro Asn Val Gln Ile His Thr Ile Asp Gly Ser Ser Gly Val Ala Asn
 245 250 255

Pro Ala Met Asp Pro Ile Tyr Asp Glu Pro Thr Thr Thr Thr Ser Val
 260 265 270

Pro Leu

<210> SEQ ID NO 6
 <211> LENGTH: 154
 <212> TYPE: PRT
 <213> ORGANISM: Coronavirus

<400> SEQUENCE: 6

Met Met Pro Thr Thr Leu Phe Ala Gly Thr His Ile Thr Met Thr Thr
 1 5 10 15

Val Tyr His Ile Thr Val Ser Gln Ile Gln Leu Ser Leu Leu Lys Val
 20 25 30

Thr Ala Phe Gln His Gln Asn Ser Lys Lys Thr Thr Lys Leu Val Val
 35 40 45

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Ile Leu Arg Ile Gly Thr Gln Val Leu Lys Thr Met Ser Leu Tyr Met
 50 55 60

Ala Ile Ser Pro Lys Phe Thr Thr Ser Leu Ser Leu His Lys Leu Leu
 65 70 75 80

Gln Thr Leu Val Leu Lys Met Leu His Ser Ser Leu Thr Ser Leu
 85 90 95

Leu Lys Thr His Arg Met Cys Lys Tyr Thr Gln Ser Thr Ala Leu Gln
 100 105 110

Glu Leu Leu Ile Gln Gln Trp Ile Gln Phe Met Met Ser Arg Arg Arg
 115 120 125

Leu Leu Ala Cys Leu Cys Lys His Lys Lys Val Ser Thr Asn Leu Cys
 130 135 140

Thr His Ser Phe Arg Lys Lys Gln Val Arg
 145 150

<210> SEQ ID NO 7
 <211> LENGTH: 76
 <212> TYPE: PRT
 <213> ORGANISM: Coronavirus

<400> SEQUENCE: 7

Met Tyr Ser Phe Val Ser Glu Glu Thr Gly Thr Leu Ile Val Asn Ser
 1 5 10 15

Val Leu Leu Phe Leu Ala Phe Val Val Phe Leu Leu Val Thr Leu Ala
 20 25 30

Ile Leu Thr Ala Leu Arg Leu Cys Ala Tyr Cys Cys Asn Ile Val Asn
 35 40 45

Val Ser Leu Val Lys Pro Thr Val Tyr Val Tyr Ser Arg Val Lys Asn
 50 55 60

Leu Asn Ser Ser Glu Gly Val Pro Asp Leu Leu Val
 65 70 75

<210> SEQ ID NO 8
 <211> LENGTH: 221
 <212> TYPE: PRT
 <213> ORGANISM: Coronavirus

<400> SEQUENCE: 8

Met Ala Asp Asn Gly Thr Ile Thr Val Glu Glu Leu Lys Gln Leu Leu
 1 5 10 15

Glu Gln Trp Asn Leu Val Ile Gly Phe Leu Phe Leu Ala Trp Ile Met
 20 25 30

Leu Leu Gln Phe Ala Tyr Ser Asn Arg Asn Arg Phe Leu Tyr Ile Ile
 35 40 45

Lys Leu Val Phe Leu Trp Leu Leu Trp Pro Val Thr Leu Ala Cys Phe
 50 55 60

Val Leu Ala Ala Val Tyr Arg Ile Asn Trp Val Thr Gly Gly Ile Ala
 65 70 75 80

Ile Ala Met Ala Cys Ile Val Gly Leu Met Trp Leu Ser Tyr Phe Val
 85 90 95

Ala Ser Phe Arg Leu Phe Ala Arg Thr Arg Ser Met Trp Ser Phe Asn
 100 105 110

Pro Glu Thr Asn Ile Leu Leu Asn Val Pro Leu Arg Gly Thr Ile Val
 115 120 125

Thr Arg Pro Leu Met Glu Ser Glu Leu Val Ile Gly Ala Val Ile Ile
 130 135 140

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Arg Gly His Leu Arg Met Ala Gly His Pro Leu Gly Arg Cys Asp Ile
 145 150 155 160

Lys Asp Leu Pro Lys Glu Ile Thr Val Ala Thr Ser Arg Thr Leu Ser
 165 170 175

Tyr Tyr Lys Leu Gly Ala Ser Gln Arg Val Gly Thr Asp Ser Gly Phe
 180 185 190

Ala Ala Tyr Asn Arg Tyr Arg Ile Gly Asn Tyr Lys Leu Asn Thr Asp
 195 200 205

His Ala Gly Ser Asn Asp Asn Ile Ala Leu Leu Val Gln
 210 215 220

<210> SEQ ID NO 9
 <211> LENGTH: 63
 <212> TYPE: PRT
 <213> ORGANISM: Coronavirus

