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(54) Title: IMMUNOGENS DERIVED FROM SARS-COV2 SPIKE PROTEIN

SARS-CoV-2 Spike shows 2 main conformations: Pre and Post-fusion State

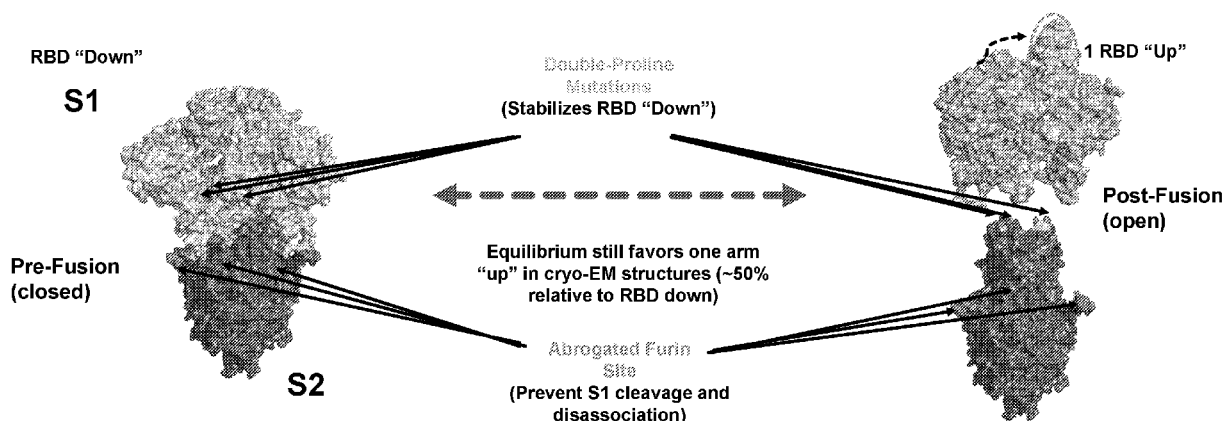


Fig. 1

(57) Abstract: The present invention relates to severe acute respiratory syndrome coronavirus 2 ("SARS-CoV2") immunogens useful for the generation of therapeutic antibodies and vaccine development. Such therapeutic antibodies include human antibodies and antigen-binding portions thereof that specifically bind to human SARS-CoV2 S protein, and that function to neutralize SARS-CoV2. The present invention also relates to methods of generating antibodies and antigen-binding portions thereof that specifically bind to human SARS-CoV2 S protein.

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IMMUNOGENS DERIVED FROM SARS-COV2 SPIKE PROTEIN

SEQUENCE LISTING

[0001] The present application is being filed along with a sequence listing in electronic format. The sequence listing is provided as a file entitled A-2657-WO-PCT_SeqList_07212021_ST25, created on July 21, 2021, which is 873 KB in size. The information in the electronic format of the sequence listing is incorporated herein by reference in its entirety.

BACKGROUND OF THE INVENTION

[0002] With the rise of COVID-19, the SARS CoV-2 spike (S) glycoprotein is a popular target for neutralizing antibodies and vaccine development. SARS-CoV2 mediates infection of target cells via the spike (S) protein expressed on the surface. The SARS CoV-2 Spike glycoprotein exists as a homotrimer, where each protomer consists of an N-terminal domain (NTD), Receptor Binding Domain (RBD), and S2 subunit. The NTD and RBD are part of the larger S1 subunit, which dissociates from the S2 subunit after binding ACE2 on the host cell. This induces global conformational change, leading to viral entry into the host cell. The three RBDs in the S protein trimer can exist in an “open” and “closed” configuration, but is sterically prevented from binding ACE2 in the “closed” conformation. Thus, the closed conformation is often described as the prefusion state and the open conformation is thought to be the initiation of the postfusion state, leading to S1 instability and dissociation.

[0003] The dynamic nature of the native S glycoprotein and structural transitions between pre- and postfusion states represent a challenge for prefusion targeting. With the dynamic nature of the S protein, there is a need and interest in stabilizing and further driving the S protein into the RBD-down, “prefusion” conformation. The present invention describes viable disulfides between the S1 and S2 subunits to produce several candidates to achieve the desired result of increased stability and conformational homogeneity.

SUMMARY OF THE INVENTION

[0004] In certain aspects, the disclosure provides an immunogen comprising a severe acute respiratory syndrome coronavirus 2 spike (“SARS-CoV2 S”) polypeptide, wherein the polypeptide comprises one or more pairs of amino acid substitutions that correspond to residues selected from the group consisting of:

- a) V382C and R983C of SEQ ID NO: 1;
- b) A520C and K41C of SEQ ID NO: 1;
- c) S383C and D985C of SEQ ID NO: 1;

- d) D614C and T859C of SEQ ID NO: 1;
- e) T547C and N978C of SEQ ID NO: 1;
- f) A570C and V963C of SEQ ID NO: 1;
- g) P665C and L864C of SEQ ID NO: 1;
- h) F562C and P225C of SEQ ID NO: 1; and
- i) P589C and F855C of SEQ ID NO: 1;

and wherein the polypeptide is 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, and 98% identical to SEQ ID NO: 1.

[0005] In certain aspects, the disclosure provides an immunogen comprising a severe acute respiratory syndrome coronavirus 2 spike (“SARS-CoV2 S”) polypeptide, wherein the polypeptide comprises one or more pairs of amino acid substitutions that correspond to residues selected from the group consisting of:

- a) V382C and R983C of SEQ ID NO: 1;
- b) A520C and K41C of SEQ ID NO: 1;
- c) S383C and D985C of SEQ ID NO: 1;
- d) D614C and T859C of SEQ ID NO: 1;
- e) T547C and N978C of SEQ ID NO: 1;
- f) A570C and V963C of SEQ ID NO: 1;
- g) P665C and L864C of SEQ ID NO: 1;
- h) F562C and P225C of SEQ ID NO: 1; and
- i) P589C and F855C of SEQ ID NO: 1.

[0006] In certain embodiments, the polypeptide comprises amino acid substitutions that correspond to residues D614C, T859C, T547C and N978C.

[0007] In certain embodiments, the polypeptide further comprises one or more groups of amino acid substitutions that correspond to residues selected from the group consisting of:

- a) K986P and V987P of SEQ ID NO: 1;
- b) R682G, R683S, and R685S of SEQ ID NO: 1;
- c) R682S, R683G, and R685G of SEQ ID NO: 1;
- d) R682G, R683S, R685S, K986P and V987P of SEQ ID NO: 1; and
- e) R682S, R683G, R685G, K986P and V987P of SEQ ID NO: 1.

[0008] In certain embodiments, the polypeptide has at least 97% sequence identity to SEQ ID NO: 1.

[0009] In certain embodiments, the polypeptide has at least 98% sequence identity to SEQ ID NO: 1.

[0010] In certain embodiments, the polypeptide has at least 99% sequence identity to SEQ ID NO: 1.

[0011] In certain embodiments, the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 13-21.

[0012] In certain embodiments, the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 4-12 and 44-61.

[0013] In certain embodiments, the polypeptide comprises a trimerization domain attached to the C-terminus of the immunogen.

[0014] In certain embodiments, the trimerization domain comprises the amino acid sequence of SEQ ID NO: 84 or SEQ ID NO: 85.

[0015] In certain embodiments, the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 23-40 and 63-80.

[0016] In certain aspects, the disclosure provides a method of producing antibodies that specifically bind SARS-CoV2 S polypeptide comprising administering to a non-human subject an immunogen of the present invention and a pharmaceutically acceptable delivery vehicle and/or adjuvant.

[0017] In certain aspects, the disclosure provides a method of treating COVID-19 in a subject comprising administering a therapeutically effective amount of an antibody produced by a method of the present invention and a pharmaceutically acceptable delivery vehicle to the subject.

[0018] In certain aspects, the disclosure provides a composition capable of producing an immunological response in a human subject, the composition comprising an immunogen of the present invention and a pharmaceutically acceptable delivery vehicle and/or adjuvant.

[0019] The invention contemplates combinations of any of the foregoing aspects and embodiments of the invention.

BRIEF DESCRIPTION OF THE DRAWINGS

[0020] Fig. 1 depicts how the SARS-CoV-2 spike protein shows 2 main conformations: pre and post-fusion state.

[0021] Fig. 2 depicts various engineered disulfides and where they are located within the spike trimer.

[0022] Fig. 3 depicts the positions and structural design of RCC1.

[0023] Fig. 4 depicts the positions and structural design of RCC2.

[0024] Fig. 5 depicts the positions and structural design of RCC3.

[0025] Fig. 6 depicts the positions and structural design of RCC4.

[0026] Fig. 7 depicts the positions and structural design of RCC5.

[0027] Fig. 8 depicts the positions and structural design of RCC6.

[0028] Fig. 9 depicts the positions and structural design of RCC7.

[0029] Fig. 10 depicts the positions and structural design of RCC8.

[0030] Fig. 11 depicts the positions and structural design of RCC9.

DETAILED DESCRIPTION OF THE INVENTION

[0031] Unless otherwise defined herein, scientific and technical terms used in connection with the present invention shall have the meanings that are commonly understood by those of ordinary skill in the art. Further, unless otherwise required by context, singular terms shall include pluralities and plural terms shall include the singular. Generally, nomenclature used in connection with, and techniques of, cell and tissue culture, molecular biology, immunology, microbiology, genetics and protein and nucleic acid chemistry and hybridization described herein are those well known and commonly used in the art.

[0032] The methods and techniques of the present invention are generally performed according to conventional methods well known in the art and as described in various general and more specific references that are cited and discussed throughout the present specification unless otherwise indicated. See, e.g., Sambrook et al. *Molecular Cloning: A Laboratory Manual*, second ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989) and Ausubel et al, *Current Protocols in Molecular Biology*, Greene Publishing Associates (1992), and Harlow and Lane *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1990), incorporated herein by reference. Enzymatic reactions and purification techniques are performed according to manufacturer's specifications, as commonly accomplished in the art or as described herein. The nomenclature used in connection with, and the laboratory procedures and techniques of, analytical chemistry, synthetic organic chemistry, and medicinal and pharmaceutical chemistry described herein are those well known and commonly used in the art. Standard techniques are used for chemical syntheses, chemical analyses, pharmaceutical preparation, formulation, and delivery, and treatment of patients.

[0033] The following terms, unless otherwise indicated, shall be understood to have the following meanings:

[0034] The term "polypeptide" encompasses native or artificial proteins, protein fragments and polypeptide analogs of a protein sequence. A polypeptide may be monomeric or polymeric.

[0035] The term "isolated protein", "isolated polypeptide" or "isolated antibody" is a protein, polypeptide or antibody that by virtue of its origin or source of derivation (1) is not associated with naturally associated components that accompany it in its native state, (2) is free of other proteins from the same species, (3) is expressed by a cell from a different species, or (4) does not occur in nature. Thus, a polypeptide that is chemically synthesized or synthesized in a cellular system different from the cell from which it naturally originates will be "isolated" from its naturally associated components. A protein may also be rendered substantially free of naturally-associated components by isolation, using protein purification techniques well known in the art.

[0036] A protein or polypeptide is "substantially pure," "substantially homogeneous," or "substantially purified" when at least about 60 to 75% of a sample exhibits a single species of polypeptide. The polypeptide or protein may be monomeric or multimeric. A substantially pure polypeptide or protein will typically comprise about 50%, 60%, 70%, 80% or 90% W/W of a protein sample, more usually about 95%, and preferably will be over 99% pure. Protein purity or homogeneity may be indicated by a number of means well known in the art, such as polyacrylamide gel electrophoresis of a protein sample, followed by visualizing a single polypeptide band upon staining the gel with a stain well known in the art. For certain purposes, higher resolution may be provided by using HPLC or other means well known in the art for purification.

[0037] The term "polypeptide fragment" as used herein refers to a polypeptide that has an amino-terminal and/or carboxy-terminal deletion, but where the remaining amino acid sequence is identical to the corresponding positions in the naturally-occurring sequence. In some embodiments, fragments are at least 5, 6, 8 or 10 amino acids long. In other embodiments, the fragments are at least 14, at least 20, at least 50, or at least 70, 80, 90, 100, 150 or 200 amino acids long.

[0038] The term "immunogen" means a molecule, often a polypeptide, which, when presented to the immune system of a healthy animal to which the molecule is foreign, will elicit some form of immune response against the molecule or a cell, or other organism, displaying the molecule.

[0039] The term "antigen" means an immunogen in which, at least part of, the immune response consists of the production of antibodies against the immunogen.

[0040] Examples of isolated antibodies include an anti- SARS-CoV2 S protein antibody that has been affinity purified using SARS-CoV2 S protein or a portion thereof, an anti- SARS-CoV2 S protein antibody that has been synthesized by a hybridoma or other cell line in vitro, and a human anti- SARS-CoV2 S protein antibody derived from a transgenic mouse.

[0041] In certain embodiments, amino acid substitutions to an anti- SARS-CoV2 S polypeptide are those which: (1) reduce susceptibility to proteolysis, (2) reduce susceptibility to oxidation, (3) alter binding affinity for forming protein complexes, and (4) confer or modify other physicochemical or functional properties of such analogs, but still retain its conformation and ability to act as an immunogen. Analogs can include various muteins of a sequence other than the normally-occurring peptide sequence. For example, single or multiple amino acid substitutions, preferably conservative amino acid substitutions, may be made in the normally-occurring sequence, preferably in the portion of the polypeptide outside the domain(s) forming intermolecular contacts. A conservative amino acid substitution should not substantially change the structural characteristics of the parent sequence; e.g., a replacement amino acid should not alter the anti-parallel β -sheet that makes up the immunoglobulin binding domain that occurs in the parent sequence, or disrupt other types of secondary structure that characterizes the parent sequence. In general, glycine and

proline would not be used in an anti-parallel β -sheet. Examples of art-recognized polypeptide secondary and tertiary structures are described in *Proteins, Structures and Molecular Principles* (Creighton, Ed., W. H. Freeman and Company, New York (1984)); *Introduction to Protein Structure* (C. Branden and J. Tooze, eds., Garland Publishing, New York, N.Y. (1991)); and Thornton et al, *Nature* 354:105 (1991), incorporated herein by reference.

[0042] Where an "antibody" is referred to herein with respect to the invention, it is normally understood that an antigen-binding portion thereof may also be used. An antigen-binding portion competes with the intact antibody for specific binding. See generally, *Fundamental Immunology*, Ch. 7 (Paul, W., ed., second ed. Raven Press, N.Y. (1989)) (incorporated by reference in its entirety for all purposes). Antigen-binding portions may be produced by recombinant DNA techniques or by enzymatic or chemical cleavage of intact antibodies. In some embodiments, antigen-binding portions include Fab, Fab', F(ab')₂, Fd, Fv, , and complementarity determining region (CDR) fragments. Single-chain antibodies (scFv), chimeric antibodies, diabodies and polypeptides that contain at least a portion of an antibody that is sufficient to confer specific antigen binding to the polypeptide can also be prepared.

[0043] From N-terminus to C-terminus, both the mature light and heavy chain variable domains comprise the regions FR1, CDR1, FR2, CDR2, FR3, CDR3 and FR4. The assignment of amino acids to each domain herein is in accordance with the definitions of Kabat, *Sequences of Proteins of Immunological Interest* (National Institutes of Health, Bethesda, Md. (1987 and 1991)), Chothia & Lesk, *J Mol Biol.* 196:901-917 (1987) or Chothia et al, *Nature* 342:878-883 (1989).

[0044] As used herein, a Fd fragment means an antibody fragment that consists of the VH and CH 1 domains; an Fv fragment consists of the VL and VH domains of a single arm of an antibody; and a dAb fragment (Ward et al, *Nature* 341 :544-546 (1989)) consists of a VH domain.

[0045] The term "polynucleotide" as referred to herein means a polymeric form of nucleotides of at least 10 bases in length, either ribonucleotides or deoxynucleotides or a modified form of either type of nucleotide. The term includes single and double stranded forms.

[0046] The term "isolated polynucleotide" as used herein means a polynucleotide of genomic, cDNA, or synthetic origin or some combination thereof, which by virtue of its origin the "isolated polynucleotide" (1) is not associated with all or a portion of a polynucleotides with which the "isolated polynucleotide" is found in nature, (2) is operably linked to a polynucleotide to which it is not linked in nature, or (3) does not occur in nature as part of a larger sequence.

[0047] The term "naturally occurring nucleotides" as used herein includes deoxyribonucleotides and ribonucleotides. The term "modified nucleotides" as used herein includes nucleotides with modified or substituted sugar groups and the like. The term "oligonucleotide linkages" referred to herein includes oligonucleotides linkages such as phosphorothioate, phosphorodithioate, phosphoroselenoate,

phosphorodiselenoate, phosphoroanilothioate, phosphoraniladate, phosphoroamidate, and the like. See e.g., LaPlanche et al., Nucl. Acids Res. 14:9081 (1986); Stec et al, J. Am. Chem. Soc. 106:6077 (1984); Stein et al., Nucl. Acids Res. 16:3209 (1988); Zon et al., Anti-Cancer Drug Design 6:539 (1991); Zon et al., Oligonucleotides and Analogues: A Practical Approach, pp. 87-108 (F. Eckstein, Ed., Oxford University Press, Oxford England (1991)); U.S. Patent No. 5,151,510; Uhlmann and Peyman, Chemical Reviews 90:543 (1990), the disclosures of which are hereby incorporated by reference. An oligonucleotide can include a label for detection, if desired.

[0048] "Operably linked" sequences include both expression control sequences that are contiguous with the gene of interest and expression control sequences that act in trans or at a distance to control the gene of interest. The term "expression control sequence" as used herein means polynucleotide sequences that are necessary to effect the expression and processing of coding sequences to which they are ligated. Expression control sequences include appropriate transcription initiation, termination, promoter and enhancer sequences; efficient RNA processing signals such as splicing and polyadenylation signals; sequences that stabilize cytoplasmic mRNA; sequences that enhance translation efficiency (i.e., Kozak consensus sequence); sequences that enhance protein stability; and when desired, sequences that enhance protein secretion. The nature of such control sequences differs depending upon the host organism; in prokaryotes, such control sequences generally include promoter, ribosomal binding site, and transcription termination sequence; in eukaryotes, generally, such control sequences include promoters and transcription termination sequence. The term "control sequences" is intended to include, at a minimum, all components whose presence is essential for expression and processing, and can also include additional components whose presence is advantageous, for example, leader sequences and fusion partner sequences.

[0049] The term "vector", as used herein, means a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. In some embodiments, the vector is a plasmid, i.e., a circular double stranded piece of DNA into which additional DNA segments may be ligated. In some embodiments, the vector is a viral vector, wherein additional DNA segments may be ligated into the viral genome. In some embodiments, the vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). In other embodiments, the vectors (e.g., non-episomal mammalian vectors) can be integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "recombinant expression vectors" (or simply, "expression vectors").

[0050] The term "recombinant host cell" (or simply "host cell"), as used herein, means a cell into which a recombinant expression vector has been introduced. It should be understood that "recombinant host cell"

and "host cell" mean not only the particular subject cell but also the progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term "host cell" as used herein.

[0051] The term "selectively hybridize" referred to herein means to detectably and specifically bind. Polynucleotides, oligonucleotides and fragments thereof in accordance with the invention selectively hybridize to nucleic acid strands under hybridization and wash conditions that minimize appreciable amounts of detectable binding to nonspecific nucleic acids. "High stringency" or "highly stringent" conditions can be used to achieve selective hybridization conditions as known in the art and discussed herein. One example of "high stringency" or "highly stringent" conditions is the incubation of a polynucleotide with another polynucleotide, wherein one polynucleotide may be affixed to a solid surface such as a membrane, in a hybridization buffer of 6X SSPE or SSC, 50% formamide, 5X Denhardt's reagent, 0.5% SDS, 100 µg/ml denatured, fragmented salmon sperm DNA at a hybridization temperature of 42°C for 12-16 hours, followed by twice washing at 55°C using a wash buffer of 1X SSC, 0.5% SDS. See also Sambrook et al, supra, pp. 9.50-9.55.

[0052] The term "percent sequence identity" in the context of nucleotide sequences means the residues in two sequences that are the same when aligned for maximum correspondence. The length of sequence identity comparison may be over a stretch of at least about nine nucleotides, usually at least about 18 nucleotides, more usually at least about 24 nucleotides, typically at least about 28 nucleotides, more typically at least about 32 nucleotides, and preferably at least about 36, 48 or more nucleotides. There are a number of different algorithms known in the art which can be used to measure nucleotide sequence identity. For instance, polynucleotide sequences can be compared using FASTA, Gap or Bestfit, which are programs in Wisconsin Package Version 10.0, Genetics Computer Group (GCG), Madison, Wisconsin. FASTA, which includes, e.g., the programs FASTA2 and FASTA3, provides alignments and percent sequence identity of the regions of the best overlap between the query and search sequences (Pearson, Methods Enzymol. 183:63-98 (1990); Pearson, Methods Mol. Biol. 132:185-219 (2000); Pearson, Methods Enzymol. 266:227-258 (1996); Pearson, J Mol. Biol. 276:71-84 (1998); incorporated herein by reference). Unless otherwise specified, default parameters for a particular program or algorithm are used. For instance, percent sequence identity between nucleotide sequences can be determined using FASTA with its default parameters (a word size of 6 and the

[0053] NOPAM factor for the scoring matrix) or using Gap with its default parameters as provided in GCG Version 6.1, incorporated herein by reference.

[0054] A reference to a nucleotide sequence encompasses its complement unless otherwise specified. Thus, a reference to a nucleic acid having a particular sequence should be understood to encompass its complementary strand, with its complementary sequence.

[0055] As used herein, the terms "percent sequence identity" and "percent sequence homology" are used interchangeably.

[0056] The term "substantial similarity" or "substantial sequence similarity," when referring to a nucleic acid or fragment thereof, means that when optimally aligned with appropriate nucleotide insertions or deletions with another nucleic acid (or its complementary strand), there is nucleotide sequence identity in at least about 85%, preferably at least about 90%, and more preferably at least about 95%, 96%, 97%, 98% or 99% of the nucleotide bases, as measured by any well-known algorithm of sequence identity, such as FASTA, BLAST or Gap, as discussed above.

[0057] As applied to polypeptides, the term "substantial identity" means that two peptide sequences, when optimally aligned, such as by the programs GAP or BESTFIT using default gap weights as supplied with the programs, share at least 70%, 75% or 80% sequence identity, preferably at least 90% or 95% sequence identity, and more preferably at least 97%, 98% or 99% sequence identity. In certain embodiments, residue positions that are not identical differ by conservative amino acid substitutions. A "conservative amino acid substitution" is one in which an amino acid residue is substituted by another amino acid residue having a side chain R group with similar chemical properties (e.g., charge or hydrophobicity). In general, a conservative amino acid substitution will not substantially change the functional properties of a protein. In cases where two or more amino acid sequences differ from each other by conservative substitutions, the percent sequence identity may be adjusted upwards to correct for the conservative nature of the substitution. Means for making this adjustment are well-known to those of skill in the art. See, e.g., Pearson, *Methods Mol. Biol.* 243:307-31 (1994). Examples of groups of amino acids that have side chains with similar chemical properties include 1) aliphatic side chains: glycine, alanine, valine, leucine, and isoleucine; 2) aliphatic-hydroxyl side chains: serine and threonine; 3) amide-containing side chains: asparagine and glutamine; 4) aromatic side chains: phenylalanine, tyrosine, and tryptophan; 5) basic side chains: lysine, arginine, and histidine; 6) acidic side chains: aspartic acid and glutamic acid; and 7) sulfur-containing side chains: cysteine and methionine. Conservative amino acids substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, glutamate-aspartate, and asparagine-glutamine.

[0058] Alternatively, a conservative replacement is any change having a positive value in the PAM250 log-likelihood matrix disclosed in Gonnet et al, *Science* 256:1443-45 (1992), incorporated herein by reference. A "moderately conservative" replacement is any change having a nonnegative value in the PAM250 log-likelihood matrix.

[0059] Amino acid positions or residues are said to “correspond to” each other when two sequences are optimally aligned. Such residues that correspond to each other are often in the same numbered position, but not always, such as when an N-terminally truncated polypeptide is compared to its wild-type counterpart. Often, residues that correspond to each other will be same amino acid, or conservative amino acids to each other. However, in certain situations, including alignments between variants or isoforms, the residues may be different and not conservative amino acids to each other.

[0060] Sequence identity for polypeptides is typically measured using sequence analysis software. Protein analysis software matches sequences using measures of similarity assigned to various substitutions, deletions and other modifications, including conservative amino acid substitutions. For instance, GCG contains programs such as "Gap" and "Bestfit" which can be used with default parameters as specified by the programs to determine sequence homology or sequence identity between closely related polypeptides, such as homologous polypeptides from different species of organisms or between a wild type protein and a mutein thereof. See, e.g., GCG Version 6.1 (University of Wisconsin, WI). Polypeptide sequences also can be compared using FASTA using default or recommended parameters, see GCG Version 6.1. FASTA (e.g., FASTA2 and FASTA3) provides alignments and percent sequence identity of the regions of the best overlap between the query and search sequences (Pearson, *Methods Enzymol.* 183:63-98 (1990); Pearson, *Methods Mol. Biol.* 132:185-219 (2000)). Another preferred algorithm when comparing a sequence of the invention to a database containing a large number of sequences from different organisms is the computer program BLAST, especially blastp or tblastn, using default parameters as supplied with the programs. See, e.g., Altschul et al, *J. Mol. Biol.* 215:403-410 (1990); Altschul et al, *Nucleic Acids Res.* 25:3389-402 (1997).

[0061] Human Anti-SARS-CoV2 S protein Antibodies and Characterization Thereof

[0062] In one embodiment, the invention provides humanized anti-SARS-CoV2 S protein antibodies. In another embodiment, the invention provides human anti-SARS-CoV2 S protein antibodies. In some embodiments, human anti-SARS-CoV2 S protein antibodies are produced by immunizing a non-human transgenic animal, e.g., a rodent, whose genome comprises human immunoglobulin genes so that the transgenic animal produces human antibodies.

[0063] Binding Affinity of Anti-SARS-CoV2 S protein Antibodies to SARS-CoV2 S protein

[0064] In some embodiments of the invention, the anti-SARS-CoV2 S protein antibodies bind to SARS-CoV2 S protein with high affinity.

[0065] The binding affinity and dissociation rate of an anti-SARS-CoV2 S protein antibody to SARS-CoV2 S protein can be determined by methods known in the art. The binding affinity can be measured by ELISAs, RIAs, flow cytometry, surface plasmon resonance, such as BIACORE™. The dissociate rate can be measured by surface plasmon resonance. Preferably, the binding affinity and dissociation rate is measured by surface plasmon resonance. More preferably, the binding affinity and dissociation rate are

measured using BIAcore™. One can determine whether an antibody has substantially the same KD as an anti-SARS-CoV2 S protein antibody by using methods known in the art. Example V exemplifies a method for determining affinity constants of anti-SARS-CoV2 S protein monoclonal antibodies. Identification of SARS-CoV2 S protein Epitopes Recognized by Anti-SARS-CoV2 S protein Antibodies

[0066] In another embodiment, the invention provides an anti-SARS-CoV2 S protein antibody that inhibits, blocks, or decreases SARS-CoV2 S protein binding to a receptor, in particular, to angiotensin-converting enzyme 2 (ACE2). In another embodiment, the invention provides an anti-SARS-CoV2 S protein antibody that inhibits, blocks, or decreases SARS-CoV2 S protein-mediated viral entry into cells. In another embodiment, the invention provides an anti-SARS-CoV2 S protein antibody that inhibits, blocks, or decreases fusion of viral and cell membranes. In another embodiment, the invention provides an anti-SARS-CoV S protein antibody that decreases viral load. In another embodiment, the invention provides an anti-SARS-CoV2 S protein antibody that inhibits, blocks, or decreases in severity for any period of time symptoms or conditions resulting from SARS-CoV2 infection. In certain embodiments, the invention provides an anti-SARS-CoV2 S protein antibody that inhibits, blocks, or decreases in severity for a day, a week, a month, 6 months, a year, or for the remainder of the subjects life symptoms or conditions resulting from SARS-CoV2 infection by 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100%. In certain embodiments, the invention provides an anti-SARS-CoV2 S protein antibody that may perform any combination of the preceding embodiments.

Methods of Producing Antibodies and Antibody Producing Cell Lines

Immunization

[0067] In some embodiments, human antibodies are produced by immunizing a non-human, transgenic animal comprising within its genome some or all of human immunoglobulin heavy chain and light chain loci with a SARS-CoV2 S immunogen. In one embodiment, the non-human animal is a XENOMOUSE™ animal. (Abgenix, Inc., Fremont, CA). XENOMOUSE™ mice are engineered mouse strains that comprise large fragments of human immunoglobulin heavy chain and light chain loci and are deficient in mouse antibody production. See, e.g., Green et al, Nature Genetics 7:13-21 (1994) and U.S. Patents 5,916,771, 5,939,598, 5,985,615, 5,998,209, 6,075,181, 6,091,001, 6,114,598, 6,130,364, 6,162,963 and 6,150,584. See also WO 91/10741, WO 94/02602, WO 96/34096, WO 96/33735, WO 98/16654, WO 98/24893, WO 98/50433, WO 99/45031, WO 99/53049, WO 00/09560, and WO 00/037504.

[0068] In another aspect, the invention provides a method for making anti-SARS-CoV2 S protein antibodies from non-human, non-mouse animals by immunizing non-human transgenic animals that comprise human immunoglobulin loci with a SARS-CoV2 S immunogen. One can produce such animals

using the methods described in the above-cited documents. The methods disclosed in these documents can be modified as described in U.S. Patent 5,994,619, which is hereby incorporated by reference. U.S. Patent 5,994,619 describes methods for producing novel cultured inner cell mass (CICM) cells and cell lines, derived from pigs and cows, and transgenic CICM cells into which heterologous DNA has been inserted. CICM transgenic cells can be used to produce cloned transgenic embryos, fetuses, and offspring. The '619 patent also describes methods of producing transgenic animals that are capable of transmitting the heterologous DNA to their progeny. In preferred embodiments of the current invention, the non-human animals are mammals, particularly rats, sheep, pigs, goats, cattle or horses.

[0069] XENOMOUSE™ mice produce an adult-like human repertoire of fully human antibodies and generate antigen-specific human antibodies. In some embodiments, the XENOMOUSE™ mice contain approximately 80% of the human antibody V gene repertoire through introduction of megabase sized, germline configuration fragments of the human heavy chain loci and kappa light chain loci in yeast artificial chromosome (YAC). In other embodiments, XENOMOUSE™ mice further contain approximately all of the human lambda light chain locus. See Mendez et al, *Nature Genetics* 15:146-156 (1997), Green and Jakobovits, *J. Exp. Med.* 188:483-495 (1998), and WO 98/24893, the disclosures of which are hereby incorporated by reference.