<400> SEQUENCE: 9

Met Phe His Leu Val Asp Phe Gln Val Thr Ile Ala Glu Ile Leu Ile
 1 5 10 15

Ile Ile Met Arg Thr Phe Arg Ile Ala Ile Trp Asn Leu Asp Val Ile
 20 25 30

Ile Ser Ser Ile Val Arg Gln Leu Phe Lys Pro Leu Thr Lys Lys Asn
 35 40 45

Tyr Ser Glu Leu Asp Asp Glu Glu Pro Met Glu Leu Asp Tyr Pro
 50 55 60

<210> SEQ ID NO 10
 <211> LENGTH: 122
 <212> TYPE: PRT
 <213> ORGANISM: Coronavirus

<400> SEQUENCE: 10

Met Lys Ile Ile Leu Phe Leu Thr Leu Ile Val Phe Thr Ser Cys Glu
 1 5 10 15

Leu Tyr His Tyr Gln Glu Cys Val Arg Gly Thr Thr Val Leu Leu Lys
 20 25 30

Glu Pro Cys Pro Ser Gly Thr Tyr Glu Gly Asn Ser Pro Phe His Pro
 35 40 45

Leu Ala Asp Asn Lys Phe Ala Leu Thr Cys Thr Ser Thr His Phe Ala
 50 55 60

Phe Ala Cys Ala Asp Gly Thr Arg His Thr Tyr Gln Leu Arg Ala Arg
 65 70 75 80

Ser Val Ser Pro Lys Leu Phe Ile Arg Gln Glu Glu Val Gln Gln Glu
 85 90 95

Leu Tyr Ser Pro Leu Phe Leu Ile Val Ala Ala Leu Val Phe Leu Ile
 100 105 110

Leu Cys Phe Thr Ile Lys Arg Lys Thr Glu
 115 120

<210> SEQ ID NO 11
 <211> LENGTH: 84
 <212> TYPE: PRT
 <213> ORGANISM: Coronavirus

<400> SEQUENCE: 11

Met Cys Leu Lys Ile Leu Val Arg Tyr Asn Thr Arg Gly Asn Thr Tyr
 1 5 10 15

-continued

Ser Thr Ala Trp Leu Cys Ala Leu Gly Lys Val Leu Pro Phe His Arg
 20 25 30
 Trp His Thr Met Val Gln Thr Cys Thr Pro Asn Val Thr Ile Asn Cys
 35 40 45
 Gln Asp Pro Ala Gly Gly Ala Leu Ile Ala Arg Cys Trp Tyr Leu His
 50 55 60
 Glu Gly His Gln Thr Ala Ala Phe Arg Asp Val Leu Val Val Leu Asn
 65 70 75 80
 Lys Arg Thr Asn

<210> SEQ ID NO 12
 <211> LENGTH: 422
 <212> TYPE: PRT
 <213> ORGANISM: Coronavirus

<400> SEQUENCE: 12

Met Ser Asp Asn Gly Pro Gln Ser Asn Gln Arg Ser Ala Pro Arg Ile
 1 5 10 15
 Thr Phe Gly Gly Pro Thr Asp Ser Thr Asp Asn Asn Gln Asn Gly Gly
 20 25 30
 Arg Asn Gly Ala Arg Pro Lys Gln Arg Arg Pro Gln Gly Leu Pro Asn
 35 40 45
 Asn Thr Ala Ser Trp Phe Thr Ala Leu Thr Gln His Gly Lys Glu Glu
 50 55 60
 Leu Arg Phe Pro Arg Gly Gln Gly Val Pro Ile Asn Thr Asn Ser Gly
 65 70 75 80
 Pro Asp Asp Gln Ile Gly Tyr Tyr Arg Arg Ala Thr Arg Arg Val Arg
 85 90 95
 Gly Gly Asp Gly Lys Met Lys Glu Leu Ser Pro Arg Trp Tyr Phe Tyr
 100 105 110
 Tyr Leu Gly Thr Gly Pro Glu Ala Ser Leu Pro Tyr Gly Ala Asn Lys
 115 120 125
 Glu Gly Ile Val Trp Val Ala Thr Glu Gly Ala Leu Asn Thr Pro Lys
 130 135 140
 Asp His Ile Gly Thr Arg Asn Pro Asn Asn Asn Ala Ala Thr Val Leu
 145 150 155 160
 Gln Leu Pro Gln Gly Thr Thr Leu Pro Lys Gly Phe Tyr Ala Glu Gly
 165 170 175
 Ser Arg Gly Gly Ser Gln Ala Ser Ser Arg Ser Ser Ser Arg Ser Arg
 180 185 190
 Gly Asn Ser Arg Asn Ser Thr Pro Gly Ser Ser Arg Gly Asn Ser Pro
 195 200 205
 Ala Arg Met Ala Ser Gly Gly Glu Thr Ala Leu Ala Leu Leu Leu
 210 215 220
 Leu Asp Arg Leu Asn Gln Leu Glu Ser Lys Val Ser Gly Lys Gly Gln
 225 230 235 240
 Gln Gln Gln Gly Gln Thr Val Thr Lys Lys Ser Ala Ala Glu Ala Ser
 245 250 255
 Lys Lys Pro Arg Gln Lys Arg Thr Ala Thr Lys Gln Tyr Asn Val Thr
 260 265 270
 Gln Ala Phe Gly Arg Arg Gly Pro Glu Gln Thr Gln Gly Asn Phe Gly
 275 280 285
 Asp Gln Asp Leu Ile Arg Gln Gly Thr Asp Tyr Lys His Trp Pro Gln
 290 295 300