[0070] In some embodiments, the non-human animal comprising human immunoglobulin genes are animals that have a human immunoglobulin "minilocus". In the minilocus approach, an exogenous Ig locus is mimicked through the inclusion of individual genes from the Ig locus. Thus, one or more VH genes, one or more DH genes, one or more JH genes, a mu constant domain, and a second constant domain (preferably a gamma constant domain) are formed into a construct for insertion into an animal. This approach is described, inter alia, in U.S. Patent Nos. 5,545,807, 5,545,806, 5,569,825, 5,625,126, 5,633,425, 5,661,016, 5,770,429, 5,789,650, 5,814,318, 5,591,669, 5,612,205, 5,721,367, 5,789,215, and 5,643,763, hereby incorporated by reference.

[0071] In another aspect, the invention provides a method for making humanized anti- SARS-CoV2 S immunogen antibodies. In some embodiments, non-human animals are immunized with a SARS-CoV2 S immunogen as described below under conditions that permit antibody production. Antibody-producing cells are isolated from the animals, fused with myelomas to produce hybridomas, and nucleic acids encoding the heavy and light chains of an anti-SARS-CoV S protein antibody of interest are isolated. These nucleic acids are subsequently engineered using techniques known to those of skill in the art and as described further below to reduce the amount of non-human sequence, i.e., to humanize the antibody to reduce the immune response in humans.

[0072] In certain aspects, the disclosure provides an immunogen comprising a severe acute respiratory syndrome coronavirus 2 spike (“SARS-CoV2 S”) polypeptide, wherein the polypeptide comprises one or more pairs of amino acid substitutions that correspond to residues selected from the group consisting of:

- a) V382C and R983C of SEQ ID NO: 1;
- b) A520C and K41C of SEQ ID NO: 1;
- c) S383C and D985C of SEQ ID NO: 1;
- d) D614C and T859C of SEQ ID NO: 1;
- e) T547C and N978C of SEQ ID NO: 1;
- f) A570C and V963C of SEQ ID NO: 1;
- g) P665C and L864C of SEQ ID NO: 1;
- h) F562C and P225C of SEQ ID NO: 1; and
- i) P589C and F855C of SEQ ID NO: 1;

and wherein the polypeptide is 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, and 98% identical to SEQ ID NO:1.

[0073] In certain aspects, the disclosure provides an immunogen comprising a severe acute respiratory syndrome coronavirus 2 spike (“SARS-CoV2 S”) polypeptide, wherein the polypeptide comprises one or more pairs of amino acid substitutions that correspond to residues selected from the group consisting of:

- a) V382C and R983C of SEQ ID NO: 1;
- b) A520C and K41C of SEQ ID NO: 1;
- c) S383C and D985C of SEQ ID NO: 1;
- d) D614C and T859C of SEQ ID NO: 1;
- e) T547C and N978C of SEQ ID NO: 1;
- f) A570C and V963C of SEQ ID NO: 1;
- g) P665C and L864C of SEQ ID NO: 1;
- h) F562C and P225C of SEQ ID NO: 1; and
- i) P589C and F855C of SEQ ID NO: 1.

[0074] In certain embodiments, the immunogen can comprise more than one of the pairs of amino acid substitutions as shown in a)-i), above. In certain embodiments, the polypeptide comprises amino acid substitutions that correspond to residues D614C, T859C, T547C and N978C.

[0075] In certain embodiments, the immunogen can comprise substitutions that can abrogate the cleavage of the SARS-CoV2 S polypeptide by furin. Such substitutions include substitutions of residues that correspond to R682, R683, and R685 of SEQ ID NO: 1. In certain embodiments, the polypeptide further comprises one or more groups of amino acid substitutions that correspond to residues selected from the group consisting of:

- a) K986P and V987P of SEQ ID NO: 1;
- b) R682G, R683S, and R685S of SEQ ID NO: 1;
- c) R682S, R683G, and R685G of SEQ ID NO: 1;
- d) R682G, R683S, R685S, K986P and V987P of SEQ ID NO: 1; and
- e) R682S, R683G, R685G, K986P and V987P of SEQ ID NO: 1.

[0076] In certain embodiments, the polypeptide has at least 97% sequence identity to SEQ ID NO: 1.

[0077] In certain embodiments, the polypeptide has at least 98% sequence identity to SEQ ID NO: 1.

[0078] In certain embodiments, the polypeptide has at least 99% sequence identity to SEQ ID NO: 1.

[0079] In certain embodiments, the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 13-21.

[0080] In certain embodiments, the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 4-12 and 44-61.

[0081] In certain embodiments, the polypeptide comprises a trimerization domain attached to the C-terminus of the immunogen.

[0082] In certain embodiments, the trimerization domain comprises the amino acid sequence of SEQ ID NO: 84 or SEQ ID NO: 85.

[0083] In certain embodiments, the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 23-40 and 63-80.

[0084] In certain aspects, the disclosure provides a method of producing antibodies that specifically bind SARS-CoV2 S polypeptide comprising administering to a non-human subject an immunogen of the present invention and a pharmaceutically acceptable delivery vehicle and/or adjuvant.

[0085] In certain aspects, the disclosure provides a method of treating COVID-19 in a subject comprising administering a therapeutically effective amount of an antibody produced by a method of the present invention and a pharmaceutically acceptable delivery vehicle to the subject.

[0086] In certain aspects, the disclosure provides a composition capable of producing an immunological response in a human subject, the composition comprising an immunogen of the present invention and a pharmaceutically acceptable delivery vehicle and/or adjuvant.

[0087] Immunization of animals can be by any method known in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, New York: Cold Spring Harbor Press, 1990. Methods for immunizing non-human animals such as mice, rats, sheep, goats, pigs, cattle and horses are well known in the art. See, e.g., Harlow and Lane, *supra*, and U.S. Patent 5,994,619. In one embodiment, the SARS-CoV2 S immunogen is administered with an adjuvant to stimulate the immune response. Exemplary adjuvants include complete or incomplete Freund's adjuvant, RIBI (muramyl dipeptides) or ISCOM

(immunostimulating complexes). Such adjuvants may protect the polypeptide from rapid dispersal by sequestering it in a local deposit, or they may contain substances that stimulate the host to secrete factors that are chemotactic for macrophages and other components of the immune system. Preferably, if a polypeptide is being administered, the immunization schedule will involve two or more administrations of the polypeptide, spread out over several weeks.

[0088] After immunization of an animal with a SARS-CoV2 S immunogen, antibodies and/or antibody-producing cells can be obtained from the animal. In some embodiments, anti-SARS-CoV2 S protein antibody-containing serum is obtained from the animal by bleeding or sacrificing the animal. The serum may be used as it is obtained from the animal, an immunoglobulin fraction may be obtained from the serum, or the anti-SARS-CoV S protein antibodies may be purified from the serum.

[0089] In some embodiments, antibody-producing immortalized cell lines are prepared from cells isolated from the immunized animal. After immunization, the animal is sacrificed and lymph node and/or splenic B cells are immortalized by any means known in the art. Methods of immortalizing cells include, but are not limited to, transfecting them with oncogenes, infecting them with an oncogenic virus and cultivating them under conditions that select for immortalized cells, subjecting them to carcinogenic or mutating compounds, fusing them with an immortalized cell, e.g., a myeloma cell, and inactivating a tumor suppressor gene. See, e.g., Harlow and Lane, *supra*. If fusion with myeloma cells is used, the myeloma cells preferably do not secrete immunoglobulin polypeptides (a non-secretory cell line). Immortalized cells are screened using SARS-CoV2 S protein, a portion thereof, or a cell expressing SARS-CoV2 S protein. In one embodiment, the initial screening is performed using an enzyme-linked immunoassay (ELISA) or a radioimmunoassay. An example of ELISA screening is provided in WO 00/37504, incorporated herein by reference.

[0090] Anti-SARS-CoV2 S protein antibody-producing cells, e.g., hybridomas, are selected, cloned and further screened for desirable characteristics, including robust growth, high antibody production and desirable antibody characteristics, as discussed further below. Hybridomas can be expanded *in vivo* in syngeneic animals, in animals that lack an immune system, e.g., nude mice, or in cell culture *in vitro*. Methods of selecting, cloning and expanding hybridomas are well known to those of ordinary skill in the art.

[0091] In one embodiment, the immunized animal is a non-human animal that expresses human immunoglobulin genes and the splenic B cells are fused to a myeloma cell line from the same species as the non-human animal. In a more preferred embodiment, the immunized animal is a XENOMOUSE™ mouse and the myeloma cell line is a non-secretory mouse myeloma. In an even more preferred embodiment, the myeloma cell line is P3-X63-Ag8.653 (American Type Culture Collection. See, e.g., Example I. [0124] Thus, in one embodiment, the invention provides methods for producing a cell line that

produces a human monoclonal antibody or a fragment thereof directed to SARS-CoV2 S protein comprising (a) immunizing a non-human transgenic animal described herein with SARS-CoV2 S immunogen ; (b) allowing the transgenic animal to mount an immune response to SARS-CoV2 S immunogen ; (c) isolating antibody-producing cells from the transgenic animal; (d) immortalizing the antibody-producing cells; (e) creating individual monoclonal populations of the immortalized antibody-producing cells; and (f) screening the immortalized antibody-producing cells to identify an antibody directed to SARS-CoV2 S.

[0092] In another aspect, the invention provides hybridomas that produce a human anti- SARS-CoV2 S protein antibody. In one embodiment, the human anti-SARS-CoV2 S protein antibody produced by the hybridoma is an antagonist of SARS-CoV2 S protein. In some embodiments, the anti-SARS-CoV2 S protein monoclonal antibody does not mediate antibody dependent enhancement of viral infection. In one embodiment, the hybridomas are mouse hybridomas, as described above. In other embodiments, the hybridomas are produced in a non-human, non-mouse species such as rats, sheep, pigs, goats, cattle or horses. In another embodiment, the hybridomas are human hybridomas.

[0093] In one embodiment of the invention, antibody-producing cells are isolated and expressed in a host cell, for example myeloma cells. In still another embodiment, a transgenic animal is immunized with a SARS-CoV2 S protein immunogen as described herein, primary cells, e.g., spleen or peripheral blood cells, are isolated from an immunized transgenic animal and individual cells producing antibodies specific for the desired antigen are identified. Polyadenylated mRNA from each individual cell is isolated and reverse transcription polymerase chain reaction (RT-PCR) is performed using sense primers that anneal to variable region sequences, e.g., degenerate primers that recognize most or all of the FRI regions of human heavy and light chain variable region genes and anti-sense primers that anneal to constant or joining region sequences. cDNAs of the heavy and light chain variable domains are then cloned and expressed in any suitable host cell, e.g., a myeloma cell, as chimeric antibodies with respective immunoglobulin constant regions, such as the heavy chain and K or λ constant domains. See Babcook, J. S. et al. (1996) Proc. Natl. Acad. Sci. USA 93: 7843-48, incorporated herein by reference. Anti SARS-CoV2 S protein antibodies may then be identified and isolated as described herein.

[0094] In certain embodiments, a pharmaceutical composition comprising SARS-CoV2 S immunogens is used to elicit an immune response to the SARS-CoV2 S in a vaccine host. Pharmaceutical compositions containing SARS-CoV2 S immunogens of the present invention can be used as a vaccine for prevention and treatment of COVID-19.

[0095] Additionally, compositions can contain carriers and/or other additives in a pharmaceutically acceptable delivery system. Accordingly, a composition containing the SARS-CoV2 S immunogens can be formulated as a pharmaceutical vaccine formulation using adjuvants, pharmaceutically-acceptable carriers or other ingredients including immunological adjuvants routinely provided in vaccine formulations. An

immunologic adjuvant is defined as "any substance that acts to accelerate, prolong, or enhance antigen-specific immune responses without having any specific antigenic effect in itself when used in combination with specific vaccine antigens." There are many known adjuvants in widespread use, including oils, aluminum salts, and virosomes. Two common salts including aluminum phosphate (e.g. Adjuphos) and aluminum hydroxide (e.g. Alhydrogel) are the most common adjuvants in human vaccines. Methods for selecting mineral salts and determining the preferred concentration of mineral salt to employ or combinations thereof are well known to those skilled in the art.

[0096] Among other ingredients that can also be used as adjuvants in this invention include liposyn, saponin, squalene, L121, Emulsigen, monophosphoryl lipid A (MPL), QS21, ISA35, ISA206, ISA50V, ISA51, and ISA720 as well as the other efficacious adjuvants and emulsifiers. In a particular embodiment, the delivery vehicle and adjuvant is Montanide™ ISA51 (an oil vaccine adjuvant composition comprised of vegetable oil and mannide oleate for production of water-in-oil emulsions), Tween® 80 (also known as: Polysorbate 80 or Polyoxyethylene (20) sorbitan monooleate), a CpG oligonucleotide, and/or any combination thereof. In another embodiment, the pharmaceutical composition is a water-in-oil-in-water (i.e. w/o/w) emulsion with Emulsigen or Emulsigen D as the adjuvant.

[0097] Pharmaceutical compositions as vaccines can be formulated as immediate-release or sustained-release formulations. Additionally, the pharmaceutical compositions can be formulated for induction of systemic or localized mucosal, immunity through immunogen entrapment and co-administration with microparticles. Such delivery systems are readily determined by one of ordinary skill in the art.

[0098] Various vaccine formulations containing SARS-CoV2 S immunogens of the present disclosure are effective for protecting and treatment of SARS-CoV2 infection and COVID-19.

[0099] The present invention also encompasses nucleic acid molecules encoding SARS-CoV2 S immunogens. In one embodiment, the nucleic acid encodes a SARS-CoV2 immunogen of the invention.

[00100] The invention provides vectors comprising nucleic acid molecules that encode the SARS-CoV2 immunogen of the invention.

[00101] In some embodiments, the SARS-CoV2 immunogen of the invention are expressed by inserting DNAs encoding SARS-CoV2 immunogen into expression vectors such that the DNA is operatively linked to necessary expression control sequences such as transcriptional and translational control sequences. Expression vectors include plasmids, retroviruses, adenoviruses, adeno-associated viruses (AAV), plant viruses such as cauliflower mosaic virus, tobacco mosaic virus, cosmids, YACs, EBV derived episomes, and the like. The DNA is ligated into a vector such that transcriptional and translational control sequences within the vector serve their intended function of regulating the transcription and translation of the SARS-CoV2 immunogen. The expression vector and expression control sequences are chosen to be compatible with the expression host cell used. The DNA is inserted into the expression vector by standard methods

(e.g., ligation of complementary restriction sites on the antibody gene fragment and vector, or blunt end ligation if no restriction sites are present).

[00102] A convenient vector is one that encodes a functionally complete SARS-CoV2 immunogen DNA sequence, with appropriate restriction sites engineered. Polyadenylation and transcription termination occur at native chromosomal sites downstream of the coding regions. The recombinant expression vector also can encode a signal peptide that facilitates secretion of the SARS-CoV2 immunogen from a host cell. The DNA may be cloned into the vector such that the signal peptide is linked in-frame to the amino terminus of the SARS-CoV2 immunogen. The signal peptide can be an immunoglobulin signal peptide or a heterologous signal peptide (i.e., a signal peptide from a non-immunoglobulin protein). In certain embodiments, a signal peptide having the amino acid sequence of MFVFLVLLPLVSSQCV (SEQ ID NO: 86) is fused to the amino terminus of any of the polypeptide sequences of the present invention. In certain embodiments, a signal peptide having the amino acid sequence of MDMRVPAQLLGLLLLWLRGARC (SEQ ID NO: 87) is fused to the amino terminus of any of the polypeptide sequences of the present invention. In other embodiments, a signal peptide having the amino acid sequence of MAWALLLLTLLTQGTGSWA (SEQ ID NO: 88) is fused to the amino terminus of any of the polypeptide sequences of the present invention. In still other embodiments, a signal peptide having the amino acid sequence of MTCSPLLLTLLIHCTGSWA (SEQ ID NO: 89) is fused to the amino terminus of any of the polypeptide sequences of the present invention. Other suitable signal peptide sequences that can be fused to the amino terminus of the polypeptide sequences described herein include: MEAPAQLLFLLLLWLPDDTG (SEQ ID NO: 90), MEWTWRVFLVAAATGAHS (SEQ ID NO: 91), METPAQLLFLLLLWLPDDTG (SEQ ID NO: 92), METPAQLLFLLLLWLPDDTG (SEQ ID NO: 93), MKHLWFFLLLVAAPRWVLS (SEQ ID NO: 94), and MEWSWVFLFFLSVTTGVHS (SEQ ID NO: 95), and MGILPSPGMPALLSLVSLLSVLLMGCVAETGTQC (SEQ ID NO: 96). Other signal peptides are known to those of skill in the art and may be fused to any of the polypeptide chains of the present invention, for example, to facilitate or optimize expression in particular host cells.

[00103] In addition to the antibody chain genes, the recombinant expression vectors of the invention carry regulatory sequences that control the expression of the SARS-CoV2 immunogen in a host cell. It will be appreciated by those skilled in the art that the design of the expression vector, including the selection of regulatory sequences may depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. Preferred regulatory sequences for mammalian host cell expression include viral elements that direct high levels of protein expression in mammalian cells, such as promoters and/or enhancers derived from retroviral LTRs, cytomegalovirus (CMV) (such as the CMV promoter/enhancer), Simian Virus 40 (SV40) (such as the SV40 promoter/enhancer), adenovirus, (e.g., the adenovirus major late promoter (AdMLP)), polyoma and strong mammalian promoters such as native

immunoglobulin and actin promoters. For further description of viral regulatory elements, and sequences thereof, see e.g., U.S. Patent No. 5,168,062, U.S. Patent No. 4,510,245 and U.S. Patent No. 4,968,615. Methods for expressing antibodies in plants, including a description of promoters and vectors, as well as transformation of plants is known in the art. See, e.g., United States Patent 6,517,529, incorporated herein by reference. Methods of expressing polypeptides in bacterial cells or fungal cells, e.g., yeast cells, are also well known in the art.

[00104] In addition to the SARS-CoV2 immunogen DNA and regulatory sequences, the recombinant expression vectors of the invention may carry additional sequences, such as sequences that regulate replication of the vector in host cells (e.g., origins of replication) and selectable marker genes. The selectable marker gene facilitates selection of host cells into which the vector has been introduced (see e.g., U.S. Patent Nos. 4,399,216, 4,634,665 and 5,179,017, incorporated herein by reference). For example, typically the selectable marker gene confers resistance to drugs, such as G418, hygromycin or methotrexate, on a host cell into which the vector has been introduced. Preferred selectable marker genes include the dihydrofolate reductase (DHFR) gene (for use in dhfr-host cells with methotrexate selection/amplification), the neo gene (for G418 selection), and the glutamate synthetase gene.

[00105] Nucleic acid molecules encoding SARS-CoV2 immunogen and vectors comprising these nucleic acid molecules can be used for transfection of a suitable mammalian, plant, bacterial or yeast host cell. Transformation can be by any known method for introducing polynucleotides into a host cell. Methods for introduction of heterologous polynucleotides into mammalian cells are well known in the art and include dextran-mediated transfection, calcium phosphate precipitation, polybrene-mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei. In addition, nucleic acid molecules may be introduced into mammalian cells by viral vectors. Methods of transforming cells are well known in the art. See, e.g., U.S. Patent Nos. 4,399,216, 4,912,040, 4,740,461, and 4,959,455, incorporated herein by reference). Methods of transforming plant cells are well known in the art, including, e.g., *Agrobacterium*-mediated transformation, biolistic transformation, direct injection, electroporation and viral transformation. Methods of transforming bacterial and yeast cells are also well known in the art.

[00106] Mammalian cell lines available as hosts for expression are well known in the art and include many immortalized cell lines available from the American Type Culture Collection (ATCC). These include, inter alia, Chinese hamster ovary (CHO) cells, N50 cells, SP2 cells, HEK-293T cells, NIH-3T3 cells, HeLa cells, baby hamster kidney (BHK) cells, African green monkey kidney cells (COS), human hepatocellular carcinoma cells (e.g., Hep G2), A549 cells, and a number of other cell lines. Cell lines of particular preference are selected through determining which cell lines have high expression levels. Other cell lines that may be used are insect cell lines, such as Sf9 or Sf21 cells. When recombinant expression vectors

encoding SARS-CoV2 immunogens are introduced into mammalian host cells, the immunogens are produced by culturing the host cells for a period of time sufficient to allow for expression of the immunogen in the host cells or, more preferably, secretion of the SARS-CoV2 immunogen into the culture medium in which the host cells are grown. SARS-CoV2 immunogens can be recovered from the culture medium using standard protein purification methods. Plant host cells include, e.g., *Nicotiana*, *Arabidopsis*, duckweed, corn, wheat, potato, etc. Bacterial host cells include *E. coli* and *Streptomyces* species. Yeast host cells include *Schizosaccharomyces pombe*, *Saccharomyces cerevisiae* and *Pichia pastoris*.

[00107] Further, expression of SARS-CoV2 immunogens of the invention from production cell lines can be enhanced using a number of known techniques. For example, the glutamine synthetase gene expression system (the GS system) is a common approach for enhancing expression under certain conditions. The GS system is discussed in whole or part in connection with European Patent Nos. 0 216 846, 0 256 055, 0 323 997 and 0 338 841.

[00108] In another aspect, the invention provides diagnostic methods. The SARS-CoV2 immunogen can be used to detect SARS-CoV2 S antibodies in a biological sample in vitro or in vivo. In one embodiment, the invention provides a method for diagnosing the presence or location of SARS-CoV2 antibodies in a subject in need thereof.

[00109] The SARS-CoV2 immunogen can be used in a conventional immunoassay, including, without limitation, an ELISA, an RIA, flow cytometry, tissue immunohistochemistry, Western blot or immunoprecipitation. The SARS-CoV2 immunogen of the invention can be used to detect SARS-CoV2 S antibodies from humans.

[00110] The invention provides a method for detecting SARS-CoV2 S antibody in a biological sample comprising contacting the biological sample with an SARS-CoV2 immunogen of the invention and detecting the bound antibody. In one embodiment, the SARS-CoV2 immunogen is directly labeled with a detectable label. In another embodiment, the SARS-CoV2 immunogen is unlabeled and a second antibody or other molecule that can bind the SARS-CoV2 immunogen is labeled.

[00111] Suitable labels include various enzymes, prosthetic groups, fluorescent materials, luminescent materials and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

[00112] In another embodiment, the invention provides a method for neutralizing SARS-CoV by administering an anti-SARS-CoV2 S protein antibody produced using a SARS-CoV2 immunogen of the

invention to a patient in need thereof. Any of the types of antibodies described herein may be used therapeutically. In various embodiments, the anti-SARS-CoV S protein antibody is a human antibody.

[00113] In some embodiments, the patient is a human patient. Alternatively, the patient may be a mammal infected with SARS-CoV2. The antibody may be administered to a non-human mammal infected with SARS for veterinary purposes or as an animal model of human disease. Such animal models may be useful for evaluating the therapeutic efficacy of antibodies of this invention.

[00114] In one embodiment, the invention provides methods of treating, aiding in the treatment, preventing or aiding in the prevention of, SARS-CoV2 infection and conditions or disorders resulting from such infection, in a subject by administering to the subject a therapeutically-effective amount of an anti-SARS-CoV2 S protein antibody of the invention.

[00115] The antibody may be administered once, but more preferably is administered multiple times. The antibody may be administered from three times daily to once every six months or longer. The administering may be on a schedule such as three times daily, twice daily, once daily, once every two days, once every three days, once weekly, once every two weeks, once every month, once every two months, once every three months and once every six months. The antibody may also be administered continuously via a minipump. The antibody may be administered via an oral, mucosal, buccal, intranasal, inhalable, intravenous, subcutaneous, intramuscular, parenteral, intratumor or topical route. The antibody may be administered locally or systemically.

[00116] The therapeutic compositions comprising anti-SARS-CoV S protein antibodies may be administered to the subject, for example, orally, nasally, vaginally, buccally, rectally, via the eye, or via the pulmonary route, in a variety of pharmaceutically acceptable dosing forms, which will be familiar to those skilled in the art.

[00117] For example, the anti-SARS-CoV S protein antibodies may be administered via the nasal route using a nasal insufflator device. Examples of these are already employed for commercial powder systems intended for nasal application (e.g. Fisons Lomudal System). Details of other devices can be found in the pharmaceutical literature (see for example Bell, A. Intranasal Delivery devices, in *Drug Delivery Devices Fundamentals and Applications*, TyLe P. (ed), Dekker, New York, 1988).

[00118] The anti-SARS-CoV2 S protein antibodies can be administered to the vagina in a freeze dried powder formulation. Anti-SARS-CoV2 S protein antibodies may be administered in a vaginal applicator and once in the vagina, the formulation comprising the anti-SARS-CoV2 S protein antibodies are released by pressing a syringe-type piston or similar release mechanism on the applicator. Alternatively, the anti-SARS-CoV2 S protein antibodies may be formulated as a powder using a powder device, formulated into a vagina suppository or pessary or vaginal tablet or vaginal gel.

[00119] The anti-SARS-CoV2 S protein antibodies can also be administered to the eye in a gel formulation. For example, before administration, a formulation containing the anti- SARS-CoV2 S protein antibodies may be conveniently contained in a two compartment unit dose container, one compartment containing a freeze-dried anti-SARS-CoV2 S protein antibody preparation and the other compartment containing normal saline. Prior to application, the two compartments are mixed and a gel is formed, which is then administered to the eye.

[00120] Other delivery routes for the anti-SARS-CoV2 S protein antibodies include via the pulmonary route using a powder inhaler or metered dose inhaler, via the buccal route formulated into a tablet or a buccal patch, via the rectal route formulated into suppositories; and via the oral route in the form of a tablet, a capsule or a pellet (which compositions may administer agent via the stomach, the small intestine or the colon), all of which may be formulated in accordance with techniques which are well known to those skilled in the art.

[00121] The antibody may be administered once, at least twice or for at least the period of time until the condition is treated, palliated or cured. The antibody will generally be administered as part of a composition as described supra. The dosage of antibody will generally be in the range of 0.1-100 mg/kg, more preferably 0.5-50 mg/kg, more preferably 1-20 mg/kg, and even more preferably 1-10 mg/kg. The serum concentration of the antibody may be measured by any method known in the art.

[00122] In another embodiment, the antibodies of the present invention are administered to the subject in combination with other therapeutic agents. In one embodiment, the additional therapeutic agents may be treat the symptoms of the SARS-CoV2 infection on their own, and may optionally synergize with the effects of the antibodies. The additional agent that is administered may be selected by one skilled in the art for treating the infection.

[00123] Co-administration of the antibody with an additional therapeutic agent (combination therapy) encompasses administering a composition comprising the anti- SARS-CoV2 S protein antibody and the additional therapeutic agent as well as administering two or more separate compositions, one comprising the anti-SARS-CoV2 S protein antibody and the other(s) comprising the additional therapeutic agent(s). Further, although coadministration or combination therapy generally means that the antibody and additional therapeutic agents are administered at the same time as one another, it also encompasses instances in which the antibody and additional therapeutic agents are administered at different times. For instance, the antibody may be administered once every three days, while the additional therapeutic agent is administered once daily. Alternatively, the antibody may be administered prior to or subsequent to treatment with the additional therapeutic agent, for example after a patient has failed therapy with the additional agent. Similarly, administration of the anti-SARS-CoV2 S protein antibody may be administered prior to or subsequent to other therapy.

[00124] The antibody and one or more additional therapeutic agents (the combination therapy) may be administered once, twice or at least the period of time until the condition is treated, palliated or cured. Preferably, the combination therapy is administered multiple times. The combination therapy may be administered from three times daily to once every six months. The administering may be on a schedule such as three times daily, twice daily, once daily, once every two days, once every three days, once weekly, once every two weeks, once every month, once every two months, once every three months and once every six months, or may be administered continuously via a minipump. The combination therapy may be administered via an oral, mucosal, buccal, intranasal, inhalable, intravenous, subcutaneous, intramuscular, or parenteral.

[00125] In certain aspects, the disclosure provides a method for treating, preventing or alleviating the symptoms of a SARS-CoV2-mediated disorder in a subject in need thereof, comprising the step of administering to the subject an antibody or antigen-binding portion according to any one of the preceding embodiments.

[00126] In certain embodiments, antibodies with different binding specificities may be used in combination to simultaneously target several neutralizing epitopes and prevent emergence of escape mutants. In certain embodiments, neutralizing epitopes may include regions of S1 or S2, other SARS-CoV2 proteins, or S protein receptors. In certain embodiments, the neutralizing epitopes are in the S1 RBD domain or upstream of the RBD.

[00127] In certain embodiments, antibodies with binding specificities to a plurality of viral strains may be used in combination to simultaneously target multiple viral strains. In certain embodiments, an antibody may bind to a single strain or multiple strains. A number of SARS-CoV2 strains have been described and are known to one of skill in the art.

[00128] In order that this invention may be better understood, the following examples are set forth. These examples are for purposes of illustration only and are not to be construed as limiting the scope of the invention in any manner.

EXAMPLE 1

[00129] Proline mutations in the coiled-coiled regions of coronavirus S proteins and other viruses have been shown to improve expression levels and stability. However, cryo-EM studies demonstrate that roughly 50% of all molecules still maintain one RBD in the “up” conformation, suggesting these methods are only partially successful at stabilizing the S protein in the prefusion state (Figure 1). A structure-based, rational design was used to design covalent disulfides between different domains of the S-protein. Nine double-cysteine mutations were identified that have the potential to form inter-domain and inter-protomer disulfides with the express goal of limiting the capability of the RBD to transition to the “up” conformation.

[00130] These mutations were identified by scanning a recent cryo-EM structure of the closed CoV-2 S ectodomain (pdb: 6VXX). Briefly, all residue pairs existing either inter-domain or inter-protomer with a C β of < 6.5Å were computationally modeled as a disulfide pair and scored for energetic potential, emphasizing variants which minimized perturbations to the original structure. Variants were filtered by score, and nine were selected for further evaluation (Fig. 2). These 9 disulfide variants could be classified into 3 broad clusters: linking the RBD to the NTD, linking the RBD to the S2, and linking the SD1/SD2 to the S2.

[00131] These efforts represent a strategy for further development into prefusion stabilized viral proteins. Although the disulfides described here are specific to SARS-CoV-2 S proteins, this method can be adapted to other coronaviruses and proteins (viral or otherwise) where a preferred conformation is desired.

EXAMPLE 2

[00132] Immunization and hybridoma production

[00133] Five micrograms of purified S protein is emulsified in Titermax Gold adjuvant (Sigma) and 6-10 week old IgG2K XenoMouse animals are immunized intraperitoneally. Subsequent boosts are performed sequentially using TiterMax Gold or alum (Sigma) as adjuvants. When the animals developed an anti-S antibody response, a final boost in PBS is performed, four days later the spleen and lymph cells are harvested, fused with P3 myeloma cells and HPRT⁺ hybridomas are selected in hypoxanthine-azaserine (HA) using a standard protocol (Davis).

[00134] Hybridoma supernatants are individually screened for S reactivity by ELISA against S-V5-HIS with a counter screen against OVA-V5-HIS as a control. Hybridoma supernatants yielding OD values above 0.7 when tested against S-V5- HIS (Tor2) are further tested against various SI-Ig fragments by ELISA.

SEQUENCE LISTING

SEQ ID NO: 1

>ECD SARS_CoV_2_S protein (1-1208)

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SEQ ID NO: 2

>full_length_unmodified SARS_CoV_2_S protein (1-1273)

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SEQ ID NO: 3

>COV2_S_(K986P_V987P)

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SEQ ID NO: 4

>COV2_S_(A570C_V963C_K986P_V987P)

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SEQ ID NO: 5

>COV2_S_(D614C_T859C_K986P_V987P)

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SEQ ID NO: 6

>COV2_S_(K41C_A520C_K986P_V987P)

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SEQ ID NO: 7

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>COV2_S_(P589C_F855C_K986P_V987P)

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SEQ ID NO: 9

>COV2_S_(P665C_L864C_K986P_V987P)

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KNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSEYCDICIGAGICASYQTQTNSPR
RARSVASQSI IAYTMSLGAENSVAYSNN SIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLQY
GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVT LAD
AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPCLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQ MAY
RFNGIGV TQNVLYENQKLIANQFN SAI GKI QD SLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
DILSRLDPPEAEVQIDRLITGR LQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
PQSAPHGVVFLHVTYVPAQEKNFTTAPAICH DGKAHFPREGVFVSN GTHWFVTQRNFYEPQIITTDNTFVSGNC
DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
QELGKYEQ

SEQ ID NO: 10

>COV2_S_(S383C_D985C_K986P_V987P)

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
YFASTEKSNIIRGWI FGTTLD SKTQSL L I V N N A T N V V I K V C E F Q F C N D P F L G V Y Y H K N N K S W M E S E F R V Y S S A N
NCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
QTLLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSF TVEKGI
YQTSNFRVQPTESIVRFPNITNLCPFGVEFNATRFASVYAWNRRKRISNCVADYSVLVNSASFSTFKCYGVCP TK
LNDLCFTNVYADSFVIRGDEVRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGN YNYLYRLFRKSN
LKPFFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
KNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSEYCDIPIGAGICASYQTQTNSPR
RARSVASQSI IAYTMSLGAENSVAYSNN SIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLQY
GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVT LAD
AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQ MAY
RFNGIGV TQNVLYENQKLIANQFN SAI GKI QD SLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
DILSRLCPPEAEVQIDRLITGR LQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
PQSAPHGVVFLHVTYVPAQEKNFTTAPAICH DGKAHFPREGVFVSN GTHWFVTQRNFYEPQIITTDNTFVSGNC
DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
QELGKYEQ

SEQ ID NO: 11

>COV2_S_(T547C_N978C_K986P_V987P)

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
YFASTEKSNIIRGWI FGTTLD SKTQSL L I V N N A T N V V I K V C E F Q F C N D P F L G V Y Y H K N N K S W M E S E F R V Y S S A N
NCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
QTLLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSF TVEKGI
YQTSNFRVQPTESIVRFPNITNLCPFGVEFNATRFASVYAWNRRKRISNCVADYSVLVNSASFSTFKCYGVSP TK
LNDLCFTNVYADSFVIRGDEVRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGN YNYLYRLFRKSN
LKPFFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
KNKCVNFNFNGLCGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV

AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGNSVVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNspr
 RARSVASQSI IAYTMSLGAENSVAYSNNsIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECsnlllQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLAD
 AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNsAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLC
 DILSRLDPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQ

SEQ ID NO: 12

>COV2_S_(V382C_R983C_K986P_V987P)

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWI FGTTLDsktQsllivNNATNVVIKVECFQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
 NCTFEYVSQPFLLMDLEGKQGNFKNLREFVFKNIDGYFKIYskHTPINLVRDLPQGFSalePLVDLPIGINITRF
 QTLALHRSYLTpgdSSSGWtagAAAYYVGYLQPRTFLLKYNGTITDAVDCALDPLSETKCTLKSFTVEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGCSPTK
 LNDLCFTNVYADSFVIRGDEVrQIAPGQTGKIADYNYKLpDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGNSVVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNspr
 RARSVASQSI IAYTMSLGAENSVAYSNNsIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECsnlllQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLAD
 AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNsAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
 DILSCLDPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQ

SEQ ID NO: 13

>COV2_S_(A570C_V963C)

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWI FGTTLDsktQsllivNNATNVVIKVECFQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
 NCTFEYVSQPFLLMDLEGKQGNFKNLREFVFKNIDGYFKIYskHTPINLVRDLPQGFSalePLVDLPIGINITRF
 QTLALHRSYLTpgdSSSGWtagAAAYYVGYLQPRTFLLKYNGTITDAVDCALDPLSETKCTLKSFTVEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVrQIAPGQTGKIADYNYKLpDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDICDTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGNSVVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNspr
 RARSVASQSI IAYTMSLGAENSVAYSNNsIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECsnlllQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLAD
 AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNsAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
 DILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQ

SEQ ID NO: 14

>COV2_S_(D614C_T859C)

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWI FGTTLDsktQsllivNNATNVVIKVECFQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN

NCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
 QTLLALHRSYLTTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGVEFNATRFASVYAWNRRKISNCVADYSVLNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQCVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPR
 RARVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNSLLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLD
 AGFIKQYGDCLGDIAARDLCAQKFNGLCVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
 DILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQ

SEQ ID NO: 15

>COV2_S_(K41C_A520C)

NLTTRTQLPPAYTNSFTRGVYYPDCVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWI FGTTLDLSDKTQSLILVNNATNVVIKVEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
 NCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
 QTLLALHRSYLTTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGVEFNATRFASVYAWNRRKISNCVADYSVLNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPR
 RARVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNSLLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLD
 AGFIKQYGDCLGDIAARDLCAQKFNGLCVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
 DILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQ

SEQ ID NO: 16

>COV2_S_(P225C_F562C)

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWI FGTTLDLSDKTQSLILVNNATNVVIKVEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
 NCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALECLVDLPIGINITRF
 QTLLALHRSYLTTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGVEFNATRFASVYAWNRRKISNCVADYSVLNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPCQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPR
 RARVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNSLLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLD
 AGFIKQYGDCLGDIAARDLCAQKFNGLCVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
 DILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC

DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
QELGKYEQ

SEQ ID NO: 17

>COV2_S_(P589C_F855C)

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
YFASTEKSNIIRGWI FGTTLD SKTQSL LIVNNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
NCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
QTLLALHRSYLT PGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSF TVEKGI
YQTSNFRVQPTESIVRFPNITNLCPFGVEFNATRFASVYAWNRKRISNCVADYSVLVNSASFSTFKCYGVSPTK
LNDLCFTNVYADSFVIRGDEVQR IAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSN
LKPFFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
KNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITCCSFGGVSVITPGTNTSNQV
AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSECDIPIGAGICASYQTQTNSPR
RARSVASQSI IAYTMSLGAENSVAYSNNIAIPTNFTISVTTEILPVSMKTSSVDCTMYICGDSTEC SNLLLQY
GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLLAD
AGFIKQYGDCLGDIAARDLICAQKCNGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
RFNGIGVTVQNVLYENQKLIANQFN SAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
DILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
PQSAPHGVVFLHVTYVPAQEKNFTTAPAI CHDGAHFPRGVFVSNGTWHFVTQRNFYEPQIITDNTFVSGNC
DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
QELGKYEQ

SEQ ID NO: 18

>COV2_S_(P665C_L864C)

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
YFASTEKSNIIRGWI FGTTLD SKTQSL LIVNNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
NCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
QTLLALHRSYLT PGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSF TVEKGI
YQTSNFRVQPTESIVRFPNITNLCPFGVEFNATRFASVYAWNRKRISNCVADYSVLVNSASFSTFKCYGVSPTK
LNDLCFTNVYADSFVIRGDEVQR IAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSN
LKPFFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
KNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSECDICIGAGICASYQTQTNSPR
RARSVASQSI IAYTMSLGAENSVAYSNNIAIPTNFTISVTTEILPVSMKTSSVDCTMYICGDSTEC SNLLLQY
GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLLAD
AGFIKQYGDCLGDIAARDLICAQKFNGLT VLPCLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
RFNGIGVTVQNVLYENQKLIANQFN SAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
DILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
PQSAPHGVVFLHVTYVPAQEKNFTTAPAI CHDGAHFPRGVFVSNGTWHFVTQRNFYEPQIITDNTFVSGNC
DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
QELGKYEQ

SEQ ID NO: 19

>COV2_S_(S383C_D985C)

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
YFASTEKSNIIRGWI FGTTLD SKTQSL LIVNNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
NCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
QTLLALHRSYLT PGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSF TVEKGI
YQTSNFRVQPTESIVRFPNITNLCPFGVEFNATRFASVYAWNRKRISNCVADYSVLVNSASFSTFKCYGVCPTK
LNDLCFTNVYADSFVIRGDEVQR IAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSN
LKPFFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
KNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSECDIPIGAGICASYQTQTNSPR

RARSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNSNLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLLAD
 AGFIKQYGDCLGDIAARDLCAQKFNGLTVLPLLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAIISSVLN
 DILSRLCKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQ

SEQ ID NO: 20

>COV2_S_(T547C_N978C)

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWI FGTTLDSTQSLIIVNNATNVVIVKCEFCNDPFLGVYYHKNKNSWMESEFRVYSSAN
 NCTFEYVSQPFLLMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRDLPPQGFSALEPLVDLPIGINITRF
 QTLALHRSYLTTPGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLKSFTEKEGI
 YQTSNFRVQPTESIVRFPNITNLCPPGVEFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLCGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTL EILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTN SPR
 RARSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNSNLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLLAD
 AGFIKQYGDCLGDIAARDLCAQKFNGLTVLPLLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAIISSVLC
 DILSRLCKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQ

SEQ ID NO: 21

>COV2_S_(V382C_R983C)

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWI FGTTLDSTQSLIIVNNATNVVIVKCEFCNDPFLGVYYHKNKNSWMESEFRVYSSAN
 NCTFEYVSQPFLLMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRDLPPQGFSALEPLVDLPIGINITRF
 QTLALHRSYLTTPGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLKSFTEKEGI
 YQTSNFRVQPTESIVRFPNITNLCPPGVEFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGCSPTK
 LNDLCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTL EILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTN SPR
 RARSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNSNLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLLAD
 AGFIKQYGDCLGDIAARDLCAQKFNGLTVLPLLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAIISSVLN
 DILSCLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQ

SEQ ID NO: 22

>COV2_S_(K986P_V987P)_trimer_tag_2

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWI FGTTLDSTQSLIIVNNATNVVIVKCEFCNDPFLGVYYHKNKNSWMESEFRVYSSAN
 NCTFEYVSQPFLLMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRDLPPQGFSALEPLVDLPIGINITRF

QTLALHRSYLTTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLVNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQGFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNspr
 RARSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLDAD
 AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPLLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
 DILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQGGGSGYIPEAPRDGQAYVRKDGWVLLSTFLGLEVLFGQPGHHHHHHHSAWSHPQFEKGGGSGGG
 GSGGSAWSHPQFEK

SEQ ID NO: 23

>COV2_S_(A570C_V963C_K986P_V987P)_trimer_tag_2
 NLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAHIVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWIFGTTLDSTQSLILVNNATNVVIVKCEVFQFCNDPFLGVYHKNKNSWMESEFRVYSSAN
 NCTFEYVSQPFLLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPPQGSFALEPLVDLPIGINITRF
 QTLALHRSYLTTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLVNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQGFGRDICDTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNspr
 RARSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLDAD
 AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPLLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
 DILSRDLPPAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQGGGSGYIPEAPRDGQAYVRKDGWVLLSTFLGLEVLFGQPGHHHHHHHSAWSHPQFEKGGGSGGG
 GSGGSAWSHPQFEK

SEQ ID NO: 24

>COV2_S_(D614C_T859C_K986P_V987P)_trimer_tag_2
 NLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAHIVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWIFGTTLDSTQSLILVNNATNVVIVKCEVFQFCNDPFLGVYHKNKNSWMESEFRVYSSAN
 NCTFEYVSQPFLLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPPQGSFALEPLVDLPIGINITRF
 QTLALHRSYLTTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLVNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQGFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQCVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNspr
 RARSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLDAD
 AGFIKQYGDCLGDIAARDLICAQKFNGLCVLPPLLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
 DILSRDLPPAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC

DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQGGGSGYIPEAPRDGQAYVRKDGWVLLSTFLGLEVLFGQPGHHHHHHHSAWSHPQFEKGGGSGGG
 GSGGSAWSHPQFEK

SEQ ID NO: 25

>COV2_S_(K41C_A520C_K986P_V987P)_trimer_tag_2
 NLTRTRQLPPAYTNSFTRGVYYPDCVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWI FGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
 NCTFEYVSQPFLLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
 QTLALHRSYLTTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGVEFNATRFASVYAWNRKRISNCVADYSVLVNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHCPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGNSVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTN SPR
 RARSVASQSI IAYTMSLGAENSVAYSNNIAIPTNFTISVTTEILPVSMKTSTVDCTMYICGDSTECNLLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVT LAD
 AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTQNVLYENQKLIANQFN SAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
 DILSRLDPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQGGGSGYIPEAPRDGQAYVRKDGWVLLSTFLGLEVLFGQPGHHHHHHHSAWSHPQFEKGGGSGGG
 GSGGSAWSHPQFEK

SEQ ID NO: 26

>COV2_S_(P225C_F562C_K986P_V987P)_trimer_tag_2
 NLTRTRQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWI FGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
 NCTFEYVSQPFLLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALECLVDLPIGINITRF
 QTLALHRSYLTTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGVEFNATRFASVYAWNRKRISNCVADYSVLVNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPCQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGNSVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTN SPR
 RARSVASQSI IAYTMSLGAENSVAYSNNIAIPTNFTISVTTEILPVSMKTSTVDCTMYICGDSTECNLLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVT LAD
 AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTQNVLYENQKLIANQFN SAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
 DILSRLDPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQGGGSGYIPEAPRDGQAYVRKDGWVLLSTFLGLEVLFGQPGHHHHHHHSAWSHPQFEKGGGSGGG
 GSGGSAWSHPQFEK

SEQ ID NO: 27

>COV2_S_(P589C_F855C_K986P_V987P)_trimer_tag_2
 NLTRTRQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWI FGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
 NCTFEYVSQPFLLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
 QTLALHRSYLTTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGVEFNATRFASVYAWNRKRISNCVADYSVLVNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN

LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITCCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPR
 RARVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNSNLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLLAD
 AGFIKQYGDCLGDIAARDLICAQKCNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
 DILSRLDPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQGGGSGYIPEAPRDGQAYVRKDGWVLLSTFLGLEVLFGQPGHHHHHHHSAWSHPQFEKGGGSGGG
 GSGGSAWSHPQFEK

SEQ ID NO: 28

>COV2_S_(P665C_L864C_K986P_V987P)_trimer_tag_2

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAHIVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWI FGTTLDSTQSLIIVNNATNVVIVKCEFCNDPFLGVYHKNKNSWMESEFRVYSSAN
 NCTFEYVSQPFLLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLPIGINITRF
 QTLALHRSYLTTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSTVEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGVSPK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDICIGAGICASYQTQTNSPR
 RARVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNSNLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLLAD
 AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
 DILSRLDPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQGGGSGYIPEAPRDGQAYVRKDGWVLLSTFLGLEVLFGQPGHHHHHHHSAWSHPQFEKGGGSGGG
 GSGGSAWSHPQFEK

SEQ ID NO: 29

>COV2_S_(S383C_D985C_K986P_V987P)_trimer_tag_2

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAHIVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWI FGTTLDSTQSLIIVNNATNVVIVKCEFCNDPFLGVYHKNKNSWMESEFRVYSSAN
 NCTFEYVSQPFLLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLPIGINITRF
 QTLALHRSYLTTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSTVEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGVCPK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPR
 RARVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNSNLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLLAD
 AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
 DILSRLCPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQGGGSGYIPEAPRDGQAYVRKDGWVLLSTFLGLEVLFGQPGHHHHHHHSAWSHPQFEKGGGSGGG
 GSGGSAWSHPQFEK

SEQ ID NO: 30

>COV2_S_(T547C_N978C_K986P_V987P)_trimer_tag_2

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
 NCTFEYVSQPFLLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLPIGINITRF
 QTLLALHRSYLTTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSTVEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKISNCVADYSVLVNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCFYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLCGTGVLTESNKKFLPFQGFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAETHVNSYECDIPIGAGICASYQTQTNSPR
 RARVASQSIIAYTMSLGAENSVAYSNNIAIPTNFTISVTTEILPVSMKTSTVDCTMYICGDSTECNNLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLDL
 AGFIKQYGDCLGDIAARDLCAQKFNGLTVLPLLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLC
 DILSRLDPPEAEVQIDRLITGRQLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQGGGSGYIPEAPRDGQAYVRKDGWVLLSTFLGLEVLFGQPGHHHHHHHSAWSHPQFEKGGGSGGG
 GSGGSAWSHPQFEK

SEQ ID NO: 31

>COV2_S_(V382C_R983C_K986P_V987P)_trimer_tag_2

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
 NCTFEYVSQPFLLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLPIGINITRF
 QTLLALHRSYLTTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSTVEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKISNCVADYSVLVNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCFYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQGFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAETHVNSYECDIPIGAGICASYQTQTNSPR
 RARVASQSIIAYTMSLGAENSVAYSNNIAIPTNFTISVTTEILPVSMKTSTVDCTMYICGDSTECNNLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLDL
 AGFIKQYGDCLGDIAARDLCAQKFNGLTVLPLLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
 DILSCLDPPEAEVQIDRLITGRQLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQGGGSGYIPEAPRDGQAYVRKDGWVLLSTFLGLEVLFGQPGHHHHHHHSAWSHPQFEKGGGSGGG
 GSGGSAWSHPQFEK

SEQ ID NO: 32

>COV2_S_(A570C_V963C)_trimer_tag_2

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
 NCTFEYVSQPFLLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLPIGINITRF
 QTLLALHRSYLTTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSTVEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKISNCVADYSVLVNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCFYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQGFGRDICDTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAETHVNSYECDIPIGAGICASYQTQTNSPR

RARSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNSNLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLLAD
 AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPLLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLCKQLSSNFGAIISSVLN
 DILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQGGGSGYIPEAPRDGQAYVRKDGGEWVLLSTFLGLEVLVFQGPGRHHHHHHHSAWSHPQFEKGGGSGGG
 GSGGSAWSHPQFEK

SEQ ID NO: 33

>COV2_S_(D614C_T859C)_trimer_tag_2

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVYHKNKNSWMESEFRVYSSAN
 NCTFEYVSQPFLLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLPIGINITRF
 QTLALHRSYLTTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTEKGI
 YQTSNFRVQPTESIVRFPNITNLCPPGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQGFGRDIADTTDAVRDPQTLLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQCVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNspr
 RARSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNSNLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLLAD
 AGFIKQYGDCLGDIAARDLICAQKFNGLCVLPPLLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAIISSVLN
 DILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQGGGSGYIPEAPRDGQAYVRKDGGEWVLLSTFLGLEVLVFQGPGRHHHHHHHSAWSHPQFEKGGGSGGG
 GSGGSAWSHPQFEK

SEQ ID NO: 34

>COV2_S_(K41C_A520C)_trimer_tag_2

NLTTRTQLPPAYTNSFTRGVYYPDCVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVYHKNKNSWMESEFRVYSSAN
 NCTFEYVSQPFLLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLPIGINITRF
 QTLALHRSYLTTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTEKGI
 YQTSNFRVQPTESIVRFPNITNLCPPGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHCPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQGFGRDIADTTDAVRDPQTLLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNspr
 RARSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNSNLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLLAD
 AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPLLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAIISSVLN
 DILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQGGGSGYIPEAPRDGQAYVRKDGGEWVLLSTFLGLEVLVFQGPGRHHHHHHHSAWSHPQFEKGGGSGGG
 GSGGSAWSHPQFEK

SEQ ID NO: 35

>COV2_S_(P225C_F562C)_trimer_tag_2

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWI FGTTLD SKTQSL LIVNNATNVVIK VCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
 NCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALECLVDLPIGINITRF
 QTLLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSF TVEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLVNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFENGLTGTGVLTESNKKFLPCQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSECDIPIGAGICASYQTQTNSPR
 RARVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMKT SV DCTMYICGDSTEC SNLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVT LAD
 AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFN SAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
 DILSRDLKVEAEVQIDRLITGR LQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICH DGKAHFPREGV FVSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQGGGSGYIPEAPRDGQAYVRKDG EWVLLSTFLGLEVL FQGPGHHHHHHHSAWSHPQFEKGGGSGGG
 GSGGSAWSHPQFEK

SEQ ID NO: 36

>COV2_S_(P589C_F855C)_trimer_tag_2

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWI FGTTLD SKTQSL LIVNNATNVVIK VCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
 NCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
 QTLLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSF TVEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLVNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFENGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITCCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSECDIPIGAGICASYQTQTNSPR
 RARVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMKT SV DCTMYICGDSTEC SNLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVT LAD
 AGFIKQYGDCLGDIAARDLICAQKCNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFN SAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
 DILSRDLKVEAEVQIDRLITGR LQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICH DGKAHFPREGV FVSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQGGGSGYIPEAPRDGQAYVRKDG EWVLLSTFLGLEVL FQGPGHHHHHHHSAWSHPQFEKGGGSGGG
 GSGGSAWSHPQFEK

SEQ ID NO: 37

>COV2_S_(P665C_L864C)_trimer_tag_2

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWI FGTTLD SKTQSL LIVNNATNVVIK VCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
 NCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
 QTLLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSF TVEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLVNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFENGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSECDICIGAGICASYQTQTNSPR
 RARVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMKT SV DCTMYICGDSTEC SNLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVT LAD
 AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPCLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY

RFNGIGVTONVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAIISSVLN
DILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNC
DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
QELGKYEQGGGSGYIPEAPRDGQAYVRKDGWVLLSTFLGLEVLVFQGPGRHHHHHHHSAWSHPQFEKGGGSGGG
GSGGSAWSHPQFEK

SEQ ID NO: 38

>COV2_S_(S383C_D985C)_trimer_tag_2

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
YFASTEKSNIIRGWI FGTTLD SKTQSL LIVNNATNVV IKVCE FQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
NCTFEYVSQPF LMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
QTLALHRSYLT PGDSSSGW TAGAAAYYVGYLQPRTFLLKYNGTITDAVDCALDPLSETKCTLKSF TVEKGI
YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNYSASFSTFKCYGVCPTK
LNDLCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSN
LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
KNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSYECDIPIGAGICASYQTQTNSPR
RARSVASQSIIAYTMSLGAENSVAYSNN SIAIPTNFTISVTTEILPVSMKT SV DCTMYICGDSTEC SNLLQY
GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVT LAD
AGFIKQYGDCLGDIAARDLICAQKFNGLT VLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
RFNGIGVTONVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAIISSVLN
DILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNC
DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
QELGKYEQGGGSGYIPEAPRDGQAYVRKDGWVLLSTFLGLEVLVFQGPGRHHHHHHHSAWSHPQFEKGGGSGGG
GSGGSAWSHPQFEK

SEQ ID NO: 39

>COV2_S_(T547C_N978C)_trimer_tag_2

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
YFASTEKSNIIRGWI FGTTLD SKTQSL LIVNNATNVV IKVCE FQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
NCTFEYVSQPF LMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
QTLALHRSYLT PGDSSSGW TAGAAAYYVGYLQPRTFLLKYNGTITDAVDCALDPLSETKCTLKSF TVEKGI
YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNYSASFSTFKCYGVSPTK
LNDLCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSN
LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
KNKCVNFNFNGLCGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSYECDIPIGAGICASYQTQTNSPR
RARSVASQSIIAYTMSLGAENSVAYSNN SIAIPTNFTISVTTEILPVSMKT SV DCTMYICGDSTEC SNLLQY
GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVT LAD
AGFIKQYGDCLGDIAARDLICAQKFNGLT VLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
RFNGIGVTONVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAIISSVLC
DILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNC
DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
QELGKYEQGGGSGYIPEAPRDGQAYVRKDGWVLLSTFLGLEVLVFQGPGRHHHHHHHSAWSHPQFEKGGGSGGG
GSGGSAWSHPQFEK

SEQ ID NO: 40

>COV2_S_(V382C_R983C)_trimer_tag_2

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
YFASTEKSNIIRGWI FGTTLD SKTQSL LIVNNATNVV IKVCE FQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
NCTFEYVSQPF LMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF

QTLALHRSYLTTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNYSASFSTFKCYGCSPTK
 LNDLCFTNVYADSFVIRGDEVRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQGFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAETHVNNSECDIPIGAGICASYQTQTNSPR
 RARSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLLAD
 AGFIKQYGDCLGDIAARDLICAQKFNGLTVL PPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAIISSVLN
 DILSCLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQGGGSGYIPEAPRDGQAYVRKDGWVLLSTFLGLEVLFGQPGHHHHHHHSAWSHPQFEKGGGSGGG
 GSGGSAWSHPQFEK

SEQ ID NO: 41

>ECD SARS_CoV_2_S protein (1-1208; R682G_R683S_R685S)

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWI FGTTLD SKTQSL L I V N N A T N V V I K V C E F Q F C N D P F L G V Y Y H K N N K S W M E S E F R V Y S S A N
 NCTFEYVSQPF LMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLV RDLPQGFSALEPLVDLPIGINITRF
 QTLALHRSYLTTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNYSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQGFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAETHVNNSECDIPIGAGICASYQTQTNSPG
 SASSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLLAD
 AGFIKQYGDCLGDIAARDLICAQKFNGLTVL PPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAIISSVLN
 DILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQ

SEQ ID NO: 42

>full_length_unmodified SARS_CoV_2_S protein (1-1273; R682G_R683S_R685S)

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWI FGTTLD SKTQSL L I V N N A T N V V I K V C E F Q F C N D P F L G V Y Y H K N N K S W M E S E F R V Y S S A N
 NCTFEYVSQPF LMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLV RDLPQGFSALEPLVDLPIGINITRF
 QTLALHRSYLTTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNYSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQGFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAETHVNNSECDIPIGAGICASYQTQTNSPG
 SASSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLLAD
 AGFIKQYGDCLGDIAARDLICAQKFNGLTVL PPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAIISSVLN
 DILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC

DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
QELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSCCCLKGCCSCGSCCKFDEDDSEPV LKGVLHYT

SEQ ID NO: 43

>COV2_S_(R682G_R683S_R685S_K986P_V987P)

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
YFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVCEQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
NCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
QTLLALHRSYLTTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTEKGI
YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLVNSASFSTFKCYGVSPTK
LNDLCFTNVYADSFVIRGDEVRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSN
LKPFFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
KNKCVNFNFNGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPG
SASSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMKTSTVDCTMYICGDSTECNLLLQY
GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLLAD
AGFIKQYGDCLGDIAARDLCAQKFNGLTVLPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
RFNGIGVTVQNVLYENQKLIANQFNLSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAIISSVLN
DILSRLDPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC
DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
QELGKYEQ

SEQ ID NO: 44

>COV2_S_(R682G_R683S_R685S_A570C_V963C_K986P_V987P)

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
YFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVCEQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
NCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
QTLLALHRSYLTTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTEKGI
YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLVNSASFSTFKCYGVSPTK
LNDLCFTNVYADSFVIRGDEVRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSN
LKPFFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
KNKCVNFNFNGLTGTGVLTESNKKFLPFQFGRDICDTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPG
SASSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMKTSTVDCTMYICGDSTECNLLLQY
GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLLAD
AGFIKQYGDCLGDIAARDLCAQKFNGLTVLPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
RFNGIGVTVQNVLYENQKLIANQFNLSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAIISSVLN
DILSRLDPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC
DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
QELGKYEQ

SEQ ID NO: 45

>COV2_S_(R682G_R683S_R685S_D614C_T859C_K986P_V987P)

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
YFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVCEQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
NCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
QTLLALHRSYLTTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTEKGI
YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLVNSASFSTFKCYGVSPTK
LNDLCFTNVYADSFVIRGDEVRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSN
LKPFFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
KNKCVNFNFNGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
AVLYQCVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPG

SASSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNSNLLQY
GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLLAD
AGFIKQYGDCLGDIAARDLICAQKFNGLCVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAIISSVLN
DILSRLDPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNC
DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
QELGKYEQ

SEQ ID NO: 46

>COV2_S_(R682G_R683S_R685S_K41C_A520C_K986P_V987P)

NLTTRTQLPPAYTNSFTRGVYYPDCVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
YFASTEKSNIIRGWI FGTTLD SKTQSL LIVNNATNVVIK VCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
NCTFEYVSQPF LMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
QTLLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNGTITDAVDCALDPLSETKCTLKSF TVEKGI
YQTSNFRVQPTESIVRFPNITNLC PFGEVFNATRFASVYAWNRKRISNCVADYSVLNYSASFSTFKCYGVSPTK
LNDLCFTNVYADSFVIRGDEVRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHCPATVCGPKKSTNLV
KNKCVNFNFNGLTGTGVLTESNKKFLPQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSYECDIPIGAGICASYQTQTNSPG
SASSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNSNLLQY
GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLLAD
AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAIISSVLN
DILSRLDPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNC
DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
QELGKYEQ

SEQ ID NO: 47

>COV2_S_(R682G_R683S_R685S_P225C_F562C_K986P_V987P)

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
YFASTEKSNIIRGWI FGTTLD SKTQSL LIVNNATNVVIK VCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
NCTFEYVSQPF LMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALECLVDLPIGINITRF
QTLLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNGTITDAVDCALDPLSETKCTLKSF TVEKGI
YQTSNFRVQPTESIVRFPNITNLC PFGEVFNATRFASVYAWNRKRISNCVADYSVLNYSASFSTFKCYGVSPTK
LNDLCFTNVYADSFVIRGDEVRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
KNKCVNFNFNGLTGTGVLTESNKKFLPQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSYECDIPIGAGICASYQTQTNSPG
SASSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNSNLLQY
GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLLAD
AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAIISSVLN
DILSRLDPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNC
DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
QELGKYEQ

SEQ ID NO: 48

>COV2_S_(R682G_R683S_R685S_P589C_F855C_K986P_V987P)

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
YFASTEKSNIIRGWI FGTTLD SKTQSL LIVNNATNVVIK VCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
NCTFEYVSQPF LMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF

QTLALHRSYLTTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLVNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTL EILDITCCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSECDIPIGAGICASYQTQTNSPG
 SASSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLLAD
 AGFIKQYGDCLGDIAARDLICAQKCNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
 DILSRLDPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQ

SEQ ID NO: 49

>COV2_S_(R682G_R683S_R685S_P665C_L864C_K986P_V987P)