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Ile Ala Gln Phe Ala Pro Ser Ala Ser Ala Phe Phe Gly Met Ser Arg
 305 310 315 320

Ile Gly Met Glu Val Thr Pro Ser Gly Thr Trp Leu Thr Tyr His Gly
 325 330 335

Ala Ile Lys Leu Asp Asp Lys Asp Pro Gln Phe Lys Asp Asn Val Ile
 340 345 350

Leu Leu Asn Lys His Ile Asp Ala Tyr Lys Thr Phe Pro Pro Thr Glu
 355 360 365

Pro Lys Lys Asp Lys Lys Lys Lys Thr Asp Glu Ala Gln Pro Leu Pro
 370 375 380

Gln Arg Gln Lys Lys Gln Pro Thr Val Thr Leu Leu Pro Ala Ala Asp
 385 390 395 400

Met Asp Asp Phe Ser Arg Gln Leu Gln Asn Ser Met Ser Gly Ala Ser
 405 410 415

Ala Asp Ser Thr Gln Ala
 420

<210> SEQ ID NO 13
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic oligonucleotide.

<400> SEQUENCE: 13

ctaacatgct taggataatg g

21

<210> SEQ ID NO 14
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic oligonucleotide.

<400> SEQUENCE: 14

gectctcttg ttcttgctcg c

21

<210> SEQ ID NO 15
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic oligonucleotide.

<400> SEQUENCE: 15

caggtagcg taaaactcat c

21

<210> SEQ ID NO 16
 <211> LENGTH: 22
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic oligonucleotide.

<400> SEQUENCE: 16

catgtgtggc ggctcactat at

22

<210> SEQ ID NO 17
 <211> LENGTH: 28
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic oligonucleotide.

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<400> SEQUENCE: 17
gacactatta gcataagcag ttgtagca 28

<210> SEQ ID NO 18
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide.

<400> SEQUENCE: 18
ttaaaccagg tggaacatca tccggtg 27

<210> SEQ ID NO 19
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide.

<400> SEQUENCE: 19
ggagccttga atacacccaa ag 22

<210> SEQ ID NO 20
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide.

<400> SEQUENCE: 20
gcacggtggc agcattg 17

<210> SEQ ID NO 21
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide.

<400> SEQUENCE: 21
ccacattggc acccgcaatc c 21

<210> SEQ ID NO 22
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide.

<400> SEQUENCE: 22
caaacattgg cgcgaaatt 19

<210> SEQ ID NO 23
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide.

<400> SEQUENCE: 23
caatgcgtga cattccaaag a 21

<210> SEQ ID NO 24

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<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide.

<400> SEQUENCE: 24

cacaatttgc tccaagtgcc tctgca 26

<210> SEQ ID NO 25
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide.

<400> SEQUENCE: 25

gaagtacat ctggggctga g 21

<210> SEQ ID NO 26
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide.

<400> SEQUENCE: 26

ccgaagagct acccgacg 18

<210> SEQ ID NO 27
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide.

<400> SEQUENCE: 27

ctctttcatt ttgccgtcac caccac 26

<210> SEQ ID NO 28
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide.

<400> SEQUENCE: 28

agctctccct agcattattc actg 24

<210> SEQ ID NO 29
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide.

<400> SEQUENCE: 29

caccacattt tcatcgaggc 20

<210> SEQ ID NO 30
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide.

<400> SEQUENCE: 30

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taccctcgat cgtactccgc gt 22

<210> SEQ ID NO 31
 <211> LENGTH: 23
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic oligonucleotide.

<400> SEQUENCE: 31

tgtaggcact gattcagggtt ttg 23

<210> SEQ ID NO 32
 <211> LENGTH: 23
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic oligonucleotide.

<400> SEQUENCE: 32

cggcgtggtc tgtatttaaat tta 23

<210> SEQ ID NO 33
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic oligonucleotide.

<400> SEQUENCE: 33

ctgcatacaa ccgctaccgt attggaa 27

<210> SEQ ID NO 34
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic oligonucleotide.

<400> SEQUENCE: 34

gggttggac tatectaagt gtga 24

<210> SEQ ID NO 35
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic oligonucleotide.

<220> FEATURE:

<221> NAME/KEY: misc.feature

<222> LOCATION: (12)..(12)

<223> OTHER INFORMATION: "n" equals inosine.

<400> SEQUENCE: 35

taacacaaa cncatcatc a 21

<210> SEQ ID NO 36
 <211> LENGTH: 19
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic oligonucleotide.

<400> SEQUENCE: 36

agatttggac ctgagagcg 19

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<210> SEQ ID NO 37
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide.

<400> SEQUENCE: 37

gagcggctgt ctccacaagt

20

<210> SEQ ID NO 38
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide.

<400> SEQUENCE: 38

ttctgacctg aaggctctgc gcg

23

We claim:

1. An isolated nucleic acid molecule consisting of the²⁵
nucleotide sequence as set forth in SEQ ID NO: 1.

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