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWI FGTTLDLSDKTQSLILVNNATNVVIKVECFQFCNDPFLGVYHKNKNSWMESEFRVYSSAN
 NCTFEYVSQPFLLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLPIGINITRF
 QTLALHRSYLTTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLVNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTL EILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSECDICIGAGICASYQTQTNSPG
 SASSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLLAD
 AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPCLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
 DILSRLDPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQ

SEQ ID NO: 50

>COV2_S_(R682G_R683S_R685S_S383C_D985C_K986P_V987P)

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWI FGTTLDLSDKTQSLILVNNATNVVIKVECFQFCNDPFLGVYHKNKNSWMESEFRVYSSAN
 NCTFEYVSQPFLLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLPIGINITRF
 QTLALHRSYLTTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLVNSASFSTFKCYGVCPTK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTL EILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSECDIPIGAGICASYQTQTNSPG
 SASSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLLAD
 AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPCLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
 DILSRLCPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC

DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
QELGKYEQ

SEQ ID NO: 51

>COV2_S_(R682G_R683S_R685S_T547C_N978C_K986P_V987P)

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
YFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
NCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
QTLLALHRSYLTTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTEKGI
YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLVNSASFSTFKCYGVSPTK
LNDLCFTNVYADSFVIRGDEVRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSN
LKPFFERDISTEIIYQAGSTPCNGVEGFNCFYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
KNKCVNFNFNGLCGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGNSVVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPG
SASSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMKTSTVDCTMYICGDSTECNSLLLQY
GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLLAD
AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLC
DILSRLDPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
PQSAPHGVVFLHVTYVPAQEKNFTTAPAI CHDGAHFPRGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC
DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
QELGKYEQ

SEQ ID NO: 52

>COV2_S_(R682G_R683S_R685S_V382C_R983C_K986P_V987P)

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
YFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
NCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
QTLLALHRSYLTTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTEKGI
YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLVNSASFSTFKCYGCSPTK
LNDLCFTNVYADSFVIRGDEVRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSN
LKPFFERDISTEIIYQAGSTPCNGVEGFNCFYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
KNKCVNFNFNGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGNSVVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPG
SASSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMKTSTVDCTMYICGDSTECNSLLLQY
GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLLAD
AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
DILSCLDPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
PQSAPHGVVFLHVTYVPAQEKNFTTAPAI CHDGAHFPRGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC
DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
QELGKYEQ

SEQ ID NO: 53

>COV2_S_(R682G_R683S_R685S_A570C_V963C)

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
YFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
NCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
QTLLALHRSYLTTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTEKGI
YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLVNSASFSTFKCYGVSPTK
LNDLCFTNVYADSFVIRGDEVRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSN
LKPFFERDISTEIIYQAGSTPCNGVEGFNCFYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
KNKCVNFNFNGLTGTGVLTESNKKFLPFQFGRDICDTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGNSVVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPG

SASSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNSNLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLLAD
 AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLCKQLSSNFGAIISSVLN
 DILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQ

SEQ ID NO: 54

>COV2_S_(R682G_R683S_R685S_D614C_T859C)

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWI FGTTLD SKTQSL LIVNNATNVV IKVCE FQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
 NCTFEYVSQPF LMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
 QTLLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNGTITDAVDCALDPLSETKCTLKSF TVEKGI
 YQTSNFRVQPTESIVRFPNITNLC PFGEVFNATRFASVYAWNRRKRISNCVADYSVLNYSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQCVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPG
 SASSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNSNLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLLAD
 AGFIKQYGDCLGDIAARDLICAQKFNGLCVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAIISSVLN
 DILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQ

SEQ ID NO: 55

>COV2_S_(R682G_R683S_R685S_K41C_A520C)

NLTTRTQLPPAYTNSFTRGVYYPDCVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWI FGTTLD SKTQSL LIVNNATNVV IKVCE FQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
 NCTFEYVSQPF LMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
 QTLLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNGTITDAVDCALDPLSETKCTLKSF TVEKGI
 YQTSNFRVQPTESIVRFPNITNLC PFGEVFNATRFASVYAWNRRKRISNCVADYSVLNYSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHCPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPG
 SASSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNSNLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLLAD
 AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAIISSVLN
 DILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQ

SEQ ID NO: 56

>COV2_S_(R682G_R683S_R685S_P225C_F562C)

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWI FGTTLD SKTQSL LIVNNATNVV IKVCE FQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
 NCTFEYVSQPF LMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALECLVDLPIGINITRF

QTLALHRSYLTTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFSTVEKGI
YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGVSPTK
LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
LKPFFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
KNKCVNFNFNGLTGTGVLTESNKKFLPCQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPG
SASSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQY
GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLDAD
AGFIKQYGDCLGDIAARDLICAQKFNGLTVL PPLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
DILSRDLKVEAEVQIDRLITGRQLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
PQSAPHGVVFLHVTYVPAQEKNFTTAPAI CHDGAHFPRGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC
DVGIVNNTTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
QELGKYEQ

SEQ ID NO: 57

>COV2_S_(R682G_R683S_R685S_P589C_F855C)

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
YFASTEKSNIIRGWI FGTTLDLSDKTQSLILVNNATNVVIKVFCEQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
NCTFEYVSQPFLLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPPQGFSALEPLVDLPIGINITRF
QTLALHRSYLTTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFSTVEKGI
YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGVSPTK
LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
LKPFFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
KNKCVNFNFNGLTGTGVLTESNKKFLPQQFGRDIADTTDAVRDPQTLEILDITCCSFGGVSVITPGTNTSNQV
AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPG
SASSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQY
GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLDAD
AGFIKQYGDCLGDIAARDLICAQKCNGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
DILSRDLKVEAEVQIDRLITGRQLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
PQSAPHGVVFLHVTYVPAQEKNFTTAPAI CHDGAHFPRGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC
DVGIVNNTTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
QELGKYEQ

SEQ ID NO: 58

>COV2_S_(R682G_R683S_R685S_P665C_L864C)

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
YFASTEKSNIIRGWI FGTTLDLSDKTQSLILVNNATNVVIKVFCEQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
NCTFEYVSQPFLLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPPQGFSALEPLVDLPIGINITRF
QTLALHRSYLTTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFSTVEKGI
YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGVSPTK
LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
LKPFFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
KNKCVNFNFNGLTGTGVLTESNKKFLPQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDICIGAGICASYQTQTNSPG
SASSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQY
GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLDAD
AGFIKQYGDCLGDIAARDLICAQKFNGLTVL PPLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
DILSRDLKVEAEVQIDRLITGRQLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
PQSAPHGVVFLHVTYVPAQEKNFTTAPAI CHDGAHFPRGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC
DVGIVNNTTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
QELGKYEQ

SEQ ID NO: 59

>COV2_S_(R682G_R683S_R685S_S383C_D985C)

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
YFASTEKSNIIRGWI FGTTLD SKTQSL L I V N N A T N V V I K V C E F Q F C N D P F L G V Y Y H K N N K S W M E S E F R V Y S S A N
NCTFEYVSQPF L M D L E G K Q G N F K N L R E F V F K N I D G Y F K I Y S K H T P I N L V R D L P Q G F S A L E P L V D L P I G I N I T R F
Q T L L A L H R S Y L T P G D S S S G W T A G A A Y Y V G Y L Q P R T F L L K Y N E N G T I T D A V D C A L D P L S E T K C T L K S F T V E K G I
Y Q T S N F R V Q P T E S I V R F P N I T N L C P F G E V F N A T R F A S V Y A W N R K R I S N C V A D Y S V L Y N S A S F S T F K C Y G V C P T K
L N D L C F T N V Y A D S F V I R G D E V R Q I A P G Q T G K I A D Y N Y K L P D D F T G C V I A W N S N N L D S K V G G N Y N Y L R L F R K S N
L K P F E R D I S T E I Y Q A G S T P C N G V E G F N C Y F P L Q S Y G F Q P T N G V G Y Q P Y R V V L S F E L L H A P A T V C G P K K S T N L V
K N K C V N F N F N G L T G T G V L T E S N K K F L P F Q Q F G R D I A D T T D A V R D P Q T L E I L D I T P C S F G G V S V I T P G T N T S N Q V
A V L Y Q D V N C T E V P V A I H A D Q L T P T W R V Y S T G S N V F Q T R A G C L I G A E H V N N S Y E C D I P I G A G I C A S Y Q T Q T N S P G
S A S S V A S Q S I I A Y T M S L G A E N S V A Y S N N S I A I P T N F T I S V T T E I L P V S M T K T S V D C T M Y I C G D S T E C S N L L L Q Y
G S F C T Q L N R A L T G I A V E Q D K N T Q E V F A Q V K Q I Y K T P P I K D F G G F N F S Q I L P D P S K P S K R S F I E D L L F N K V T L A D
A G F I K Q Y G D C L G D I A A R D L I C A Q K F N G L T V L P P L L T D E M I A Q Y T S A L L A G T I T S G W T F G A G A A L Q I P F A M Q M A Y
R F N G I G V T Q N V L Y E N Q K L I A N Q F N S A I G K I Q D S L S S T A S A L G K L Q D V N Q N A Q A L N T L V K Q L S S N F G A I S S V L N
D I L S R L C K V E A E V Q I D R L I T G R L Q S L Q T Y V T Q Q L I R A A E I R A S A N L A A T K M S E C V L G Q S K R V D F C G K Y H L M S F
P Q S A P H G V V F L H V T Y V P A Q E K N F T T A P A I C H D G K A H F P R E G V F V S N G T H W F V T Q R N F Y E P Q I I T D N T F V S G N C
D V V I G I V N N T V Y D P L Q P E L D S F K E E L D K Y F K N H T S P D V D L G D I S G I N A S V V N I Q K E I D R L N E V A K N L N E S L I D L
Q E L G K Y E Q

SEQ ID NO: 60

>COV2_S_(R682G_R683S_R685S_T547C_N978C)

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
YFASTEKSNIIRGWI FGTTLD SKTQSL L I V N N A T N V V I K V C E F Q F C N D P F L G V Y Y H K N N K S W M E S E F R V Y S S A N
NCTFEYVSQPF L M D L E G K Q G N F K N L R E F V F K N I D G Y F K I Y S K H T P I N L V R D L P Q G F S A L E P L V D L P I G I N I T R F
Q T L L A L H R S Y L T P G D S S S G W T A G A A Y Y V G Y L Q P R T F L L K Y N E N G T I T D A V D C A L D P L S E T K C T L K S F T V E K G I
Y Q T S N F R V Q P T E S I V R F P N I T N L C P F G E V F N A T R F A S V Y A W N R K R I S N C V A D Y S V L Y N S A S F S T F K C Y G V S P T K
L N D L C F T N V Y A D S F V I R G D E V R Q I A P G Q T G K I A D Y N Y K L P D D F T G C V I A W N S N N L D S K V G G N Y N Y L R L F R K S N
L K P F E R D I S T E I Y Q A G S T P C N G V E G F N C Y F P L Q S Y G F Q P T N G V G Y Q P Y R V V L S F E L L H A P A T V C G P K K S T N L V
K N K C V N F N F N G L C G T G V L T E S N K K F L P F Q Q F G R D I A D T T D A V R D P Q T L E I L D I T P C S F G G V S V I T P G T N T S N Q V
A V L Y Q D V N C T E V P V A I H A D Q L T P T W R V Y S T G S N V F Q T R A G C L I G A E H V N N S Y E C D I P I G A G I C A S Y Q T Q T N S P G
S A S S V A S Q S I I A Y T M S L G A E N S V A Y S N N S I A I P T N F T I S V T T E I L P V S M T K T S V D C T M Y I C G D S T E C S N L L L Q Y
G S F C T Q L N R A L T G I A V E Q D K N T Q E V F A Q V K Q I Y K T P P I K D F G G F N F S Q I L P D P S K P S K R S F I E D L L F N K V T L A D
A G F I K Q Y G D C L G D I A A R D L I C A Q K F N G L T V L P P L L T D E M I A Q Y T S A L L A G T I T S G W T F G A G A A L Q I P F A M Q M A Y
R F N G I G V T Q N V L Y E N Q K L I A N Q F N S A I G K I Q D S L S S T A S A L G K L Q D V N Q N A Q A L N T L V K Q L S S N F G A I S S V L C
D I L S R L D K V E A E V Q I D R L I T G R L Q S L Q T Y V T Q Q L I R A A E I R A S A N L A A T K M S E C V L G Q S K R V D F C G K Y H L M S F
P Q S A P H G V V F L H V T Y V P A Q E K N F T T A P A I C H D G K A H F P R E G V F V S N G T H W F V T Q R N F Y E P Q I I T D N T F V S G N C
D V V I G I V N N T V Y D P L Q P E L D S F K E E L D K Y F K N H T S P D V D L G D I S G I N A S V V N I Q K E I D R L N E V A K N L N E S L I D L
Q E L G K Y E Q

SEQ ID NO: 61

>COV2_S_(R682G_R683S_R685S_V382C_R983C)

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
YFASTEKSNIIRGWI FGTTLD SKTQSL L I V N N A T N V V I K V C E F Q F C N D P F L G V Y Y H K N N K S W M E S E F R V Y S S A N
NCTFEYVSQPF L M D L E G K Q G N F K N L R E F V F K N I D G Y F K I Y S K H T P I N L V R D L P Q G F S A L E P L V D L P I G I N I T R F
Q T L L A L H R S Y L T P G D S S S G W T A G A A Y Y V G Y L Q P R T F L L K Y N E N G T I T D A V D C A L D P L S E T K C T L K S F T V E K G I
Y Q T S N F R V Q P T E S I V R F P N I T N L C P F G E V F N A T R F A S V Y A W N R K R I S N C V A D Y S V L Y N S A S F S T F K C Y G C S P T K
L N D L C F T N V Y A D S F V I R G D E V R Q I A P G Q T G K I A D Y N Y K L P D D F T G C V I A W N S N N L D S K V G G N Y N Y L R L F R K S N
L K P F E R D I S T E I Y Q A G S T P C N G V E G F N C Y F P L Q S Y G F Q P T N G V G Y Q P Y R V V L S F E L L H A P A T V C G P K K S T N L V
K N K C V N F N F N G L T G T G V L T E S N K K F L P F Q Q F G R D I A D T T D A V R D P Q T L E I L D I T P C S F G G V S V I T P G T N T S N Q V
A V L Y Q D V N C T E V P V A I H A D Q L T P T W R V Y S T G S N V F Q T R A G C L I G A E H V N N S Y E C D I P I G A G I C A S Y Q T Q T N S P G
S A S S V A S Q S I I A Y T M S L G A E N S V A Y S N N S I A I P T N F T I S V T T E I L P V S M T K T S V D C T M Y I C G D S T E C S N L L L Q Y
G S F C T Q L N R A L T G I A V E Q D K N T Q E V F A Q V K Q I Y K T P P I K D F G G F N F S Q I L P D P S K P S K R S F I E D L L F N K V T L A D

AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPLLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNLSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAIISSVLN
 DILSCLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQ

SEQ ID NO: 62

>COV2_S_(R682G_R683S_R685S_K986P_V987P)_trimer_tag_2
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 NCTFEYVSQPFLLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLPIGINITRF
 QTLALHRSYLTTPGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLKSFTEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGVSPK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCFYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQGFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPG
 SASSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMKTSTVDCTMYICGDSTECNLLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLD
 AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPLLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNLSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAIISSVLN
 DILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQGGGSGYIPEAPRDGQAYVRKDGWVLLSTFLGLEVLVFQGPGRHHHHHHHSAWSHPQFEKGGGSGGG
 GSGGSAWSHPQFEK

SEQ ID NO: 63

>COV2_S_(R682G_R683S_R685S_A570C_V963C_K986P_V987P)_trimer_tag_2
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 YFASTEKSNIIRGWI FGTTLD SKTQSLIIVNNATNVVIVKCEFCNDPFLGVYHKNKNSWMESEFRVYSSAN
 NCTFEYVSQPFLLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLPIGINITRF
 QTLALHRSYLTTPGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLKSFTEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGVSPK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCFYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQGFGRDICDTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPG
 SASSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMKTSTVDCTMYICGDSTECNLLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLD
 AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPLLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNLSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAIISSVLN
 DILSRLDPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQGGGSGYIPEAPRDGQAYVRKDGWVLLSTFLGLEVLVFQGPGRHHHHHHHSAWSHPQFEKGGGSGGG
 GSGGSAWSHPQFEK

SEQ ID NO: 64

>COV2_S_(R682G_R683S_R685S_D614C_T859C_K986P_V987P)_trimer_tag_2
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 YFASTEKSNIIRGWI FGTTLD SKTQSLIIVNNATNVVIVKCEFCNDPFLGVYHKNKNSWMESEFRVYSSAN
 NCTFEYVSQPFLLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLPIGINITRF

QTLALHRSYLTTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQGFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQCVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPG
 SASSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLDAD
 AGFIKQYGDCLGDIAARDLCAQKFNGLCVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
 DILSRLDPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQGGGSGYIPEAPRDGQAYVRKDGWVLLSTFLGLEVLFGQPGHHHHHHHSAWSHPQFEKGGGSGGG
 GSGGSAWSHPQFEK

SEQ ID NO: 65

>COV2_S_(R682G_R683S_R685S_K41C_A520C_K986P_V987P)_trimer_tag_2
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 YFASTEKSNIIRGWI FGTTLDSTQSLILVNNATNVVIKVFCEQFCNDPFLGVYHKNKNSWMESEFRVYSSAN
 NCTFEYVSQPFLLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLPIGINITRF
 QTLALHRSYLTTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQGFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPG
 SASSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLDAD
 AGFIKQYGDCLGDIAARDLCAQKFNGLCVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
 DILSRLDPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQGGGSGYIPEAPRDGQAYVRKDGWVLLSTFLGLEVLFGQPGHHHHHHHSAWSHPQFEKGGGSGGG
 GSGGSAWSHPQFEK

SEQ ID NO: 66

>COV2_S_(R682G_R683S_R685S_P225C_F562C_K986P_V987P)_trimer_tag_2
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 NCTFEYVSQPFLLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRLDPQGFSALECLVDLPIGINITRF
 QTLALHRSYLTTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPCQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPG
 SASSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLDAD
 AGFIKQYGDCLGDIAARDLCAQKFNGLCVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
 DILSRLDPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNC

DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
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 GSGGSAWSHPQFEK

SEQ ID NO: 67

>COV2_S_(R682G_R683S_R685S_P589C_F855C_K986P_V987P)_trimer_tag_2
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 YFASTEKSNIIRGWI FGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
 NCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
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 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLVNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQGFGRDIADTTDAVRDPQTLEILDITCCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPG
 SASSVASQSI IAYTMSLGAENSVAYSNNIAIPTNFTISVTTEILPVSMKTSTVDCTMYICGDSTECNLLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLD
 AGFIKQYGDCLGDIAARDLCAQKCNGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
 DILSRLDPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFHTTAPAICHGDKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQGGGSGYIPEAPRDGQAYVRKDGWVLLSTFLGLEVLFGQPGHHHHHHHSAWSHPQFEKGGGSGGG
 GSGGSAWSHPQFEK

SEQ ID NO: 68

>COV2_S_(R682G_R683S_R685S_P665C_L864C_K986P_V987P)_trimer_tag_2
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 YFASTEKSNIIRGWI FGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
 NCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
 QTLALHRSYLTTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLVNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQGFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDICIGAGICASYQTQTNSPG
 SASSVASQSI IAYTMSLGAENSVAYSNNIAIPTNFTISVTTEILPVSMKTSTVDCTMYICGDSTECNLLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLD
 AGFIKQYGDCLGDIAARDLCAQKFNGLTVLPCLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
 DILSRLDPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFHTTAPAICHGDKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQGGGSGYIPEAPRDGQAYVRKDGWVLLSTFLGLEVLFGQPGHHHHHHHSAWSHPQFEKGGGSGGG
 GSGGSAWSHPQFEK

SEQ ID NO: 69

>COV2_S_(R682G_R683S_R685S_S383C_D985C_K986P_V987P)_trimer_tag_2
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 YFASTEKSNIIRGWI FGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
 NCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
 QTLALHRSYLTTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLVNSASFSTFKCYGVCPTK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN

LKPFFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPG
 SASSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLLAD
 AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
 DILSRLCPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQGGGSGYIPEAPRDGQAYVRKDGWVLLSTFLGLEVLFGQPGHHHHHHHSAWSHPQFEKGGGSGGG
 GSGGSAWSHPQFEK

SEQ ID NO: 70

>COV2_S_(R682G_R683S_R685S_T547C_N978C_K986P_V987P)_trimer_tag_2
 NLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWIFGTTLDSTQSLIIVNNATNVVIKVFCEFCNDPFLGVYHKNKNSWMESEFRVYSSAN
 NCTFEYVSQPFLLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
 QTLALHRSYLTTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNGTITDAVDCALDPLSETKCTLKSFTEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSN
 LKPFFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLCTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPG
 SASSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLLAD
 AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLC
 DILSRLDPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQGGGSGYIPEAPRDGQAYVRKDGWVLLSTFLGLEVLFGQPGHHHHHHHSAWSHPQFEKGGGSGGG
 GSGGSAWSHPQFEK

SEQ ID NO: 71

>COV2_S_(R682G_R683S_R685S_V382C_R983C_K986P_V987P)_trimer_tag_2
 NLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWIFGTTLDSTQSLIIVNNATNVVIKVFCEFCNDPFLGVYHKNKNSWMESEFRVYSSAN
 NCTFEYVSQPFLLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
 QTLALHRSYLTTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNGTITDAVDCALDPLSETKCTLKSFTEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGCSPTK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSN
 LKPFFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPG
 SASSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLLAD
 AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
 DILSCLDPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQGGGSGYIPEAPRDGQAYVRKDGWVLLSTFLGLEVLFGQPGHHHHHHHSAWSHPQFEKGGGSGGG
 GSGGSAWSHPQFEK

SEQ ID NO: 72

>COV2_S_(R682G_R683S_R685S_A570C_V963C)_trimer_tag_2

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
 NCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
 QTLLALHRSYLTTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSTVEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKISNCVADYSVLVNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQFGRDICDITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAETHVNSYECDIPIGAGICASYQTQTNSPG
 SASSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMKTSTVDCTMYICGDSTECNNLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLD
 AGFIKQYGDCLGDIAARDLCAQKFNGLTVLPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDLSSTASALGKLQDVVNQNAQALNTLCKQLSSNFGAISSVLN
 DILSRDLKVEAEVQIDRLITGRQLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQGGGSGYIPEAPRDGQAYVRKDGWVLLSTFLGLEVLFGQPGHHHHHHHSAWSHPQFEKGGGSGGG
 GSGGSAWSHPQFEK

SEQ ID NO: 73

>COV2_S_(R682G_R683S_R685S_D614C_T859C)_trimer_tag_2

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
 NCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
 QTLLALHRSYLTTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSTVEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKISNCVADYSVLVNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQCVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAETHVNSYECDIPIGAGICASYQTQTNSPG
 SASSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMKTSTVDCTMYICGDSTECNNLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLD
 AGFIKQYGDCLGDIAARDLCAQKFNGLCVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
 DILSRDLKVEAEVQIDRLITGRQLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQGGGSGYIPEAPRDGQAYVRKDGWVLLSTFLGLEVLFGQPGHHHHHHHSAWSHPQFEKGGGSGGG
 GSGGSAWSHPQFEK

SEQ ID NO: 74

>COV2_S_(R682G_R683S_R685S_K41C_A520C)_trimer_tag_2

NLTTRTQLPPAYTNSFTRGVYYPDCVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
 NCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
 QTLLALHRSYLTTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSTVEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKISNCVADYSVLVNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHCPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAETHVNSYECDIPIGAGICASYQTQTNSPG

SASSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNSNLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLLAD
 AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPLLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
 DILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQGGGSGYIPEAPRDGQAYVRKDGWVLLSTFLGLEVLVFQGPGRHHHHHHHSAWSHPQFEKGGGSGGG
 GSGGSAWSHPQFEK

SEQ ID NO: 75

>COV2_S_(R682G_R683S_R685S_P225C_F562C)_trimer_tag_2
 NLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVYHKNKNSWMESEFRVYSSAN
 NCTFEYVSQPFLLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALECLVDLPIGINITRF
 QTLALHRSYLTTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSTVEKGI
 YQTSNFRVQPTESIVRFPNITNLCPPGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPCQQFGRDIADTTDAVRDPQTLTILEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPG
 SASSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNSNLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLLAD
 AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPLLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
 DILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQGGGSGYIPEAPRDGQAYVRKDGWVLLSTFLGLEVLVFQGPGRHHHHHHHSAWSHPQFEKGGGSGGG
 GSGGSAWSHPQFEK

SEQ ID NO: 76

>COV2_S_(R682G_R683S_R685S_P589C_F855C)_trimer_tag_2
 NLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVYHKNKNSWMESEFRVYSSAN
 NCTFEYVSQPFLLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLPIGINITRF
 QTLALHRSYLTTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSTVEKGI
 YQTSNFRVQPTESIVRFPNITNLCPPGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLTILEILDITCCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPG
 SASSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNSNLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLLAD
 AGFIKQYGDCLGDIAARDLICAQKCNGLTVLPLLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
 DILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQGGGSGYIPEAPRDGQAYVRKDGWVLLSTFLGLEVLVFQGPGRHHHHHHHSAWSHPQFEKGGGSGGG
 GSGGSAWSHPQFEK

SEQ ID NO: 77

>COV2_S_(R682G_R683S_R685S_P665C_L864C)_trimer_tag_2

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWI FGTTLD SKTQSL LIVNNATNVV IKVCE FQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
 NCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
 QTLLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLVNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVQR IAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFENGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSEYCDICIGAGICASYQTQTNSPG
 SASSVASQSI IAYTMSLGAENSVAYSNN SIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLDAD
 AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPCLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFN SAI GKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
 DILSRLDKVEAEVQIDRLITGR LQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAI CHDGAHFREGV FVSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVGIVGNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQGGGSGYIPEAPRDGQAYVRKDG EWVLLSTFLGLEVL FQGP GHHHHHHHSAWSHPQFEKGGGSGGG
 GSGGSAWSHPQFEK

SEQ ID NO: 78

>COV2_S_(R682G_R683S_R685S_S383C_D985C)_trimer_tag_2

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWI FGTTLD SKTQSL LIVNNATNVV IKVCE FQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
 NCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
 QTLLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLVNSASFSTFKCYGVCPTK
 LNDLCFTNVYADSFVIRGDEVQR IAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFENGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSEYCDIPIGAGICASYQTQTNSPG
 SASSVASQSI IAYTMSLGAENSVAYSNN SIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLDAD
 AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFN SAI GKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN
 DILSRLCKVEAEVQIDRLITGR LQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAI CHDGAHFREGV FVSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVGIVGNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQGGGSGYIPEAPRDGQAYVRKDG EWVLLSTFLGLEVL FQGP GHHHHHHHSAWSHPQFEKGGGSGGG
 GSGGSAWSHPQFEK

SEQ ID NO: 79

>COV2_S_(R682G_R683S_R685S_T547C_N978C)_trimer_tag_2

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
 YFASTEKSNIIRGWI FGTTLD SKTQSL LIVNNATNVV IKVCE FQFCNDPFLGVYYHKNNKSWMESEFRVYSSAN
 NCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
 QTLLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLVNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVQR IAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNNYNYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFENGLCGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSEYCDIPIGAGICASYQTQTNSPG
 SASSVASQSI IAYTMSLGAENSVAYSNN SIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLQY
 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLDAD
 AGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY

RFNGIGVTONVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAIISSVLC
DILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNC
DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
QELGKYEQGGGSGYIPEAPRDGQAYVRKDGWVLLSTFLGLEVLFGQPGHHHHHHHSAWSHPQFEKGGGSGGG
GSGGSAWSHPQFEK

SEQ ID NO: 80

>COV2_S_(R682G_R683S_R685S_V382C_R983C)_trimer_tag_2

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
YFASTEKSNIIRGWI FGTTLD SKTQSL LIVNNATNVV IKVCE FQFCNDPFLGVYHKNKNSWMESEFRVYSSAN
NCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
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SASSVASQSI IAYTMSLGAENSVAYSNN SIAIPTNFTISVTTEILPVSMKT SV DCTMYICGDSTEC SNLLQY
GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLAD
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PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNC
DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
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GSGGSAWSHPQFEK

SEQ ID NO: 81

>SEQ128430_-_prefusion-stabilized_trimer_tag SARS_CoV_2_S-protein (1-
1208,R682G,R683S,R685S,K986P,V987P), trimerization domain, HRV 3C Protease
Site, G, His8, SA, Strep tag, GGGSGGGSGGSA, Strep tag

NLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
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NCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
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YQTSNFRVQPTESIVRFPNITNLCPFGVEFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGVSP TK
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SASSVASQSI IAYTMSLGAENSVAYSNN SIAIPTNFTISVTTEILPVSMKT SV DCTMYICGDSTEC SNLLQY
GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLAD
AGFIKQYGDCLGDIAARDLICAQKFNGLT VLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
RFNGIGVTONVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAIISSVLN
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PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNC
DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
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SEQ ID NO: 82

>SEQ128430_-prefusion-stabilized_trimer_tag SARS_CoV_2_S-protein (1-1208,R682G,R683S,R685S,K986P,V987P), trimerization domain, HRV 3C Protease Site, G, His8, SA, Strep tag, GGGSGGGSGGSA, Strep tag
 NLTRTRQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
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 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLVNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSN
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 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLD
 AGFIKQYGDCLGDIAARDLCAQKFNGLTVLPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
 RFNGIGVTVQNVLYENQKLIANQFNSAIGKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAIISSVLN
 DILSRDLGVAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQGGGSGYIPEAPRDGQAYVRKDGWVLLSTFLGLEVLFGQPGHHHHHHHSAWSHPQFEKGGGSGGG
 GSGGSAWSHPQFEK

SEQ ID NO: 83

>COV2_S_(K986P_V987P)_trimer_tag_2

NLTRTRQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGV
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 NCTFEYVSQPFLLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF
 QTLALHRSYLTTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSTVEKGI
 YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLVNSASFSTFKCYGVSPTK
 LNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSN
 LKPFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLV
 KNKCVNFNFNGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQV
 AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAETHVNSYECDIPIGAGICASYQTQTNTPR
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 GSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLD
 AGFIKQYGDCLGDIAARDLCAQKFNGLTVLPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAY
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 DILSRDLDPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSF
 PQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNC
 DVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL
 QELGKYEQ

SEQ ID NO: 84

>fibrin trimerization domain

GYIPEAPRDGQAYVRKDGWVLLSTFL

SEQ ID NO: 85

>trimer_tag_2

GGGSGYIPEAPRDGQAYVRKDGWVLLSTFLGLEVLFGQPGHHHHHHHSAWSHPQFEKGGGSGGGSGGSAWS
 HPQFEK

SEQ ID NO: 86

>Signal peptide

MFVFLVLLPLVSSQCV

SEQ ID NO: 87
>Signal peptide
MDMRVPAQLLGLLLLWLRGARC

SEQ ID NO: 88
>Signal peptide
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SEQ ID NO: 89
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SEQ ID NO: 90
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SEQ ID NO: 91
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MEWTWRVFLVAAATGAHS

SEQ ID NO: 92
>Signal peptide
METPAQLLFLLLLWLPDTTG

SEQ ID NO: 93
>Signal peptide
METPAQLLFLLLLWLPDTTG

SEQ ID NO: 94
>Signal peptide
MKHLWFFLLLVAAPRWVLS

SEQ ID NO: 95
>Signal peptide
MEWSWVFLFFLSVTTGVHS

SEQ ID NO: 96
>Signal peptide
MGILPSPGMPALLSLVSLLSVLLMGCVAETGTQC

SEQ ID NO: 97
>Linker
GGSGGGGSGGSA

CLAIMS

We claim:

1. An immunogen comprising a severe acute respiratory syndrome coronavirus 2 spike (“SARS-CoV2 S”) polypeptide, wherein the polypeptide comprises one or more pairs of amino acid substitutions that correspond to residues selected from the group consisting of:

- a) V382C and R983C of SEQ ID NO: 1;
- b) A520C and K41C of SEQ ID NO: 1;
- c) S383C and D985C of SEQ ID NO: 1;
- d) D614C and T859C of SEQ ID NO: 1;
- e) T547C and N978C of SEQ ID NO: 1;
- f) A570C and V963C of SEQ ID NO: 1;
- g) P665C and L864C of SEQ ID NO: 1;
- h) F562C and P225C of SEQ ID NO: 1; and
- i) P589C and F855C of SEQ ID NO: 1.

2. The immunogen of claim 1, wherein the polypeptide comprises amino acid substitutions that correspond to residues D614C, T859C, T547C and N978C.

3. The immunogen of any one of claim 1 or 2, wherein the polypeptide further comprises one or more groups of amino acid substitutions that correspond to residues selected from the group consisting of:

- a) K986P and V987P of SEQ ID NO: 1;
- b) R682G, R683S, and R685S of SEQ ID NO: 1;
- c) R682S, R683G, and R685G of SEQ ID NO: 1;
- d) R682G, R683S, R685S, K986P and V987P of SEQ ID NO: 1; and
- e) R682S, R683G, R685G, K986P and V987P of SEQ ID NO: 1.

4. The immunogen of any one of claims 1-3, wherein the polypeptide has at least 97% sequence identity to SEQ ID NO: 1.

5. The immunogen of any one of claims 1-4, wherein the polypeptide has at least 98% sequence identity to SEQ ID NO: 1.

6. The immunogen of any one of claims 1-5, wherein the polypeptide has at least 98% sequence identity to SEQ ID NO: 1.
7. The immunogen of any one of claims 1-6, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 13-21.
8. The immunogen of claim 3, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 4-12 and 44-61.
9. The immunogen of any preceding claim, wherein the polypeptide comprises a trimerization domain attached to the C-terminus of the immunogen.
10. The immunogen of claim 9, wherein the trimerization domain comprises the amino acid sequence of SEQ ID NO: 84 or SEQ ID NO: 85.
11. The immunogen of claim 10, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 23-40 and 63-80.
12. A method of producing antibodies that specifically bind SARS-CoV2 S polypeptide comprising administering to a non-human subject the immunogen of any one of claims 1-10 and a pharmaceutically acceptable delivery vehicle and/or adjuvant.
13. A method of treating COVID-19 in a subject comprising administering a therapeutically effective amount of an antibody produced by the method of claim 11 and a pharmaceutically acceptable delivery vehicle to the subject.
14. A composition capable of producing an immunological response in a human subject, the composition comprising the immunogen of any one of claims 1-10 and a pharmaceutically acceptable delivery vehicle and/or adjuvant.

SARS-CoV-2 Spike shows 2 main conformations:
Pre and Post-fusion State

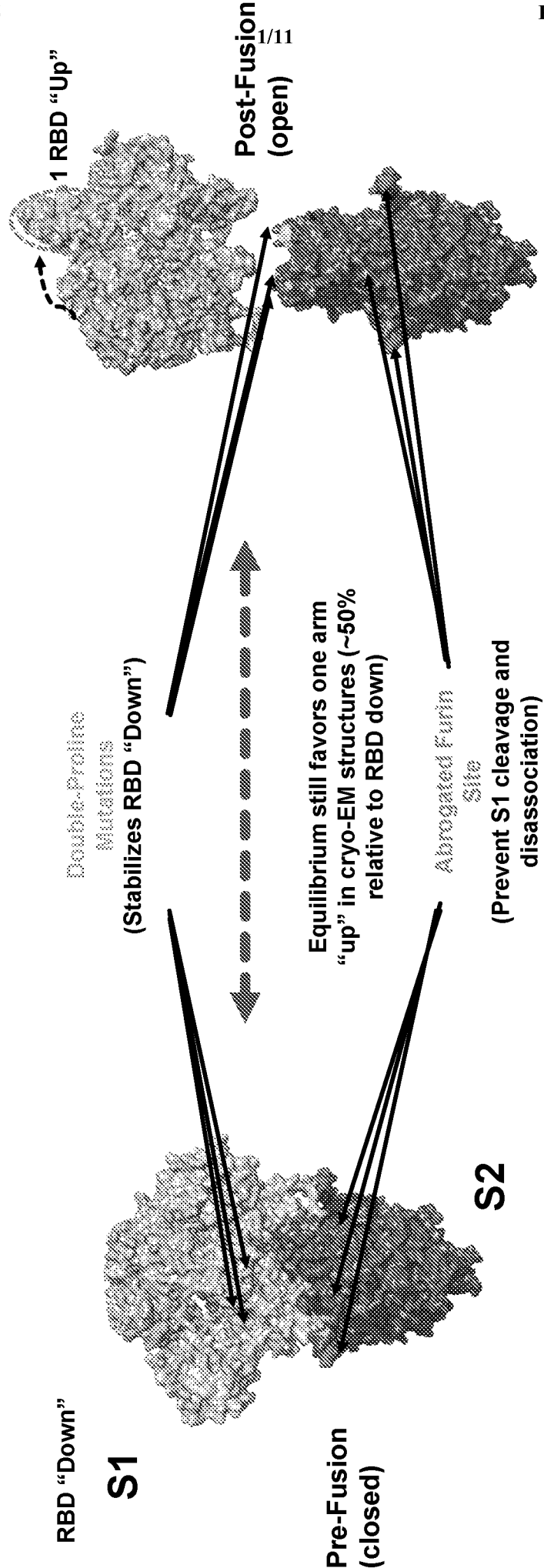
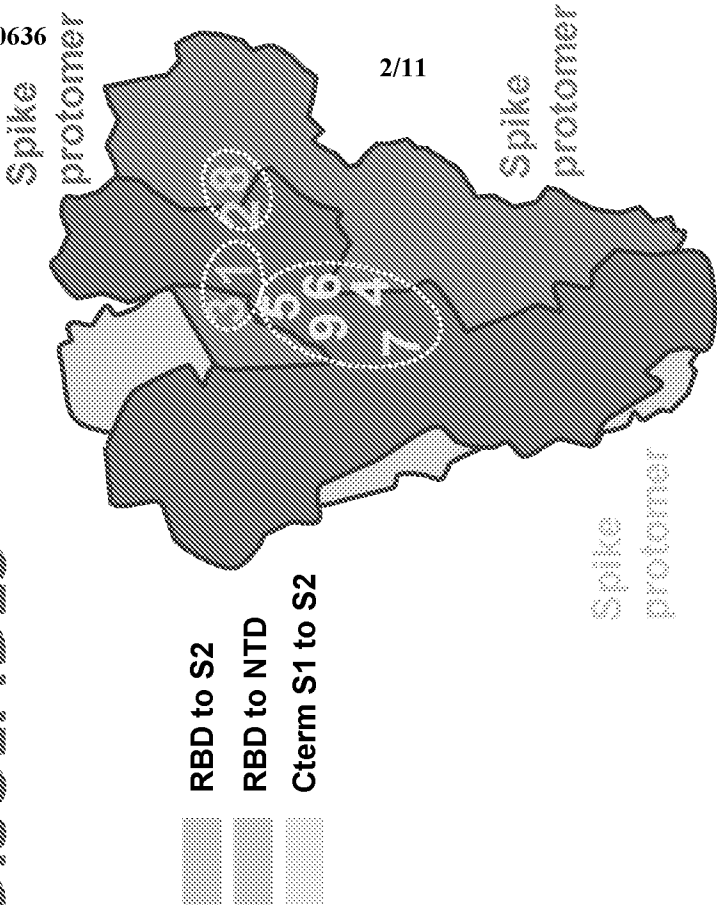


Fig. 1

THREE CLASSES OF ENGINEERED DISULFIDES



Design ID	Residue Pair	Total Energy	Disulfide Potential
RCC1	V382C - R983C	4.53	-0.42
RCC2	A520C - K41C	4.76	0.37
RCC3	S383C - D985C	6.17	1.02
RCC4	D614C - T859C	7.29	0.83
RCC5	T547C - N978C	8.84	0.88
RCC6	A570C - V963C	8.96	3.08
RCC7	P665C - L864C	9.07	0.82
RCC8	F562C - P225C	9.52	0.14
RCC9	P589C - F855C	9.74	1.48

666 S1 residues x 474 S2 residues x 3 subunits = ~900,000 possible pairs
Filter pairs with CB < 6.5Å and model disulfide residues (n = 56)
9 with good energy scores (REU<10)

Fig. 2

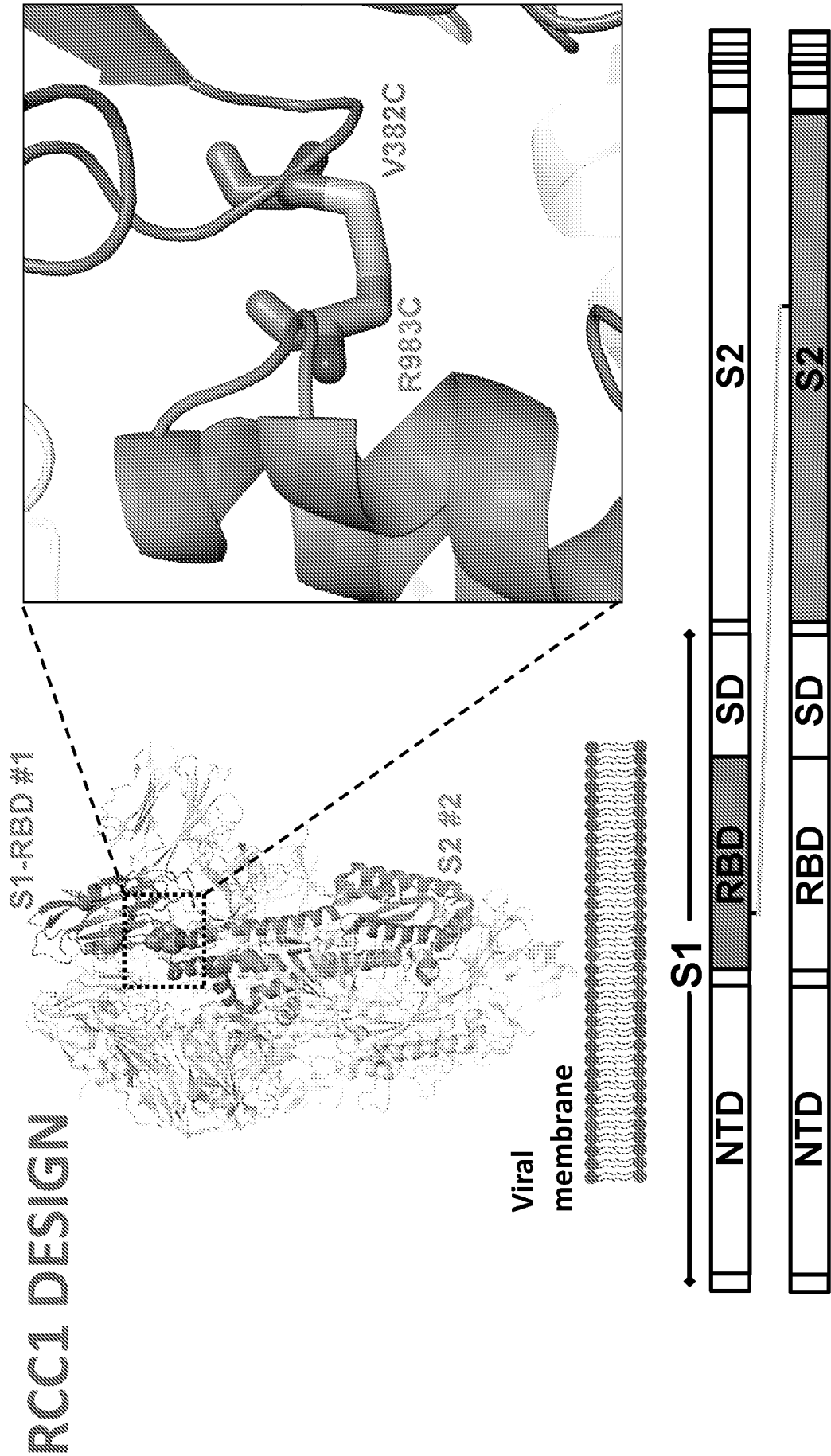


Fig. 3

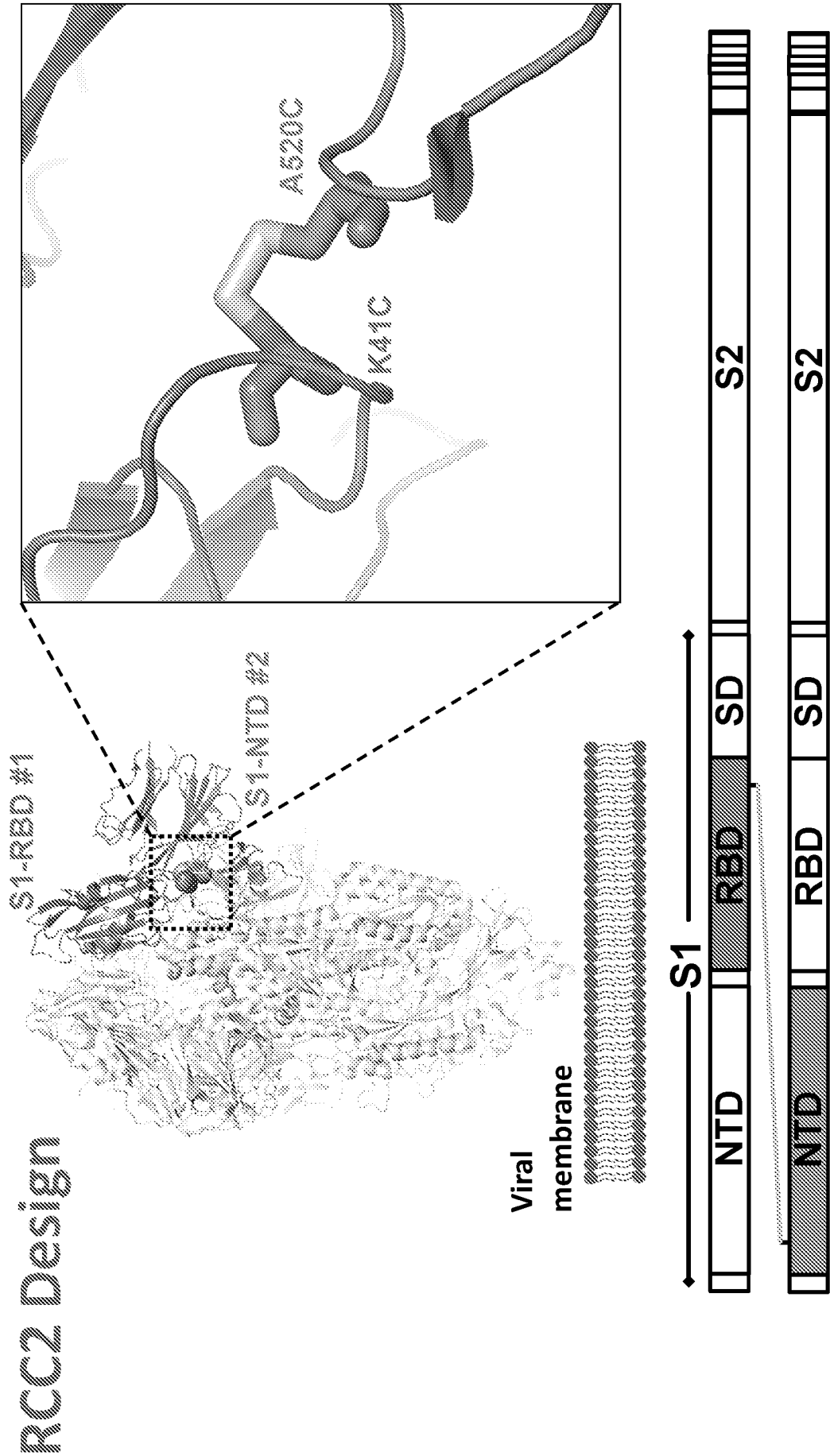


Fig. 4

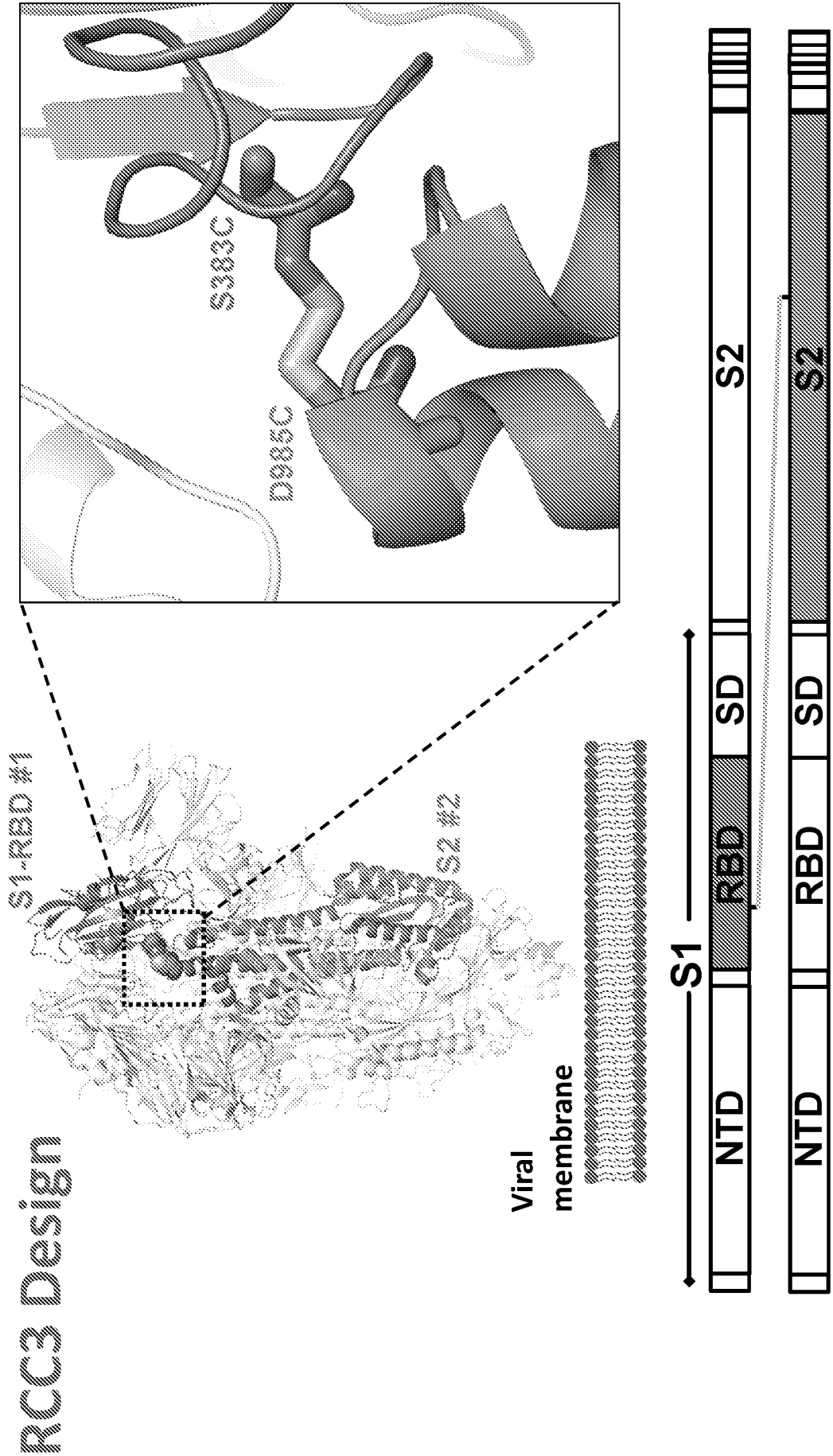


Fig. 5

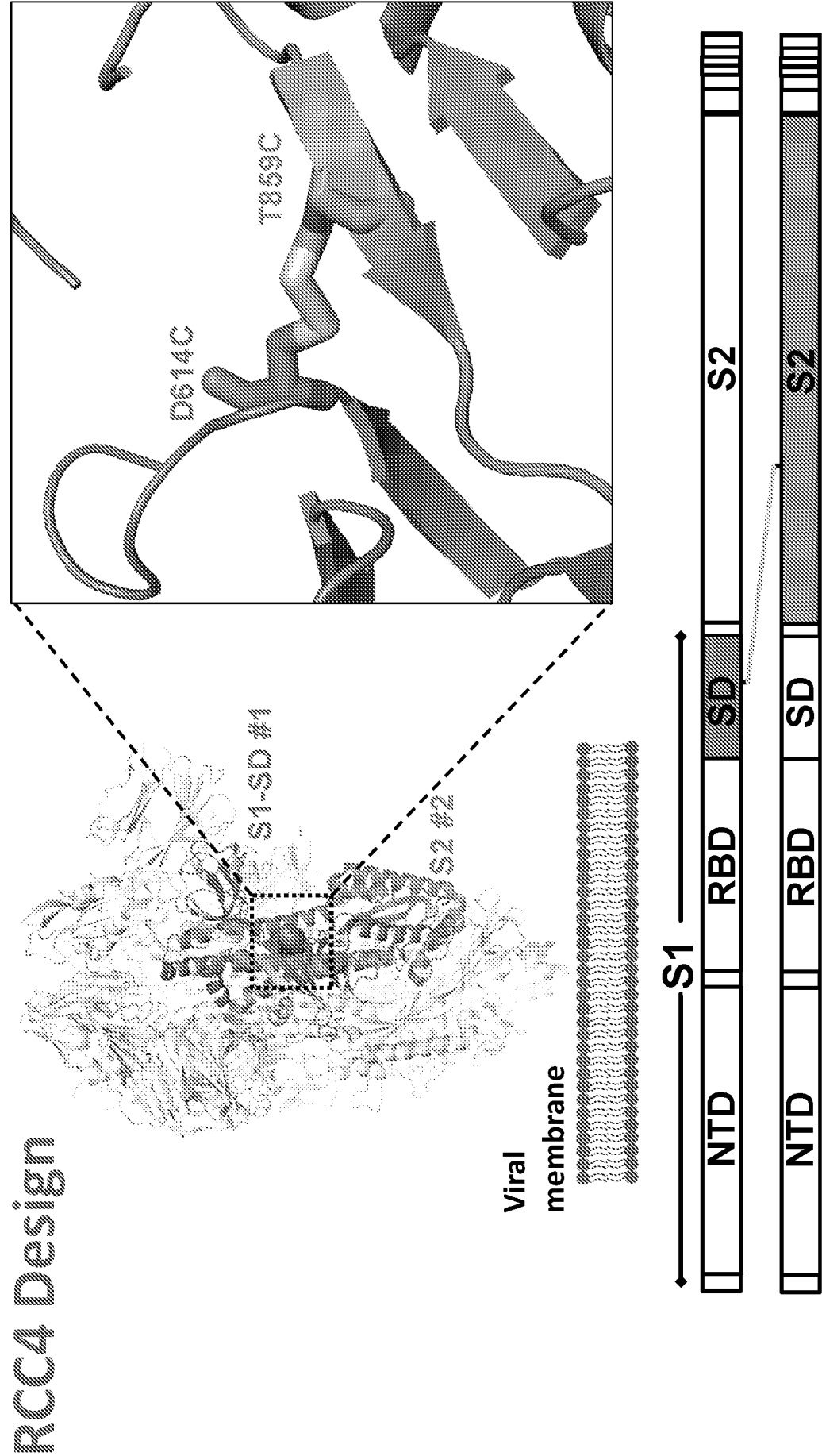


Fig. 6

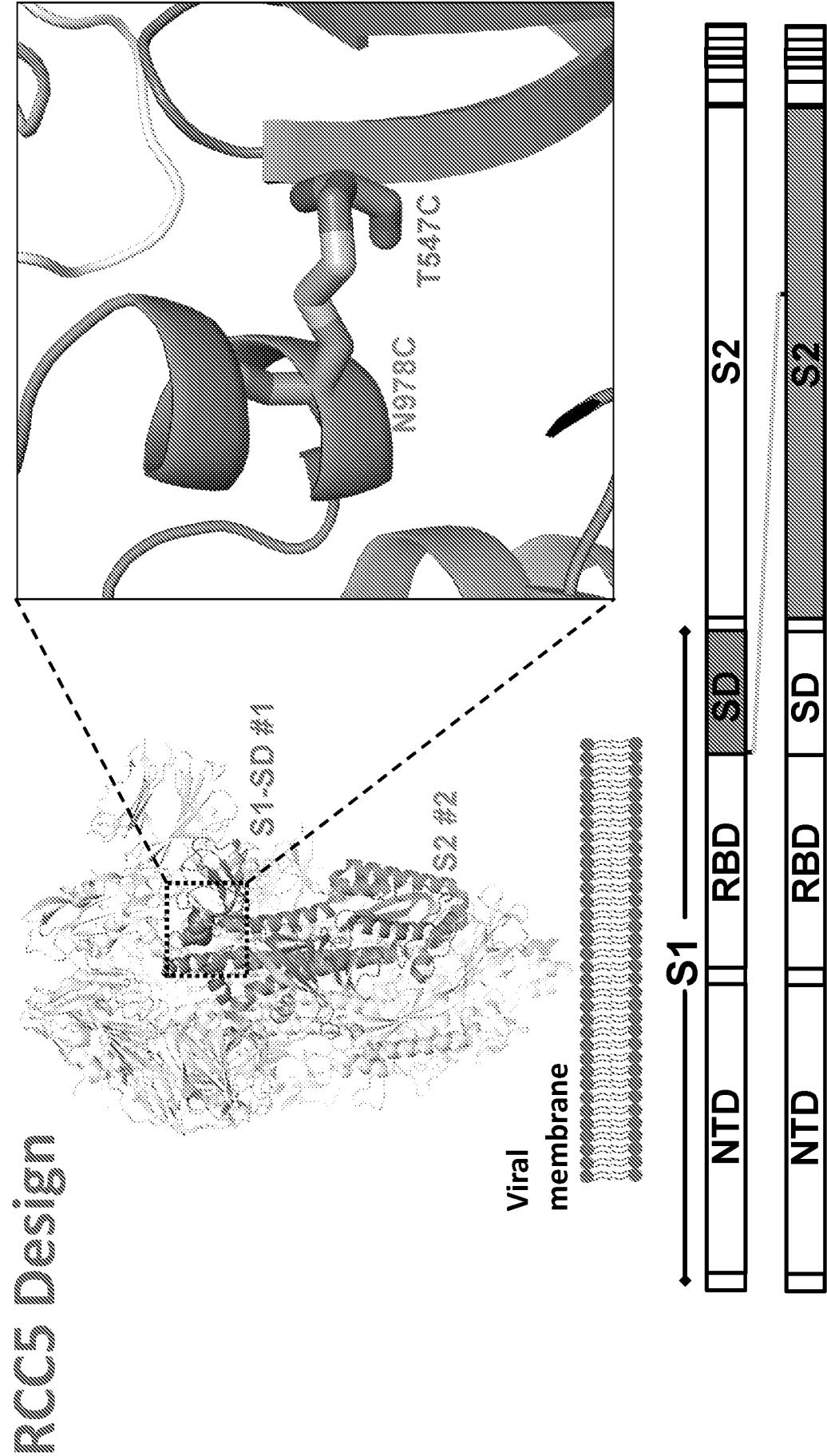


Fig. 7

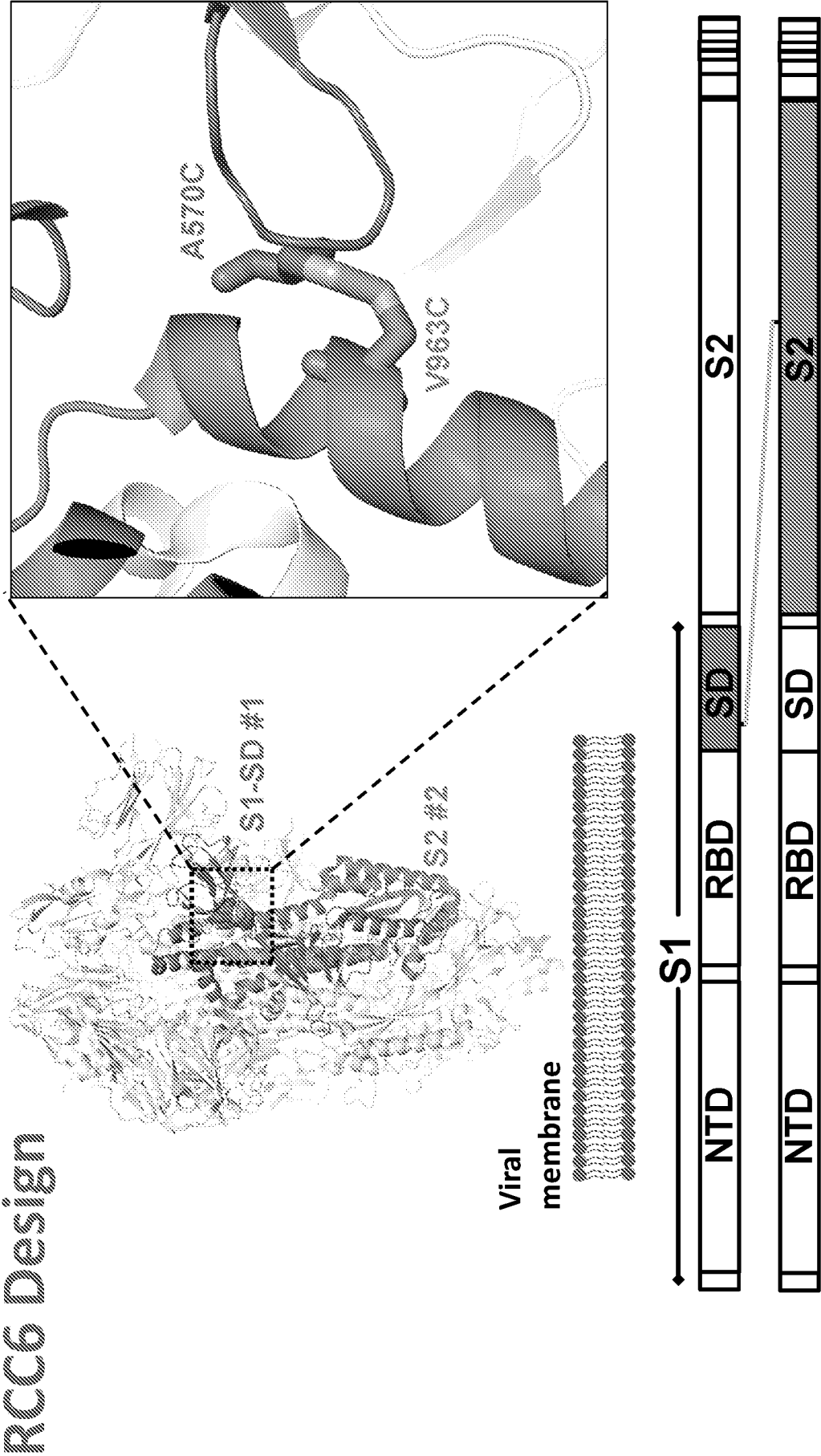


Fig.

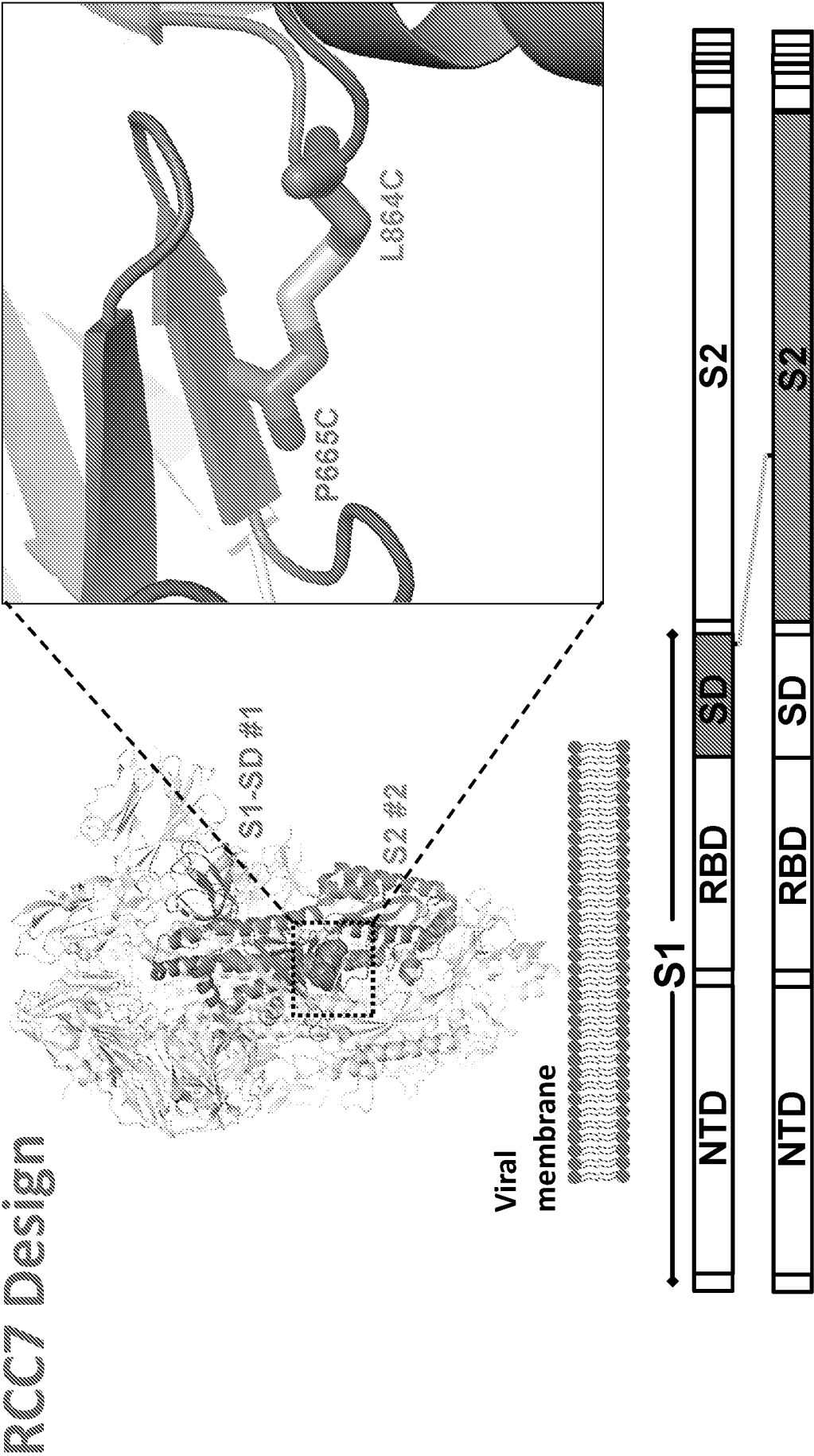


Fig.

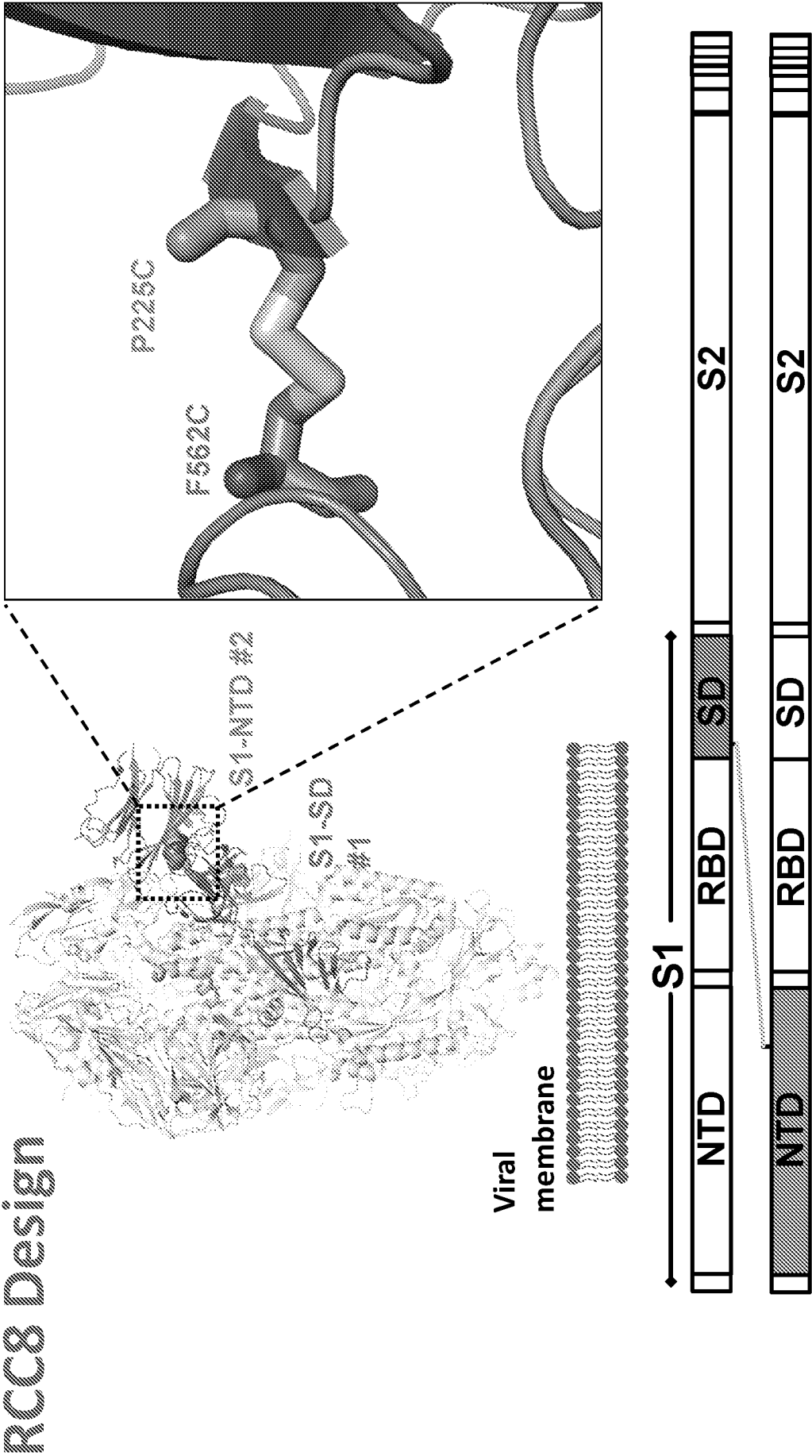


Fig. 1

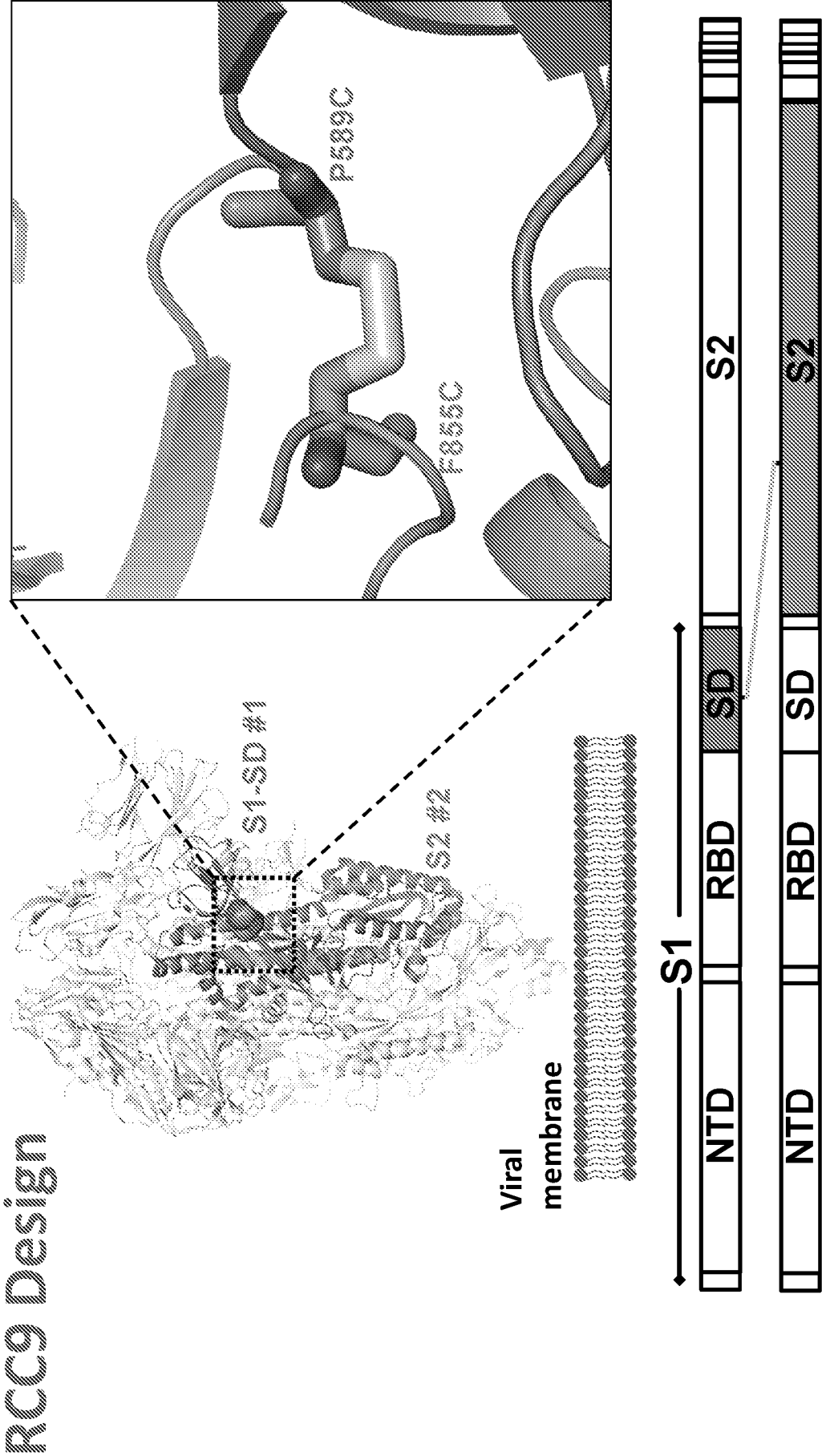


Fig. 1

SEQUENCE LISTING

<110> AMGEN INC.
GARCES, Fernando
WANG, Zhulun
RILEY, Timothy

<120> IMMUNOGENS DERIVED FROM SARS-COV2 SPIKE PROTEIN

<130> A-2657-W0-PCT

<150> 63/056,396

<151> 2020-07-24

<160> 97

<170> PatentIn version 3.5

<210> 1

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<213> SARS-CoV-2

<400> 1

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
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Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val	Phe	Lys	Asn	Ile	Asp	Gly	Tyr	Phe	Lys	Ile	Tyr	Ser	Lys	His	Thr	180	185	190	
Pro	Ile	Asn	Leu	Val	Arg	Asp	Leu	Pro	Gln	Gly	Phe	Ser	Ala	Leu	Glu	195	200	205	
Pro	Leu	Val	Asp	Leu	Pro	Ile	Gly	Ile	Asn	Ile	Thr	Arg	Phe	Gln	Thr	210	215	220	
Leu	Leu	Ala	Leu	His	Arg	Ser	Tyr	Leu	Thr	Pro	Gly	Asp	Ser	Ser	Ser	225	230	235	240
Gly	Trp	Thr	Ala	Gly	Ala	Ala	Ala	Tyr	Tyr	Val	Gly	Tyr	Leu	Gln	Pro	245	250	255	
Arg	Thr	Phe	Leu	Leu	Lys	Tyr	Asn	Glu	Asn	Gly	Thr	Ile	Thr	Asp	Ala	260	265	270	
Val	Asp	Cys	Ala	Leu	Asp	Pro	Leu	Ser	Glu	Thr	Lys	Cys	Thr	Leu	Lys	275	280	285	
Ser	Phe	Thr	Val	Glu	Lys	Gly	Ile	Tyr	Gln	Thr	Ser	Asn	Phe	Arg	Val	290	295	300	
Gln	Pro	Thr	Glu	Ser	Ile	Val	Arg	Phe	Pro	Asn	Ile	Thr	Asn	Leu	Cys	305	310	315	320
Pro	Phe	Gly	Glu	Val	Phe	Asn	Ala	Thr	Arg	Phe	Ala	Ser	Val	Tyr	Ala	325	330	335	
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Lys	Ile	Ala	Asp	Tyr	Asn	Tyr	Lys	Leu	Pro	Asp	Asp	Phe	Thr	Gly	Cys	405	410	415	
Val	Ile	Ala	Trp	Asn	Ser	Asn	Asn	Leu	Asp	Ser	Lys	Val	Gly	Gly	Asn	420	425	430	
Tyr	Asn	Tyr	Leu	Tyr	Arg	Leu	Phe	Arg	Lys	Ser	Asn	Leu	Lys	Pro	Phe	435	440	445	

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Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
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Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
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Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
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Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

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705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu

725

730

735

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Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
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Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
 770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
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Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
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Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
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Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
 900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
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Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
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Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
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Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
 965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
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Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
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Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln
1190

<210> 2
<211> 1257
<212> PRT
<213> SARS-CoV-2

<400> 2

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys

305					310						315				320
Pro	Phe	Gly	Glu	Val	Phe	Asn	Ala	Thr	Arg	Phe	Ala	Ser	Val	Tyr	Ala
				325					330					335	
Trp	Asn	Arg	Lys	Arg	Ile	Ser	Asn	Cys	Val	Ala	Asp	Tyr	Ser	Val	Leu
			340					345					350		
Tyr	Asn	Ser	Ala	Ser	Phe	Ser	Thr	Phe	Lys	Cys	Tyr	Gly	Val	Ser	Pro
		355					360					365			
Thr	Lys	Leu	Asn	Asp	Leu	Cys	Phe	Thr	Asn	Val	Tyr	Ala	Asp	Ser	Phe
	370					375					380				
Val	Ile	Arg	Gly	Asp	Glu	Val	Arg	Gln	Ile	Ala	Pro	Gly	Gln	Thr	Gly
385					390					395					400
Lys	Ile	Ala	Asp	Tyr	Asn	Tyr	Lys	Leu	Pro	Asp	Asp	Phe	Thr	Gly	Cys
				405					410					415	
Val	Ile	Ala	Trp	Asn	Ser	Asn	Asn	Leu	Asp	Ser	Lys	Val	Gly	Gly	Asn
			420					425					430		
Tyr	Asn	Tyr	Leu	Tyr	Arg	Leu	Phe	Arg	Lys	Ser	Asn	Leu	Lys	Pro	Phe
		435					440					445			
Glu	Arg	Asp	Ile	Ser	Thr	Glu	Ile	Tyr	Gln	Ala	Gly	Ser	Thr	Pro	Cys
	450					455					460				
Asn	Gly	Val	Glu	Gly	Phe	Asn	Cys	Tyr	Phe	Pro	Leu	Gln	Ser	Tyr	Gly
465					470					475					480
Phe	Gln	Pro	Thr	Asn	Gly	Val	Gly	Tyr	Gln	Pro	Tyr	Arg	Val	Val	Val
				485					490					495	
Leu	Ser	Phe	Glu	Leu	Leu	His	Ala	Pro	Ala	Thr	Val	Cys	Gly	Pro	Lys
			500					505					510		
Lys	Ser	Thr	Asn	Leu	Val	Lys	Asn	Lys	Cys	Val	Asn	Phe	Asn	Phe	Asn
		515					520					525			
Gly	Leu	Thr	Gly	Thr	Gly	Val	Leu	Thr	Glu	Ser	Asn	Lys	Lys	Phe	Leu
	530					535					540				
Pro	Phe	Gln	Gln	Phe	Gly	Arg	Asp	Ile	Ala	Asp	Thr	Thr	Asp	Ala	Val
545					550					555					560
Arg	Asp	Pro	Gln	Thr	Leu	Glu	Ile	Leu	Asp	Ile	Thr	Pro	Cys	Ser	Phe
				565					570					575	
Gly	Gly	Val	Ser	Val	Ile	Thr	Pro	Gly	Thr	Asn	Thr	Ser	Asn	Gln	Val
			580					585					590		

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
 595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
 610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
 625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
 645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
 660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
 675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
 690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
 705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
 725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
 740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
 755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
 770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
 785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
 805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
 820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
 835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
 850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln Tyr Ile Lys Trp Pro Trp Tyr Ile Trp Leu Gly
1190 1195 1200

Phe Ile Ala Gly Leu Ile Ala Ile Val Met Val Thr Ile Met Leu
1205 1210 1215

Cys Cys Met Thr Ser Cys Cys Ser Cys Leu Lys Gly Cys Cys Ser
1220 1225 1230

Cys Gly Ser Cys Cys Lys Phe Asp Glu Asp Asp Ser Glu Pro Val
1235 1240 1245

Leu Lys Gly Val Lys Leu His Tyr Thr
1250 1255

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<211> 1192
<212> PRT
<213> Artificial Sequence

<220>
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<400> 3

Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe
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Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu
20 25 30

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala

645

650

655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln
1190

<210> 4
<211> 1192
<212> PRT
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<220>
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Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe
1 5 10 15

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
 225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
 245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
 260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
 290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
 305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
 325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
 355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
 500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
 515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
 530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Cys Asp Thr Thr Asp Ala Val
 545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
 565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
 580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
 595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
 610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
 625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
 645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
 660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
 675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
 690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
 705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
 725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
 740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
 755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Cys Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro

1040		1045		1050
Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp				
1055		1060		1065
Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly				
1070		1075		1080
Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile				
1085		1090		1095
Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val				
1100		1105		1110
Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu				
1115		1120		1125
Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His				
1130		1135		1140
Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala				
1145		1150		1155
Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val				
1160		1165		1170
Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly				
1175		1180		1185
Lys Tyr Glu Gln				
1190				
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Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe				
1		5	10	15
Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu				
	20	25	30	
His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp				
	35	40	45	
Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp				
50	55	60		

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu

340

345

350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
 355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
 500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
 515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
 530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
 545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
 565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
 580 585 590

Ala Val Leu Tyr Gln Cys Val Asn Cys Thr Glu Val Pro Val Ala Ile
 595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
 610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Cys Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln
1190

<210> 6
<211> 1192
<212> PRT
<213> Artificial Sequence

<220>
<223> COV2_S_(K41C_A520C_K986P_V987P)

<400> 6

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Cys Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr

740

745

750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln
1190

<210> 7
<211> 1192
<212> PRT
<213> Artificial Sequence

<220>
<223> COV2_S_(P225C_F562C_K986P_V987P)

<400> 7

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp

35

40

45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
 65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
 85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
 100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
 115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
 130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
 145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
 165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
 180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
 195 200 205

Cys Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
 210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
 225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
 245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
 260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
 290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
 305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
 325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
 355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
 500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
 515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
 530 535 540

Pro Cys Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
 545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
 565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
 580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His

1130		1135		1140
Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala				
1145		1150		1155
Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val				
1160		1165		1170
Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly				
1175		1180		1185
Lys Tyr Glu Gln				
1190				
<210> 8				
<211> 1192				
<212> PRT				
<213> Artificial Sequence				
<220>				
<223> COV2_S_(P589C_F855C_K986P_V987P)				
<400> 8				
Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe				
1		5		10 15
Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu				
	20		25	30
His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp				
	35		40	45
Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp				
50		55		60
Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu				
65		70		75 80
Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser				
	85		90	95
Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile				
	100		105	110
Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr				
	115		120	125
Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr				
130		135		140
Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu				
145		150		155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe

435

440

445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
 500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
 515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
 530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
 545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Cys Cys Ser Phe
 565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
 580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
 595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
 610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
 625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
 645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
 660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
 675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
 690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
 705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
 725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
 740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
 755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
 770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
 785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
 805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
 820 825 830

Leu Ile Cys Ala Gln Lys Cys Asn Gly Leu Thr Val Leu Pro Pro Leu
 835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
 850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
 865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
 885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
 900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
 915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
 930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
 945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln
 965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
 980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln
1190

<210> 9
<211> 1192
<212> PRT
<213> Artificial Sequence

<220>
<223> COV2_S_(P665C_L864C_K986P_V987P)

<400> 9

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
 35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
 65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
 85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
 100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
 115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
 130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
 145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
 165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
 180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
 195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
 210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
 225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
 245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
 260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Cys Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Cys

835

840

845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
 850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
 865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
 885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
 900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
 915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
 930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
 945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln
 965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
 980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
 995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
 1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
 1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
 1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
 1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
 1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
 1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
 1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln
1190

<210> 10
<211> 1192
<212> PRT
<213> Artificial Sequence

<220>
<223> COV2_S_(S383C_D985C_K986P_V987P)

<400> 10

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr

130	135	140														
Ser 145	Ser	Ala	Asn	Asn	Cys 150	Thr	Phe	Glu	Tyr	Val 155	Ser	Gln	Pro	Phe	Leu 160	
Met	Asp	Leu	Glu	Gly 165	Lys	Gln	Gly	Asn	Phe	Lys 170	Asn	Leu	Arg	Glu	Phe 175	
Val	Phe	Lys	Asn 180	Ile	Asp	Gly	Tyr	Phe 185	Lys	Ile	Tyr	Ser	Lys 190	His	Thr	
Pro	Ile	Asn 195	Leu	Val	Arg	Asp	Leu	Pro 200	Gln	Gly	Phe	Ser 205	Ala	Leu	Glu	
Pro	Leu 210	Val	Asp	Leu	Pro	Ile 215	Gly	Ile	Asn	Ile	Thr 220	Arg	Phe	Gln	Thr	
Leu 225	Leu	Ala	Leu	His	Arg 230	Ser	Tyr	Leu	Thr	Pro 235	Gly	Asp	Ser	Ser	Ser 240	
Gly	Trp	Thr	Ala	Gly 245	Ala	Ala	Ala	Tyr	Tyr 250	Val	Gly	Tyr	Leu	Gln 255	Pro	
Arg	Thr	Phe	Leu 260	Leu	Lys	Tyr	Asn	Glu 265	Asn	Gly	Thr	Ile	Thr 270	Asp	Ala	
Val	Asp	Cys 275	Ala	Leu	Asp	Pro	Leu	Ser 280	Glu	Thr	Lys	Cys 285	Thr	Leu	Lys	
Ser	Phe	Thr	Val	Glu	Lys	Gly 295	Ile	Tyr	Gln	Thr	Ser 300	Asn	Phe	Arg	Val	
Gln 305	Pro	Thr	Glu	Ser	Ile 310	Val	Arg	Phe	Pro	Asn 315	Ile	Thr	Asn	Leu	Cys 320	
Pro	Phe	Gly	Glu	Val 325	Phe	Asn	Ala	Thr	Arg	Phe 330	Ala	Ser	Val	Tyr 335	Ala	
Trp	Asn	Arg	Lys 340	Arg	Ile	Ser	Asn	Cys 345	Val	Ala	Asp	Tyr	Ser 350	Val	Leu	
Tyr	Asn	Ser 355	Ala	Ser	Phe	Ser	Thr	Phe 360	Lys	Cys	Tyr	Gly 365	Val	Cys	Pro	
Thr	Lys 370	Leu	Asn	Asp	Leu	Cys 375	Phe	Thr	Asn	Val	Tyr 380	Ala	Asp	Ser	Phe	
Val 385	Ile	Arg	Gly	Asp	Glu 390	Val	Arg	Gln	Ile	Ala 395	Pro	Gly	Gln	Thr	Gly 400	
Lys	Ile	Ala	Asp	Tyr 405	Asn	Tyr	Lys	Leu	Pro	Asp 410	Asp	Phe	Thr	Gly 415	Cys	

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Cys Pro Pro Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln
1190

<210> 11
<211> 1192
<212> PRT
<213> Artificial Sequence

<220>

<223> COV2_S_(T547C_N978C_K986P_V987P)

<400> 11

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Cys Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu

540

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Cys Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln
1190

<210> 12
<211> 1192
<212> PRT
<213> Artificial Sequence

<220>
<223> COV2_S_(V382C_R983C_K986P_V987P)

<400> 12

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
 115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
 130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
 145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
 165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
 180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
 195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
 210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
 225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
 245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
 260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
 290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
 305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
 325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Cys Ser Pro
 355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn

930

935

940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
 945 950 955 960

Leu Asn Asp Ile Leu Ser Cys Leu Asp Pro Pro Glu Ala Glu Val Gln
 965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
 980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
 995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
 1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
 1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
 1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
 1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
 1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
 1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
 1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
 1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
 1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
 1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
 1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
 1175 1180 1185

Lys Tyr Glu Gln
 1190

<210> 13
<211> 1192
<212> PRT
<213> Artificial Sequence

<220>
<223> COV2_S_(A570C_V963C)

<400> 13

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser

225		230		235		240
Gly Trp Thr Ala	Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro	245		250		255
Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala		260		265		270
Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys		275		280		285
Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val		290		295		300
Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys		305		310		315
Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala		325		330		335
Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu		340		345		350
Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro		355		360		365
Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe		370		375		380
Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly		385		390		395
Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys		405		410		415
Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn		420		425		430
Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe		435		440		445
Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys		450		455		460
Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly		465		470		475
Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val		485		490		495
Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys		500		505		510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
 515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
 530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Cys Asp Thr Thr Asp Ala Val
 545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
 565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
 580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
 595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
 610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
 625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
 645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
 660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
 675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
 690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
 705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
 725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
 740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
 755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
 770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Cys Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln
1190

<210> 14
<211> 1192
<212> PRT
<213> Artificial Sequence

<220>
<223> COV2_S_(D614C_T859C)

<400> 14

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Cys Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val

625		630		635		640
Asn Asn Ser Tyr	Glu Cys Asp Ile Pro	Ile Gly Ala Gly	Ile Cys Ala			
	645	650	655			
Ser Tyr Gln Thr	Gln Thr Asn Ser Pro	Arg Arg Ala Arg	Ser Val Ala			
	660	665	670			
Ser Gln Ser Ile	Ile Ala Tyr Thr Met	Ser Leu Gly Ala	Glu Asn Ser			
	675	680	685			
Val Ala Tyr Ser	Asn Asn Ser Ile Ala	Ile Pro Thr Asn	Phe Thr Ile			
	690	695	700			
Ser Val Thr Thr	Glu Ile Leu Pro Val	Ser Met Thr Lys	Thr Ser Val			
	705	710	715	720		
Asp Cys Thr Met	Tyr Ile Cys Gly Asp	Ser Thr Glu Cys	Ser Asn Leu			
	725	730	735			
Leu Leu Gln Tyr	Gly Ser Phe Cys Thr	Gln Leu Asn Arg	Ala Leu Thr			
	740	745	750			
Gly Ile Ala Val	Glu Gln Asp Lys Asn	Thr Gln Glu Val	Phe Ala Gln			
	755	760	765			
Val Lys Gln Ile	Tyr Lys Thr Pro Pro	Ile Lys Asp Phe	Gly Gly Phe			
	770	775	780			
Asn Phe Ser Gln	Ile Leu Pro Asp Pro	Ser Lys Pro Ser	Lys Arg Ser			
	785	790	795	800		
Phe Ile Glu Asp	Leu Leu Phe Asn Lys	Val Thr Leu Ala	Asp Ala Gly			
	805	810	815			
Phe Ile Lys Gln	Tyr Gly Asp Cys Leu	Gly Asp Ile Ala	Ala Arg Asp			
	820	825	830			
Leu Ile Cys Ala	Gln Lys Phe Asn Gly	Leu Cys Val Leu	Pro Pro Leu			
	835	840	845			
Leu Thr Asp Glu	Met Ile Ala Gln Tyr	Thr Ser Ala Leu	Leu Ala Gly			
	850	855	860			
Thr Ile Thr Ser	Gly Trp Thr Phe Gly	Ala Gly Ala Ala	Leu Gln Ile			
	865	870	875	880		
Pro Phe Ala Met	Gln Met Ala Tyr Arg	Phe Asn Gly Ile	Gly Val Thr			
	885	890	895			
Gln Asn Val Leu	Tyr Glu Asn Gln Lys	Leu Ile Ala Asn	Gln Phe Asn			
	900	905	910			

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln
1190

<210> 15
<211> 1192
<212> PRT
<213> Artificial Sequence

<220>
<223> COV2_S_(K41C_A520C)

<400> 15

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
 210 215 220
 Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
 225 230 235 240
 Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
 245 250 255
 Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
 260 265 270
 Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 275 280 285
 Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
 290 295 300
 Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
 305 310 315 320
 Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
 325 330 335
 Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 340 345 350
 Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
 355 360 365
 Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 370 375 380
 Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 385 390 395 400
 Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 405 410 415
 Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 420 425 430
 Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 435 440 445
 Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460
 Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Cys Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln

1025	1030	1035
Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro		
1040	1045	1050
Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp		
1055	1060	1065
Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly		
1070	1075	1080
Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile		
1085	1090	1095
Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val		
1100	1105	1110
Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu		
1115	1120	1125
Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His		
1130	1135	1140
Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala		
1145	1150	1155
Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val		
1160	1165	1170
Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly		
1175	1180	1185
Lys Tyr Glu Gln		
1190		
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<400> 16		
Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe		
1	5	10 15
Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu		
20	25	30
His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp		
35	40	45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Cys Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala

325

330

335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
 355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
 500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
 515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
 530 535 540

Pro Cys Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
 545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
 565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
 580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
 595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
 610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
 625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
 645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
 660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
 675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
 690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
 705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
 725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
 740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
 755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
 770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
 785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
 805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
 820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
 835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
 850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
 865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln
1190

<210> 17

<211> 1192

<212> PRT

<213> Artificial Sequence

<220>

<223> COV2_S_(P589C_F855C)

<400> 17

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val	Phe	Lys	Asn	Ile	Asp	Gly	Tyr	Phe	Lys	Ile	Tyr	Ser	Lys	His	Thr	180	185	190	
Pro	Ile	Asn	Leu	Val	Arg	Asp	Leu	Pro	Gln	Gly	Phe	Ser	Ala	Leu	Glu	195	200	205	
Pro	Leu	Val	Asp	Leu	Pro	Ile	Gly	Ile	Asn	Ile	Thr	Arg	Phe	Gln	Thr	210	215	220	
Leu	Leu	Ala	Leu	His	Arg	Ser	Tyr	Leu	Thr	Pro	Gly	Asp	Ser	Ser	Ser	225	230	235	240
Gly	Trp	Thr	Ala	Gly	Ala	Ala	Ala	Tyr	Tyr	Val	Gly	Tyr	Leu	Gln	Pro	245	250	255	
Arg	Thr	Phe	Leu	Leu	Lys	Tyr	Asn	Glu	Asn	Gly	Thr	Ile	Thr	Asp	Ala	260	265	270	
Val	Asp	Cys	Ala	Leu	Asp	Pro	Leu	Ser	Glu	Thr	Lys	Cys	Thr	Leu	Lys	275	280	285	
Ser	Phe	Thr	Val	Glu	Lys	Gly	Ile	Tyr	Gln	Thr	Ser	Asn	Phe	Arg	Val	290	295	300	
Gln	Pro	Thr	Glu	Ser	Ile	Val	Arg	Phe	Pro	Asn	Ile	Thr	Asn	Leu	Cys	305	310	315	320
Pro	Phe	Gly	Glu	Val	Phe	Asn	Ala	Thr	Arg	Phe	Ala	Ser	Val	Tyr	Ala	325	330	335	
Trp	Asn	Arg	Lys	Arg	Ile	Ser	Asn	Cys	Val	Ala	Asp	Tyr	Ser	Val	Leu	340	345	350	
Tyr	Asn	Ser	Ala	Ser	Phe	Ser	Thr	Phe	Lys	Cys	Tyr	Gly	Val	Ser	Pro	355	360	365	
Thr	Lys	Leu	Asn	Asp	Leu	Cys	Phe	Thr	Asn	Val	Tyr	Ala	Asp	Ser	Phe	370	375	380	
Val	Ile	Arg	Gly	Asp	Glu	Val	Arg	Gln	Ile	Ala	Pro	Gly	Gln	Thr	Gly	385	390	395	400
Lys	Ile	Ala	Asp	Tyr	Asn	Tyr	Lys	Leu	Pro	Asp	Asp	Phe	Thr	Gly	Cys	405	410	415	
Val	Ile	Ala	Trp	Asn	Ser	Asn	Asn	Leu	Asp	Ser	Lys	Val	Gly	Gly	Asn	420	425	430	
Tyr	Asn	Tyr	Leu	Tyr	Arg	Leu	Phe	Arg	Lys	Ser	Asn	Leu	Lys	Pro	Phe	435	440	445	

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Cys Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu

725

730

735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
 740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
 755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
 770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
 785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
 805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
 820 825 830

Leu Ile Cys Ala Gln Lys Cys Asn Gly Leu Thr Val Leu Pro Pro Leu
 835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
 850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
 865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
 885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
 900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
 915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
 930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
 945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
 965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
 980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
 995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln
1190

<210> 18
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<212> PRT
<213> Artificial Sequence

<220>
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<400> 18

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

Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu

20

25

30

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
 35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
 65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
 85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
 100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
 115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
 130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
 145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
 165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
 180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
 195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
 210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
 225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
 245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
 260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
 290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
 580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
 595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
 610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
 625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Cys Ile Gly Ala Gly Ile Cys Ala
 645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
 660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
 675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
 690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
 705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
 725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
 740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
 755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
 770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
 785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
 805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
 820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Cys
 835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu

1115	1120	1125
Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His		
1130	1135	1140
Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala		
1145	1150	1155
Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val		
1160	1165	1170
Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly		
1175	1180	1185
Lys Tyr Glu Gln		
1190		
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Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe		
1	5	10 15
Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu		
	20	25 30
His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp		
	35	40 45
Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp		
50	55	60
Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu		
65	70	75 80
Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser		
	85	90 95
Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile		
	100	105 110
Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr		
115	120	125
Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr		
130	135	140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Cys Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn

420

425

430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
 500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
 515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
 530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
 545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
 565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
 580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
 595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
 610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
 625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
 645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
 660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
 675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
 690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
 705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
 725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
 740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
 755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
 770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
 785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
 805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
 820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
 835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
 850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
 865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
 885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
 900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
 915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
 930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
 945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Cys Lys Val Glu Ala Glu Val Gln
 965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln
1190

<210> 20

<211> 1192

<212> PRT

<213> Artificial Sequence

<220>

<223> COV2_S_(T547C_N978C)

<400> 20

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Cys Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp

820

825

830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Cys Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln
1190

<210> 21
<211> 1192
<212> PRT
<213> Artificial Sequence

<220>
<223> COV2_S_(V382C_R983C)

<400> 21

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr

115

120

125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
 130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
 145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
 165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
 180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
 195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
 210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
 225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
 245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
 260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
 290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
 305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
 325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Cys Ser Pro
 355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
 500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
 515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
 530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
 545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
 565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
 580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
 595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
 610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
 625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
 645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
 660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Cys Leu Asp Lys Val Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln
1190

<211> 1272
<212> PRT
<213> Artificial Sequence

<220>
<223> COV2_S_(K986P_V987P)_trimer_tag_2

<400> 22

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
 245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
 260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
 290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
 305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
 325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
 355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
 500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn

515

520

525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
 530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
 545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
 565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
 580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
 595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
 610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
 625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
 645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
 660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
 675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
 690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
 705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
 725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
 740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
 755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
 770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
 785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly	Lys	Ala	His	Phe	Pro	Arg	Glu	Gly	Val	Phe	Val	Ser	Asn	Gly
1070						1075					1080			
Thr	His	Trp	Phe	Val	Thr	Gln	Arg	Asn	Phe	Tyr	Glu	Pro	Gln	Ile
1085						1090					1095			
Ile	Thr	Thr	Asp	Asn	Thr	Phe	Val	Ser	Gly	Asn	Cys	Asp	Val	Val
1100						1105					1110			
Ile	Gly	Ile	Val	Asn	Asn	Thr	Val	Tyr	Asp	Pro	Leu	Gln	Pro	Glu
1115						1120					1125			
Leu	Asp	Ser	Phe	Lys	Glu	Glu	Leu	Asp	Lys	Tyr	Phe	Lys	Asn	His
1130						1135					1140			
Thr	Ser	Pro	Asp	Val	Asp	Leu	Gly	Asp	Ile	Ser	Gly	Ile	Asn	Ala
1145						1150					1155			
Ser	Val	Val	Asn	Ile	Gln	Lys	Glu	Ile	Asp	Arg	Leu	Asn	Glu	Val
1160						1165					1170			
Ala	Lys	Asn	Leu	Asn	Glu	Ser	Leu	Ile	Asp	Leu	Gln	Glu	Leu	Gly
1175						1180					1185			
Lys	Tyr	Glu	Gln	Gly	Gly	Gly	Ser	Gly	Tyr	Ile	Pro	Glu	Ala	Pro
1190						1195					1200			
Arg	Asp	Gly	Gln	Ala	Tyr	Val	Arg	Lys	Asp	Gly	Glu	Trp	Val	Leu
1205						1210					1215			
Leu	Ser	Thr	Phe	Leu	Gly	Leu	Glu	Val	Leu	Phe	Gln	Gly	Pro	Gly
1220						1225					1230			
His	His	His	His	His	His	His	His	Ser	Ala	Trp	Ser	His	Pro	Gln
1235						1240					1245			
Phe	Glu	Lys	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Ser
1250						1255					1260			
Ala	Trp	Ser	His	Pro	Gln	Phe	Glu	Lys						
1265						1270								

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 <212> PRT
 <213> Artificial Sequence

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 <400> 23

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
 35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
 65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
 85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
 100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
 115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
 130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
 145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
 165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
 180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
 195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
 210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
 225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
 245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
 260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Cys Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu

835

840

845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
 850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
 865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
 885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
 900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
 915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
 930 935 940

Thr Leu Cys Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
 945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln
 965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
 980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
 995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
 1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
 1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
 1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
 1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
 1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
 1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
 1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro
1190 1195 1200

Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu
1205 1210 1215

Leu Ser Thr Phe Leu Gly Leu Glu Val Leu Phe Gln Gly Pro Gly
1220 1225 1230

His His His His His His His His Ser Ala Trp Ser His Pro Gln
1235 1240 1245

Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser
1250 1255 1260

Ala Trp Ser His Pro Gln Phe Glu Lys
1265 1270

<210> 24

<211> 1272

<212> PRT

<213> Artificial Sequence

<220>

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<400> 24

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp

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

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
 355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
 500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
 515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
 530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
 545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
 565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
 580 585 590

Ala Val Leu Tyr Gln Cys Val Asn Cys Thr Glu Val Pro Val Ala Ile
 595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Cys Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala

1145		1150		1155
Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val				
1160		1165		1170
Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly				
1175		1180		1185
Lys Tyr Glu Gln Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro				
1190		1195		1200
Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu				
1205		1210		1215
Leu Ser Thr Phe Leu Gly Leu Glu Val Leu Phe Gln Gly Pro Gly				
1220		1225		1230
His His His His His His His His Ser Ala Trp Ser His Pro Gln				
1235		1240		1245
Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser				
1250		1255		1260
Ala Trp Ser His Pro Gln Phe Glu Lys				
1265		1270		
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Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe				
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Thr Arg Gly Val Tyr Tyr Pro Asp Cys Val Phe Arg Ser Ser Val Leu				
	20		25	30
His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp				
	35		40	45
Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp				
	50		55	60
Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu				
65		70	75	80
Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser				
	85		90	95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe

370

375

380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 485 490 495

Leu Ser Phe Glu Leu Leu His Cys Pro Ala Thr Val Cys Gly Pro Lys
 500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
 515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
 530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
 545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
 565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
 580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
 595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
 610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
 625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
 645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
 660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
 675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
 690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
 705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
 725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
 740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
 755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
 770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
 785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
 805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
 820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
 835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
 850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
 865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
 885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
 900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
 915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro
1190 1195 1200

Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu
1205 1210 1215

Leu Ser Thr Phe Leu Gly Leu Glu Val Leu Phe Gln Gly Pro Gly
1220 1225 1230

His His His His His His His His Ser Ala Trp Ser His Pro Gln
1235 1240 1245

Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser
1250 1255 1260

Ala Trp Ser His Pro Gln Phe Glu Lys
1265 1270

<210> 26
<211> 1272
<212> PRT
<213> Artificial Sequence

<220>
<223> COV2_S_(P225C_F562C_K986P_V987P)_trimer_tag_2

<400> 26

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Cys Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Cys Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile

690				695				700							
Ser 705	Val	Thr	Thr	Glu	Ile 710	Leu	Pro	Val	Ser	Met 715	Thr	Lys	Thr	Ser	Val 720
Asp	Cys	Thr	Met	Tyr 725	Ile	Cys	Gly	Asp	Ser 730	Thr	Glu	Cys	Ser	Asn 735	Leu
Leu	Leu	Gln	Tyr 740	Gly	Ser	Phe	Cys	Thr 745	Gln	Leu	Asn	Arg	Ala 750	Leu	Thr
Gly	Ile	Ala 755	Val	Glu	Gln	Asp	Lys 760	Asn	Thr	Gln	Glu	Val 765	Phe	Ala	Gln
Val	Lys 770	Gln	Ile	Tyr	Lys	Thr 775	Pro	Pro	Ile	Lys	Asp 780	Phe	Gly	Gly	Phe
Asn 785	Phe	Ser	Gln	Ile	Leu 790	Pro	Asp	Pro	Ser	Lys 795	Pro	Ser	Lys	Arg	Ser 800
Phe	Ile	Glu	Asp	Leu 805	Leu	Phe	Asn	Lys	Val 810	Thr	Leu	Ala	Asp	Ala 815	Gly
Phe	Ile	Lys	Gln 820	Tyr	Gly	Asp	Cys	Leu 825	Gly	Asp	Ile	Ala	Ala 830	Arg	Asp
Leu	Ile	Cys 835	Ala	Gln	Lys	Phe	Asn 840	Gly	Leu	Thr	Val	Leu 845	Pro	Pro	Leu
Leu	Thr 850	Asp	Glu	Met	Ile	Ala 855	Gln	Tyr	Thr	Ser	Ala 860	Leu	Leu	Ala	Gly
Thr 865	Ile	Thr	Ser	Gly	Trp 870	Thr	Phe	Gly	Ala	Gly 875	Ala	Ala	Leu	Gln	Ile 880
Pro	Phe	Ala	Met	Gln 885	Met	Ala	Tyr	Arg	Phe 890	Asn	Gly	Ile	Gly	Val 895	Thr
Gln	Asn	Val	Leu 900	Tyr	Glu	Asn	Gln	Lys 905	Leu	Ile	Ala	Asn	Gln 910	Phe	Asn
Ser	Ala	Ile 915	Gly	Lys	Ile	Gln	Asp 920	Ser	Leu	Ser	Ser	Thr 925	Ala	Ser	Ala
Leu	Gly 930	Lys	Leu	Gln	Asp	Val 935	Val	Asn	Gln	Asn	Ala 940	Gln	Ala	Leu	Asn
Thr 945	Leu	Val	Lys	Gln	Leu 950	Ser	Ser	Asn	Phe	Gly 955	Ala	Ile	Ser	Ser	Val 960
Leu	Asn	Asp	Ile	Leu 965	Ser	Arg	Leu	Asp	Pro 970	Pro	Glu	Ala	Glu	Val 975	Gln

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro
1190 1195 1200

Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu
1205 1210 1215

Leu Ser Thr Phe Leu Gly Leu Glu Val Leu Phe Gln Gly Pro Gly
1220 1225 1230

His His His His His His His Ser Ala Trp Ser His Pro Gln
1235 1240 1245

Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser
1250 1255 1260

Ala Trp Ser His Pro Gln Phe Glu Lys
1265 1270

<210> 27
<211> 1272
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<400> 27

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
 195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
 210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
 225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
 245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
 260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
 290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
 305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
 325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
 355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Cys Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Cys Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg

1010		1015		1020
Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln 1025 1030 1035				
Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro 1040 1045 1050				
Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp 1055 1060 1065				
Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly 1070 1075 1080				
Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile 1085 1090 1095				
Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val 1100 1105 1110				
Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu 1115 1120 1125				
Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His 1130 1135 1140				
Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala 1145 1150 1155				
Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val 1160 1165 1170				
Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly 1175 1180 1185				
Lys Tyr Glu Gln Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro 1190 1195 1200				
Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu 1205 1210 1215				
Leu Ser Thr Phe Leu Gly Leu Glu Val Leu Phe Gln Gly Pro Gly 1220 1225 1230				
His His His His His His His His Ser Ala Trp Ser His Pro Gln 1235 1240 1245				
Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser 1250 1255 1260				
Ala Trp Ser His Pro Gln Phe Glu Lys 1265 1270				

<210> 28
<211> 1272
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<213> Artificial Sequence

<220>
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<400> 28

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser

225		230		235		240
Gly Trp Thr Ala	Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro	245		250		255
Arg Thr Phe Leu	Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala	260		265		270
Val Asp Cys Ala	Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys	275		280		285
Ser Phe Thr Val	Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val	290		295		300
Gln Pro Thr Glu	Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys	305		310		315
Pro Phe Gly Glu	Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala	325		330		335
Trp Asn Arg Lys	Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu	340		345		350
Tyr Asn Ser Ala	Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro	355		360		365
Thr Lys Leu Asn	Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe	370		375		380
Val Ile Arg Gly	Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly	385		390		395
Lys Ile Ala Asp	Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys	405		410		415
Val Ile Ala Trp	Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn	420		425		430
Tyr Asn Tyr Leu	Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe	435		440		445
Glu Arg Asp Ile	Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys	450		455		460
Asn Gly Val Glu	Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly	465		470		475
Phe Gln Pro Thr	Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val	485		490		495
Leu Ser Phe Glu	Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys	500		505		510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
 515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
 530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
 545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
 565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
 580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
 595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
 610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
 625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Cys Ile Gly Ala Gly Ile Cys Ala
 645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
 660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
 675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
 690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
 705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
 725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
 740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
 755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
 770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Cys
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro
1190 1195 1200

Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu
1205 1210 1215

Leu Ser Thr Phe Leu Gly Leu Glu Val Leu Phe Gln Gly Pro Gly
1220 1225 1230

His His His His His His His His Ser Ala Trp Ser His Pro Gln
1235 1240 1245

Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser
1250 1255 1260

Ala Trp Ser His Pro Gln Phe Glu Lys
1265 1270

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<213> Artificial Sequence

<220>

<223> COV2_S_(S383C_D985C_K986P_V987P)_trimer_tag_2

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

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Cys Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val

545		550		555		560
Arg Asp Pro Gln Thr	Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe					
	565		570		575	
Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val						
	580		585		590	
Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile						
	595		600		605	
His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser						
	610		615		620	
Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val						
	625		630		635	640
Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala						
	645		650		655	
Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala						
	660		665		670	
Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser						
	675		680		685	
Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile						
	690		695		700	
Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val						
	705		710		715	720
Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu						
	725		730		735	
Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr						
	740		745		750	
Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln						
	755		760		765	
Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe						
	770		775		780	
Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser						
	785		790		795	800
Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly						
	805		810		815	
Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp						
	820		825		830	

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Cys Pro Pro Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro
1190 1195 1200

Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu
1205 1210 1215

Leu Ser Thr Phe Leu Gly Leu Glu Val Leu Phe Gln Gly Pro Gly
1220 1225 1230

His His His His His His His His Ser Ala Trp Ser His Pro Gln
1235 1240 1245

Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser
1250 1255 1260

Ala Trp Ser His Pro Gln Phe Glu Lys
1265 1270

<210> 30

<211> 1272

<212> PRT

<213> Artificial Sequence

<220>

<223> COV2_S_(T547C_N978C_K986P_V987P)_trimer_tag_2

<400> 30

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Cys Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile

865		870		875		880
Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr						
	885			890		895
Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn						
	900			905		910
Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala						
	915			920		925
Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn						
	930			935		940
Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val						
	945			950		955
						960
Leu Cys Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln						
				965		970
						975
Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val						
	980			985		990
Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu						
	995			1000		1005
Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg						
	1010			1015		1020
Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln						
	1025			1030		1035
Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro						
	1040			1045		1050
Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp						
	1055			1060		1065
Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly						
	1070			1075		1080
Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile						
	1085			1090		1095
Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val						
	1100			1105		1110
Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu						
	1115			1120		1125
Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His						
	1130			1135		1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro
1190 1195 1200

Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu
1205 1210 1215

Leu Ser Thr Phe Leu Gly Leu Glu Val Leu Phe Gln Gly Pro Gly
1220 1225 1230

His His His His His His His His Ser Ala Trp Ser His Pro Gln
1235 1240 1245

Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser
1250 1255 1260

Ala Trp Ser His Pro Gln Phe Glu Lys
1265 1270

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<400> 31

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser

85

90

95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
 100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
 115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
 130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
 145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
 165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
 180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
 195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
 210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
 225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
 245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
 260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
 290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
 305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
 325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Cys Ser Pro
 355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
 500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
 515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
 530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
 545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
 565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
 580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
 595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
 610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
 625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Cys Leu Asp Pro Pro Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly

1175		1180		1185
Lys Tyr Glu Gln Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro				
1190		1195		1200
Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu				
1205		1210		1215
Leu Ser Thr Phe Leu Gly Leu Glu Val Leu Phe Gln Gly Pro Gly				
1220		1225		1230
His His His His His His His His Ser Ala Trp Ser His Pro Gln				
1235		1240		1245
Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser				
1250		1255		1260
Ala Trp Ser His Pro Gln Phe Glu Lys				
1265		1270		
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<400> 32				
Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe				
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Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu				
	20		25	30
His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp				
	35		40	45
Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp				
	50		55	60
Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu				
65		70		75 80
Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser				
	85		90	95
Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile				
	100		105	110
Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr				
	115		120	125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys

405

410

415

Val	Ile	Ala	Trp	Asn	Ser	Asn	Asn	Leu	Asp	Ser	Lys	Val	Gly	Gly	Asn		
			420					425					430				
Tyr	Asn	Tyr	Leu	Tyr	Arg	Leu	Phe	Arg	Lys	Ser	Asn	Leu	Lys	Pro	Phe		
		435					440					445					
Glu	Arg	Asp	Ile	Ser	Thr	Glu	Ile	Tyr	Gln	Ala	Gly	Ser	Thr	Pro	Cys		
	450					455					460						
Asn	Gly	Val	Glu	Gly	Phe	Asn	Cys	Tyr	Phe	Pro	Leu	Gln	Ser	Tyr	Gly		
465					470					475					480		
Phe	Gln	Pro	Thr	Asn	Gly	Val	Gly	Tyr	Gln	Pro	Tyr	Arg	Val	Val	Val		
				485					490					495			
Leu	Ser	Phe	Glu	Leu	Leu	His	Ala	Pro	Ala	Thr	Val	Cys	Gly	Pro	Lys		
			500					505					510				
Lys	Ser	Thr	Asn	Leu	Val	Lys	Asn	Lys	Cys	Val	Asn	Phe	Asn	Phe	Asn		
		515					520					525					
Gly	Leu	Thr	Gly	Thr	Gly	Val	Leu	Thr	Glu	Ser	Asn	Lys	Lys	Phe	Leu		
	530					535					540						
Pro	Phe	Gln	Gln	Phe	Gly	Arg	Asp	Ile	Cys	Asp	Thr	Thr	Asp	Ala	Val		
545					550					555					560		
Arg	Asp	Pro	Gln	Thr	Leu	Glu	Ile	Leu	Asp	Ile	Thr	Pro	Cys	Ser	Phe		
				565					570					575			
Gly	Gly	Val	Ser	Val	Ile	Thr	Pro	Gly	Thr	Asn	Thr	Ser	Asn	Gln	Val		
			580					585					590				
Ala	Val	Leu	Tyr	Gln	Asp	Val	Asn	Cys	Thr	Glu	Val	Pro	Val	Ala	Ile		
		595					600					605					
His	Ala	Asp	Gln	Leu	Thr	Pro	Thr	Trp	Arg	Val	Tyr	Ser	Thr	Gly	Ser		
	610					615					620						
Asn	Val	Phe	Gln	Thr	Arg	Ala	Gly	Cys	Leu	Ile	Gly	Ala	Glu	His	Val		
625					630					635					640		
Asn	Asn	Ser	Tyr	Glu	Cys	Asp	Ile	Pro	Ile	Gly	Ala	Gly	Ile	Cys	Ala		
				645					650					655			
Ser	Tyr	Gln	Thr	Gln	Thr	Asn	Ser	Pro	Arg	Arg	Ala	Arg	Ser	Val	Ala		
			660					665					670				
Ser	Gln	Ser	Ile	Ile	Ala	Tyr	Thr	Met	Ser	Leu	Gly	Ala	Glu	Asn	Ser		
		675					680					685					

Val	Ala	Tyr	Ser	Asn	Asn	Ser	Ile	Ala	Ile	Pro	Thr	Asn	Phe	Thr	Ile	690	695	700
Ser	Val	Thr	Thr	Glu	Ile	Leu	Pro	Val	Ser	Met	Thr	Lys	Thr	Ser	Val	705	710	715
Asp	Cys	Thr	Met	Tyr	Ile	Cys	Gly	Asp	Ser	Thr	Glu	Cys	Ser	Asn	Leu	725	730	735
Leu	Leu	Gln	Tyr	Gly	Ser	Phe	Cys	Thr	Gln	Leu	Asn	Arg	Ala	Leu	Thr	740	745	750
Gly	Ile	Ala	Val	Glu	Gln	Asp	Lys	Asn	Thr	Gln	Glu	Val	Phe	Ala	Gln	755	760	765
Val	Lys	Gln	Ile	Tyr	Lys	Thr	Pro	Pro	Ile	Lys	Asp	Phe	Gly	Gly	Phe	770	775	780
Asn	Phe	Ser	Gln	Ile	Leu	Pro	Asp	Pro	Ser	Lys	Pro	Ser	Lys	Arg	Ser	785	790	795
Phe	Ile	Glu	Asp	Leu	Leu	Phe	Asn	Lys	Val	Thr	Leu	Ala	Asp	Ala	Gly	805	810	815
Phe	Ile	Lys	Gln	Tyr	Gly	Asp	Cys	Leu	Gly	Asp	Ile	Ala	Ala	Arg	Asp	820	825	830
Leu	Ile	Cys	Ala	Gln	Lys	Phe	Asn	Gly	Leu	Thr	Val	Leu	Pro	Pro	Leu	835	840	845
Leu	Thr	Asp	Glu	Met	Ile	Ala	Gln	Tyr	Thr	Ser	Ala	Leu	Leu	Ala	Gly	850	855	860
Thr	Ile	Thr	Ser	Gly	Trp	Thr	Phe	Gly	Ala	Gly	Ala	Ala	Leu	Gln	Ile	865	870	875
Pro	Phe	Ala	Met	Gln	Met	Ala	Tyr	Arg	Phe	Asn	Gly	Ile	Gly	Val	Thr	885	890	895
Gln	Asn	Val	Leu	Tyr	Glu	Asn	Gln	Lys	Leu	Ile	Ala	Asn	Gln	Phe	Asn	900	905	910
Ser	Ala	Ile	Gly	Lys	Ile	Gln	Asp	Ser	Leu	Ser	Ser	Thr	Ala	Ser	Ala	915	920	925
Leu	Gly	Lys	Leu	Gln	Asp	Val	Val	Asn	Gln	Asn	Ala	Gln	Ala	Leu	Asn	930	935	940
Thr	Leu	Cys	Lys	Gln	Leu	Ser	Ser	Asn	Phe	Gly	Ala	Ile	Ser	Ser	Val	945	950	955
																960		

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro
1190 1195 1200

Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu
1205 1210 1215

Leu Ser Thr Phe Leu Gly Leu Glu Val Leu Phe Gln Gly Pro Gly
1220 1225 1230

His His His His His His His His Ser Ala Trp Ser His Pro Gln
1235 1240 1245

Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser
1250 1255 1260

Ala Trp Ser His Pro Gln Phe Glu Lys
1265 1270

<210> 33

<211> 1272

<212> PRT

<213> Artificial Sequence

<220>

<223> COV2_S_(D614C_T859C)_trimer_tag_2

<400> 33

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Cys Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu

725

730

735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
 740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
 755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
 770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
 785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
 805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
 820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Cys Val Leu Pro Pro Leu
 835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
 850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
 865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
 885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
 900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
 915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
 930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
 945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
 965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
 980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
 995 1000 1005

Ala	Ala	Thr	Lys	Met	Ser	Glu	Cys	Val	Leu	Gly	Gln	Ser	Lys	Arg
1010						1015					1020			
Val	Asp	Phe	Cys	Gly	Lys	Gly	Tyr	His	Leu	Met	Ser	Phe	Pro	Gln
1025						1030					1035			
Ser	Ala	Pro	His	Gly	Val	Val	Phe	Leu	His	Val	Thr	Tyr	Val	Pro
1040						1045					1050			
Ala	Gln	Glu	Lys	Asn	Phe	Thr	Thr	Ala	Pro	Ala	Ile	Cys	His	Asp
1055						1060					1065			
Gly	Lys	Ala	His	Phe	Pro	Arg	Glu	Gly	Val	Phe	Val	Ser	Asn	Gly
1070						1075					1080			
Thr	His	Trp	Phe	Val	Thr	Gln	Arg	Asn	Phe	Tyr	Glu	Pro	Gln	Ile
1085						1090					1095			
Ile	Thr	Thr	Asp	Asn	Thr	Phe	Val	Ser	Gly	Asn	Cys	Asp	Val	Val
1100						1105					1110			
Ile	Gly	Ile	Val	Asn	Asn	Thr	Val	Tyr	Asp	Pro	Leu	Gln	Pro	Glu
1115						1120					1125			
Leu	Asp	Ser	Phe	Lys	Glu	Glu	Leu	Asp	Lys	Tyr	Phe	Lys	Asn	His
1130						1135					1140			
Thr	Ser	Pro	Asp	Val	Asp	Leu	Gly	Asp	Ile	Ser	Gly	Ile	Asn	Ala
1145						1150					1155			
Ser	Val	Val	Asn	Ile	Gln	Lys	Glu	Ile	Asp	Arg	Leu	Asn	Glu	Val
1160						1165					1170			
Ala	Lys	Asn	Leu	Asn	Glu	Ser	Leu	Ile	Asp	Leu	Gln	Glu	Leu	Gly
1175						1180					1185			
Lys	Tyr	Glu	Gln	Gly	Gly	Gly	Ser	Gly	Tyr	Ile	Pro	Glu	Ala	Pro
1190						1195					1200			
Arg	Asp	Gly	Gln	Ala	Tyr	Val	Arg	Lys	Asp	Gly	Glu	Trp	Val	Leu
1205						1210					1215			
Leu	Ser	Thr	Phe	Leu	Gly	Leu	Glu	Val	Leu	Phe	Gln	Gly	Pro	Gly
1220						1225					1230			
His	His	His	His	His	His	His	His	Ser	Ala	Trp	Ser	His	Pro	Gln
1235						1240					1245			
Phe	Glu	Lys	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Ser
1250						1255					1260			

Ala Trp Ser His Pro Gln Phe Glu Lys
1265 1270

<210> 34
<211> 1272
<212> PRT
<213> Artificial Sequence

<220>
<223> COV2_S_(K41C_A520C)_trimer_tag_2

<400> 34

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
 225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
 245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
 260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
 290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
 305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
 325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
 355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 485 490 495

Leu Ser Phe Glu Leu Leu His Cys Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro

1040														
Ala	Gln	Glu	Lys	Asn	Phe	Thr	Thr	Ala	Pro	Ala	Ile	Cys	His	Asp
1055						1060					1065			
Gly	Lys	Ala	His	Phe	Pro	Arg	Glu	Gly	Val	Phe	Val	Ser	Asn	Gly
1070						1075					1080			
Thr	His	Trp	Phe	Val	Thr	Gln	Arg	Asn	Phe	Tyr	Glu	Pro	Gln	Ile
1085						1090					1095			
Ile	Thr	Thr	Asp	Asn	Thr	Phe	Val	Ser	Gly	Asn	Cys	Asp	Val	Val
1100						1105					1110			
Ile	Gly	Ile	Val	Asn	Asn	Thr	Val	Tyr	Asp	Pro	Leu	Gln	Pro	Glu
1115						1120					1125			
Leu	Asp	Ser	Phe	Lys	Glu	Glu	Leu	Asp	Lys	Tyr	Phe	Lys	Asn	His
1130						1135					1140			
Thr	Ser	Pro	Asp	Val	Asp	Leu	Gly	Asp	Ile	Ser	Gly	Ile	Asn	Ala
1145						1150					1155			
Ser	Val	Val	Asn	Ile	Gln	Lys	Glu	Ile	Asp	Arg	Leu	Asn	Glu	Val
1160						1165					1170			
Ala	Lys	Asn	Leu	Asn	Glu	Ser	Leu	Ile	Asp	Leu	Gln	Glu	Leu	Gly
1175						1180					1185			
Lys	Tyr	Glu	Gln	Gly	Gly	Gly	Ser	Gly	Tyr	Ile	Pro	Glu	Ala	Pro
1190						1195					1200			
Arg	Asp	Gly	Gln	Ala	Tyr	Val	Arg	Lys	Asp	Gly	Glu	Trp	Val	Leu
1205						1210					1215			
Leu	Ser	Thr	Phe	Leu	Gly	Leu	Glu	Val	Leu	Phe	Gln	Gly	Pro	Gly
1220						1225					1230			
His	His	His	His	His	His	His	His	Ser	Ala	Trp	Ser	His	Pro	Gln
1235						1240					1245			
Phe	Glu	Lys	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Ser
1250						1255					1260			
Ala	Trp	Ser	His	Pro	Gln	Phe	Glu	Lys						
1265						1270								

<210> 35
 <211> 1272
 <212> PRT
 <213> Artificial Sequence

 <220>

<223> COV2_S_(P225C_F562C)_trimer_tag_2

<400> 35

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Cys Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala

260

265

270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
 290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
 305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
 325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
 355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
 500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
 515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
 530 535 540

Pro Cys Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro
1190 1195 1200

Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu
1205 1210 1215

Leu Ser Thr Phe Leu Gly Leu Glu Val Leu Phe Gln Gly Pro Gly
1220 1225 1230

His His His His His His His His Ser Ala Trp Ser His Pro Gln
1235 1240 1245

Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser
1250 1255 1260

Ala Trp Ser His Pro Gln Phe Glu Lys
1265 1270

<210> 36
<211> 1272
<212> PRT
<213> Artificial Sequence

<220>
<223> COV2_S_(P589C_F855C)_trimer_tag_2

<400> 36

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
 35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
 65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
 85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
 100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
 115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
 130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
 145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
 165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
 180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
 195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
 210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
 225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
 245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
 260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
 290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Cys Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val

580

585

590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
 595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
 610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
 625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
 645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
 660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
 675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
 690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
 705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
 725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
 740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
 755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
 770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
 785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
 805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
 820 825 830

Leu Ile Cys Ala Gln Lys Cys Asn Gly Leu Thr Val Leu Pro Pro Leu
 835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
 850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro
1190 1195 1200

Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu
1205 1210 1215

Leu Ser Thr Phe Leu Gly Leu Glu Val Leu Phe Gln Gly Pro Gly
1220 1225 1230

His His His His His His His His Ser Ala Trp Ser His Pro Gln
1235 1240 1245

Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser
1250 1255 1260

Ala Trp Ser His Pro Gln Phe Glu Lys
1265 1270

<210> 37
<211> 1272
<212> PRT
<213> Artificial Sequence

<220>
<223> COV2_S_(P665C_L864C)_trimer_tag_2

<400> 37

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
 85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
 100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
 115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
 130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
 145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
 165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
 180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
 195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
 210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
 225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
 245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
 260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
 290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
 305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
 325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Cys Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Cys
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn

900

905

910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
 915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
 930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
 945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
 965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
 980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
 995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
 1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
 1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
 1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
 1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
 1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
 1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
 1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
 1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
 1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
 1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
 1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro
1190 1195 1200

Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu
1205 1210 1215

Leu Ser Thr Phe Leu Gly Leu Glu Val Leu Phe Gln Gly Pro Gly
1220 1225 1230

His His His His His His His His Ser Ala Trp Ser His Pro Gln
1235 1240 1245

Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser
1250 1255 1260

Ala Trp Ser His Pro Gln Phe Glu Lys
1265 1270

<210> 38
<211> 1272
<212> PRT
<213> Artificial Sequence

<220>
<223> COV2_S_(S383C_D985C)_trimer_tag_2

<400> 38

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr

115

120

125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
 130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
 145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
 165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
 180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
 195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
 210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
 225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
 245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
 260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
 290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
 305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
 325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Cys Pro
 355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
 500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
 515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
 530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
 545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
 565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
 580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
 595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
 610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
 625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
 645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
 660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Cys Lys Val Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro
1190 1195 1200

Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu

1205		1210		1215
Leu Ser Thr Phe Leu Gly Leu Glu Val Leu Phe Gln Gly Pro Gly				
1220		1225		1230
His His His His His His His His Ser Ala Trp Ser His Pro Gln				
1235		1240		1245
Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser				
1250		1255		1260
Ala Trp Ser His Pro Gln Phe Glu Lys				
1265		1270		
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Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu				
	20		25	30
His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp				
	35		40	45
Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp				
50		55		60
Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu				
65		70		75 80
Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser				
	85		90	95
Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile				
	100		105	110
Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr				
	115		120	125
Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr				
130		135		140
Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu				
145		150		155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe

435

440

445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
 500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
 515 520 525

Gly Leu Cys Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
 530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
 545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
 565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
 580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
 595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
 610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
 625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
 645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
 660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
 675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
 690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
 705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
 725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
 740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
 755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
 770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
 785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
 805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
 820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
 835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
 850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
 865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
 885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
 900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
 915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
 930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
 945 950 955 960

Leu Cys Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
 965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
 980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro
1190 1195 1200

Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu
1205 1210 1215

Leu Ser Thr Phe Leu Gly Leu Glu Val Leu Phe Gln Gly Pro Gly
1220 1225 1230

His His His His His His His His Ser Ala Trp Ser His Pro Gln
1235 1240 1245

Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser
1250 1255 1260

Ala Trp Ser His Pro Gln Phe Glu Lys
1265 1270

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<400> 40

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Cys Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln

755

760

765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Cys Leu Asp Lys Val Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser	Ala	Pro	His	Gly	Val	Val	Phe	Leu	His	Val	Thr	Tyr	Val	Pro
1040						1045					1050			
Ala	Gln	Glu	Lys	Asn	Phe	Thr	Thr	Ala	Pro	Ala	Ile	Cys	His	Asp
1055						1060					1065			
Gly	Lys	Ala	His	Phe	Pro	Arg	Glu	Gly	Val	Phe	Val	Ser	Asn	Gly
1070						1075					1080			
Thr	His	Trp	Phe	Val	Thr	Gln	Arg	Asn	Phe	Tyr	Glu	Pro	Gln	Ile
1085						1090					1095			
Ile	Thr	Thr	Asp	Asn	Thr	Phe	Val	Ser	Gly	Asn	Cys	Asp	Val	Val
1100						1105					1110			
Ile	Gly	Ile	Val	Asn	Asn	Thr	Val	Tyr	Asp	Pro	Leu	Gln	Pro	Glu
1115						1120					1125			
Leu	Asp	Ser	Phe	Lys	Glu	Glu	Leu	Asp	Lys	Tyr	Phe	Lys	Asn	His
1130						1135					1140			
Thr	Ser	Pro	Asp	Val	Asp	Leu	Gly	Asp	Ile	Ser	Gly	Ile	Asn	Ala
1145						1150					1155			
Ser	Val	Val	Asn	Ile	Gln	Lys	Glu	Ile	Asp	Arg	Leu	Asn	Glu	Val
1160						1165					1170			
Ala	Lys	Asn	Leu	Asn	Glu	Ser	Leu	Ile	Asp	Leu	Gln	Glu	Leu	Gly
1175						1180					1185			
Lys	Tyr	Glu	Gln	Gly	Gly	Gly	Ser	Gly	Tyr	Ile	Pro	Glu	Ala	Pro
1190						1195					1200			
Arg	Asp	Gly	Gln	Ala	Tyr	Val	Arg	Lys	Asp	Gly	Glu	Trp	Val	Leu
1205						1210					1215			
Leu	Ser	Thr	Phe	Leu	Gly	Leu	Glu	Val	Leu	Phe	Gln	Gly	Pro	Gly
1220						1225					1230			
His	His	His	His	His	His	His	His	Ser	Ala	Trp	Ser	His	Pro	Gln
1235						1240					1245			
Phe	Glu	Lys	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Ser
1250						1255					1260			
Ala	Trp	Ser	His	Pro	Gln	Phe	Glu	Lys						
1265						1270								

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<220>

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
 260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
 290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
 305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
 325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
 355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
 500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
 515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly

1070 1075 1080
 Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
 1085 1090 1095
 Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
 1100 1105 1110
 Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
 1115 1120 1125
 Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
 1130 1135 1140
 Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
 1145 1150 1155
 Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
 1160 1165 1170
 Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
 1175 1180 1185
 Lys Tyr Glu Gln
 1190
 <210> 42
 <211> 1257
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> full_length_unmodified SARS_CoV_2_S protein (1-1273;
 R682G_R683S_R685S)
 <400> 42
 Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe
 1 5 10 15
 Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu
 20 25 30
 His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
 35 40 45
 Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp
 50 55 60
 Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
 65 70 75 80
 Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
 85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala

655

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln Tyr Ile Lys Trp Pro Trp Tyr Ile Trp Leu Gly
1190 1195 1200

Phe Ile Ala Gly Leu Ile Ala Ile Val Met Val Thr Ile Met Leu
1205 1210 1215

Cys Cys Met Thr Ser Cys Cys Ser Cys Leu Lys Gly Cys Cys Ser
1220 1225 1230

Cys Gly Ser Cys Cys Lys Phe Asp Glu Asp Asp Ser Glu Pro Val
1235 1240 1245

Leu Lys Gly Val Lys Leu His Tyr Thr
1250 1255

<210> 43
<211> 1192
<212> PRT
<213> Artificial Sequence

<220>
<223> COV2_S_(R682G_R683S_R685S_K986P_V987P)

<400> 43

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
 165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
 180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
 195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
 210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
 225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
 245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
 260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
 290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
 305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
 325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
 355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val

980

985

990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
 995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
 1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
 1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
 1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
 1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
 1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
 1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
 1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
 1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
 1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
 1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
 1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
 1175 1180 1185

Lys Tyr Glu Gln
 1190

<210> 44

<211> 1192

<212> PRT

<213> Artificial Sequence

<220>

<223> COV2_S_(R682G_R683S_R685S_A570C_V963C_K986P_V987P)

<400> 44

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys

275

280

285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
 290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
 305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
 325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
 355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
 500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
 515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
 530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Cys Asp Thr Thr Asp Ala Val
 545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Cys Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln
1190

<210> 45
<211> 1192
<212> PRT
<213> Artificial Sequence

<220>
<223> COV2_S_(R682G_R683S_R685S_D614C_T859C_K986P_V987P)

<400> 45

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Cys Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser

Leu Asn Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln
1190

<210> 46
<211> 1192
<212> PRT

<213> Artificial Sequence

<220>

<223> COV2_S_(R682G_R683S_R685S_K41C_A520C_K986P_V987P)

<400> 46

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
 260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
 290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
 305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
 325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
 355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 485 490 495

Leu Ser Phe Glu Leu Leu His Cys Pro Ala Thr Val Cys Gly Pro Lys
 500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
 515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly

1070		1075		1080
Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile				
1085		1090		1095
Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val				
1100		1105		1110
Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu				
1115		1120		1125
Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His				
1130		1135		1140
Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala				
1145		1150		1155
Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val				
1160		1165		1170
Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly				
1175		1180		1185
Lys Tyr Glu Gln				
1190				

<210> 47
 <211> 1192
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> COV2_S_(R682G_R683S_R685S_P225C_F562C_K986P_V987P)

 <400> 47

Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe				
1	5	10	15	
Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu				
20	25	30		
His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp				
35	40	45		
Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp				
50	55	60		
Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu				
65	70	75	80	
Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser				
85	90	95		

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Cys Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe

370

375

380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
 500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
 515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
 530 535 540

Pro Cys Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
 545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
 565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
 580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
 595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
 610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
 625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
 645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
 660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
 675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
 690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
 705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
 725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
 740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
 755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
 770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
 785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
 805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
 820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
 835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
 850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
 865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
 885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
 900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
 915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln
1190

<210> 48
<211> 1192
<212> PRT
<213> Artificial Sequence

<220>
<223> COV2_S_(R682G_R683S_R685S_P589C_F855C_K986P_V987P)

<400> 48

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Cys Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe

770	775	780
Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser 785 790 795 800		
Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly 805 810 815		
Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp 820 825 830		
Leu Ile Cys Ala Gln Lys Cys Asn Gly Leu Thr Val Leu Pro Pro Leu 835 840 845		
Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly 850 855 860		
Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile 865 870 875 880		
Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr 885 890 895		
Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn 900 905 910		
Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala 915 920 925		
Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn 930 935 940		
Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val 945 950 955 960		
Leu Asn Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln 965 970 975		
Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val 980 985 990		
Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu 995 1000 1005		
Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg 1010 1015 1020		
Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln 1025 1030 1035		
Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro 1040 1045 1050		

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln
1190

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu

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

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
 355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
 500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
 515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
 530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
 545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
 565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
 580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
 595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
 610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Cys Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Cys
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val

1160	1165	1170
Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly		
1175	1180	1185
Lys Tyr Glu Gln		
1190		
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<400> 50		
Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe		
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Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu		
	20	25 30
His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp		
	35	40 45
Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp		
50	55	60
Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu		
65	70	75 80
Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser		
	85	90 95
Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile		
	100	105 110
Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr		
	115	120 125
Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr		
	130	135 140
Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu		
145	150	155 160
Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe		
	165	170 175
Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr		
	180	185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Cys Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly

465		470		475		480									
Phe	Gln	Pro	Thr	Asn	Gly	Val	Gly	Tyr	Gln	Pro	Tyr	Arg	Val	Val	Val
				485					490					495	
Leu	Ser	Phe	Glu	Leu	Leu	His	Ala	Pro	Ala	Thr	Val	Cys	Gly	Pro	Lys
			500					505					510		
Lys	Ser	Thr	Asn	Leu	Val	Lys	Asn	Lys	Cys	Val	Asn	Phe	Asn	Phe	Asn
		515					520					525			
Gly	Leu	Thr	Gly	Thr	Gly	Val	Leu	Thr	Glu	Ser	Asn	Lys	Lys	Phe	Leu
	530					535					540				
Pro	Phe	Gln	Gln	Phe	Gly	Arg	Asp	Ile	Ala	Asp	Thr	Thr	Asp	Ala	Val
545					550					555					560
Arg	Asp	Pro	Gln	Thr	Leu	Glu	Ile	Leu	Asp	Ile	Thr	Pro	Cys	Ser	Phe
				565					570					575	
Gly	Gly	Val	Ser	Val	Ile	Thr	Pro	Gly	Thr	Asn	Thr	Ser	Asn	Gln	Val
			580					585					590		
Ala	Val	Leu	Tyr	Gln	Asp	Val	Asn	Cys	Thr	Glu	Val	Pro	Val	Ala	Ile
		595					600					605			
His	Ala	Asp	Gln	Leu	Thr	Pro	Thr	Trp	Arg	Val	Tyr	Ser	Thr	Gly	Ser
	610					615					620				
Asn	Val	Phe	Gln	Thr	Arg	Ala	Gly	Cys	Leu	Ile	Gly	Ala	Glu	His	Val
625					630					635					640
Asn	Asn	Ser	Tyr	Glu	Cys	Asp	Ile	Pro	Ile	Gly	Ala	Gly	Ile	Cys	Ala
				645					650					655	
Ser	Tyr	Gln	Thr	Gln	Thr	Asn	Ser	Pro	Gly	Ser	Ala	Ser	Ser	Val	Ala
			660					665					670		
Ser	Gln	Ser	Ile	Ile	Ala	Tyr	Thr	Met	Ser	Leu	Gly	Ala	Glu	Asn	Ser
		675					680					685			
Val	Ala	Tyr	Ser	Asn	Asn	Ser	Ile	Ala	Ile	Pro	Thr	Asn	Phe	Thr	Ile
	690					695					700				
Ser	Val	Thr	Thr	Glu	Ile	Leu	Pro	Val	Ser	Met	Thr	Lys	Thr	Ser	Val
705				710						715					720
Asp	Cys	Thr	Met	Tyr	Ile	Cys	Gly	Asp	Ser	Thr	Glu	Cys	Ser	Asn	Leu
				725					730					735	
Leu	Leu	Gln	Tyr	Gly	Ser	Phe	Cys	Thr	Gln	Leu	Asn	Arg	Ala	Leu	Thr
			740					745					750		

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Cys Pro Pro Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln
1190

<210> 51
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Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe
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Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu
20 25 30

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Cys Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile

865		870		875		880
Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr						
	885			890		895
Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn						
	900			905		910
Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala						
	915			920		925
Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn						
	930			935		940
Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val						
	945			950		955
Leu Cys Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln						
	965			970		975
Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val						
	980			985		990
Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu						
	995			1000		1005
Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg						
	1010			1015		1020
Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln						
	1025			1030		1035
Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro						
	1040			1045		1050
Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp						
	1055			1060		1065
Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly						
	1070			1075		1080
Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile						
	1085			1090		1095
Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val						
	1100			1105		1110
Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu						
	1115			1120		1125
Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His						
	1130			1135		1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln
1190

<210> 52
<211> 1192
<212> PRT
<213> Artificial Sequence

<220>
<223> COV2_S_(R682G_R683S_R685S_V382C_R983C_K986P_V987P)

<400> 52

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe

165

170

175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Cys Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
 500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
 515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
 530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
 545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
 565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
 580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
 595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
 610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
 625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
 645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
 660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
 675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
 690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
 705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Cys Leu Asp Pro Pro Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln
1190

<210> 53
<211> 1192
<212> PRT
<213> Artificial Sequence

<220>
<223> COV2_S_(R682G_R683S_R685S_A570C_V963C)

<400> 53

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
 35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
 65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
 85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
 100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
 115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
 130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
 145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
 165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
 180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
 195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
 210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
 225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
 245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
 260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Cys Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe

565

570

575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Cys Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln
1190

<210> 54
<211> 1192
<212> PRT
<213> Artificial Sequence

<220>
<223> COV2_S_(R682G_R683S_R685S_D614C_T859C)

<400> 54

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
 145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
 165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
 180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
 195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
 210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
 225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
 245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
 260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
 290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
 305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
 325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
 355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Cys Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Cys Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln

965

970

975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
 980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
 995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
 1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
 1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
 1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
 1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
 1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
 1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
 1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
 1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
 1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
 1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
 1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
 1175 1180 1185

Lys Tyr Glu Gln
 1190

<210> 55

<211> 1192

<212> PRT

<213> Artificial Sequence

<220>

<223> COV2_S_(R682G_R683S_R685S_K41C_A520C)

<400> 55

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala

260

265

270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
 290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
 305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
 325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
 355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 485 490 495

Leu Ser Phe Glu Leu Leu His Cys Pro Ala Thr Val Cys Gly Pro Lys
 500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
 515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
 530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
 545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
 565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
 580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
 595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
 610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
 625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
 645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
 660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
 675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
 690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
 705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
 725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
 740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
 755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
 770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
 785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
 805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln
1190

<210> 56

<211> 1192

<212> PRT

<213> Artificial Sequence

<220>

<223> COV2_S_(R682G_R683S_R685S_P225C_F562C)

<400> 56

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Cys Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Cys Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala

660

665

670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
 675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
 690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
 705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
 725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
 740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
 755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
 770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
 785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
 805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
 820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
 835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
 850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
 865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
 885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
 900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
 915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
 930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln
1190

<210> 57
<211> 1192
<212> PRT
<213> Artificial Sequence

<220>
<223> COV2_S_(R682G_R683S_R685S_P589C_F855C)

<400> 57

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
 245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
 260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
 290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
 305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
 325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
 355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
 500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Cys Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Cys Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp

1055		1060		1065
Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly				
1070		1075		1080
Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile				
1085		1090		1095
Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val				
1100		1105		1110
Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu				
1115		1120		1125
Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His				
1130		1135		1140
Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala				
1145		1150		1155
Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val				
1160		1165		1170
Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly				
1175		1180		1185
Lys Tyr Glu Gln				
1190				
<210>	58			
<211>	1192			
<212>	PRT			
<213>	Artificial Sequence			
<220>				
<223>	COV2_S_(R682G_R683S_R685S_P665C_L864C)			
<400>	58			
Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe				
1	5	10	15	
Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu				
20	25	30		
His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp				
35	40	45		
Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp				
50	55	60		
Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu				
65	70	75	80	

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

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

355

360

365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
 500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
 515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
 530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
 545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
 565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
 580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
 595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
 610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
 625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Cys Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Cys
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln
1190

<210> 59
<211> 1192
<212> PRT
<213> Artificial Sequence

<220>
<223> COV2_S_(R682G_R683S_R685S_S383C_D985C)

<400> 59

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
 210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
 225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
 245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
 260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
 290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
 305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
 325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Cys Pro
 355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln

755

760

765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Cys Lys Val Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln
1190

<210> 60

<211> 1192

<212> PRT

<213> Artificial Sequence

<220>

<223> COV2_S_(R682G_R683S_R685S_T547C_N978C)

<400> 60

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp

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

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
 355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
 500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
 515 520 525

Gly Leu Cys Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
 530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
 545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
 565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
 580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
 595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Cys Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala

1145	1150	1155
Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val		
1160	1165	1170
Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly		
1175	1180	1185
Lys Tyr Glu Gln		
1190		
<210> 61		
<211> 1192		
<212> PRT		
<213> Artificial Sequence		
<220>		
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<400> 61		
Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe		
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Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu		
	20	25 30
His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp		
	35	40 45
Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp		
50	55	60
Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu		
65	70	75 80
Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser		
	85	90 95
Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile		
	100	105 110
Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr		
	115	120 125
Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr		
	130	135 140
Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu		
145	150	155 160
Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe		
	165	170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Cys Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys

450		455		460	
Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly					
465		470		475	480
Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val					
		485		490	495
Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys					
		500		505	510
Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn					
		515		520	525
Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu					
		530		535	540
Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val					
545		550		555	560
Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe					
		565		570	575
Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val					
		580		585	590
Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile					
		595		600	605
His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser					
		610		615	620
Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val					
625		630		635	640
Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala					
		645		650	655
Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala					
		660		665	670
Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser					
		675		680	685
Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile					
		690		695	700
Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val					
705		710		715	720
Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu					
		725		730	735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Cys Leu Asp Lys Val Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln
1190

<210> 62
<211> 1272
<212> PRT
<213> Artificial Sequence

<220>
<223> COV2_S_(R682G_R683S_R685S_K986P_V987P)_trimer_tag_2

<400> 62

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
 35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
 65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
 85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
 100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
 115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
 130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
 145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
 165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
 180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
 195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
 210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
 225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
 245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
 260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
 290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly	Gly	Val	Ser	Val	Ile	Thr	Pro	Gly	Thr	Asn	Thr	Ser	Asn	Gln	Val	580	585	590	
Ala	Val	Leu	Tyr	Gln	Asp	Val	Asn	Cys	Thr	Glu	Val	Pro	Val	Ala	Ile	595	600	605	
His	Ala	Asp	Gln	Leu	Thr	Pro	Thr	Trp	Arg	Val	Tyr	Ser	Thr	Gly	Ser	610	615	620	
Asn	Val	Phe	Gln	Thr	Arg	Ala	Gly	Cys	Leu	Ile	Gly	Ala	Glu	His	Val	625	630	635	640
Asn	Asn	Ser	Tyr	Glu	Cys	Asp	Ile	Pro	Ile	Gly	Ala	Gly	Ile	Cys	Ala	645	650	655	
Ser	Tyr	Gln	Thr	Gln	Thr	Asn	Ser	Pro	Gly	Ser	Ala	Ser	Ser	Val	Ala	660	665	670	
Ser	Gln	Ser	Ile	Ile	Ala	Tyr	Thr	Met	Ser	Leu	Gly	Ala	Glu	Asn	Ser	675	680	685	
Val	Ala	Tyr	Ser	Asn	Asn	Ser	Ile	Ala	Ile	Pro	Thr	Asn	Phe	Thr	Ile	690	695	700	
Ser	Val	Thr	Thr	Glu	Ile	Leu	Pro	Val	Ser	Met	Thr	Lys	Thr	Ser	Val	705	710	715	720
Asp	Cys	Thr	Met	Tyr	Ile	Cys	Gly	Asp	Ser	Thr	Glu	Cys	Ser	Asn	Leu	725	730	735	
Leu	Leu	Gln	Tyr	Gly	Ser	Phe	Cys	Thr	Gln	Leu	Asn	Arg	Ala	Leu	Thr	740	745	750	
Gly	Ile	Ala	Val	Glu	Gln	Asp	Lys	Asn	Thr	Gln	Glu	Val	Phe	Ala	Gln	755	760	765	
Val	Lys	Gln	Ile	Tyr	Lys	Thr	Pro	Pro	Ile	Lys	Asp	Phe	Gly	Gly	Phe	770	775	780	
Asn	Phe	Ser	Gln	Ile	Leu	Pro	Asp	Pro	Ser	Lys	Pro	Ser	Lys	Arg	Ser	785	790	795	800
Phe	Ile	Glu	Asp	Leu	Leu	Phe	Asn	Lys	Val	Thr	Leu	Ala	Asp	Ala	Gly	805	810	815	
Phe	Ile	Lys	Gln	Tyr	Gly	Asp	Cys	Leu	Gly	Asp	Ile	Ala	Ala	Arg	Asp	820	825	830	
Leu	Ile	Cys	Ala	Gln	Lys	Phe	Asn	Gly	Leu	Thr	Val	Leu	Pro	Pro	Leu	835	840	845	
Leu	Thr	Asp	Glu	Met	Ile	Ala	Gln	Tyr	Thr	Ser	Ala	Leu	Leu	Ala	Gly				

850					855					860					
Thr 865	Ile	Thr	Ser	Gly	Trp 870	Thr	Phe	Gly	Ala	Gly 875	Ala	Ala	Leu	Gln	Ile 880
Pro	Phe	Ala	Met	Gln 885	Met	Ala	Tyr	Arg	Phe 890	Asn	Gly	Ile	Gly	Val 895	Thr
Gln	Asn	Val	Leu 900	Tyr	Glu	Asn	Gln	Lys 905	Leu	Ile	Ala	Asn	Gln 910	Phe	Asn
Ser	Ala	Ile 915	Gly	Lys	Ile	Gln	Asp 920	Ser	Leu	Ser	Ser	Thr 925	Ala	Ser	Ala
Leu	Gly 930	Lys	Leu	Gln	Asp	Val 935	Val	Asn	Gln	Asn	Ala 940	Gln	Ala	Leu	Asn
Thr 945	Leu	Val	Lys	Gln	Leu 950	Ser	Ser	Asn	Phe	Gly 955	Ala	Ile	Ser	Ser	Val 960
Leu	Asn	Asp	Ile	Leu 965	Ser	Arg	Leu	Asp	Lys 970	Val	Glu	Ala	Glu	Val 975	Gln
Ile	Asp	Arg	Leu 980	Ile	Thr	Gly	Arg	Leu 985	Gln	Ser	Leu	Gln 990	Thr	Tyr	Val
Thr	Gln 995	Gln	Leu	Ile	Arg	Ala	Ala 1000	Glu	Ile	Arg	Ala	Ser 1005	Ala	Asn	Leu
Ala	Ala 1010	Thr	Lys	Met	Ser	Glu 1015	Cys	Val	Leu	Gly	Gln 1020	Ser	Lys	Arg	
Val	Asp 1025	Phe	Cys	Gly	Lys	Gly 1030	Tyr	His	Leu	Met	Ser 1035	Phe	Pro	Gln	
Ser	Ala 1040	Pro	His	Gly	Val	Val 1045	Phe	Leu	His	Val	Thr 1050	Tyr	Val	Pro	
Ala	Gln 1055	Glu	Lys	Asn	Phe	Thr 1060	Thr	Ala	Pro	Ala	Ile 1065	Cys	His	Asp	
Gly	Lys 1070	Ala	His	Phe	Pro	Arg 1075	Glu	Gly	Val	Phe	Val 1080	Ser	Asn	Gly	
Thr 1085	His	Trp	Phe	Val	Thr	Gln 1090	Arg	Asn	Phe	Tyr	Glu 1095	Pro	Gln	Ile	
Ile 1100	Thr	Thr	Asp	Asn	Thr	Phe 1105	Val	Ser	Gly	Asn	Cys 1110	Asp	Val	Val	
Ile 1115	Gly	Ile	Val	Asn	Asn	Thr 1120	Val	Tyr	Asp	Pro	Leu 1125	Gln	Pro	Glu	

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro
1190 1195 1200

Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu
1205 1210 1215

Leu Ser Thr Phe Leu Gly Leu Glu Val Leu Phe Gln Gly Pro Gly
1220 1225 1230

His His His His His His His His Ser Ala Trp Ser His Pro Gln
1235 1240 1245

Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser
1250 1255 1260

Ala Trp Ser His Pro Gln Phe Glu Lys
1265 1270

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu

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

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Cys Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Cys Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val

1160	1165	1170
Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly		
1175	1180	1185
Lys Tyr Glu Gln Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro		
1190	1195	1200
Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu		
1205	1210	1215
Leu Ser Thr Phe Leu Gly Leu Glu Val Leu Phe Gln Gly Pro Gly		
1220	1225	1230
His His His His His His His His Ser Ala Trp Ser His Pro Gln		
1235	1240	1245
Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser		
1250	1255	1260
Ala Trp Ser His Pro Gln Phe Glu Lys		
1265	1270	
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Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe		
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Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu		
	20	25 30
His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp		
	35	40 45
Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp		
50	55	60
Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu		
65	70	75 80
Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser		
	85	90 95
Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile		
	100	105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly

385		390		395		400
Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys						
	405			410		415
Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn						
	420			425		430
Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe						
	435			440		445
Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys						
	450			455		460
Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly						
	465			470		480
Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val						
	485			490		495
Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys						
	500			505		510
Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn						
	515			520		525
Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu						
	530			535		540
Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val						
	545			550		555
Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe						
	565			570		575
Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val						
	580			585		590
Ala Val Leu Tyr Gln Cys Val Asn Cys Thr Glu Val Pro Val Ala Ile						
	595			600		605
His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser						
	610			615		620
Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val						
	625			630		635
Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala						
	645			650		655
Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala						
	660			665		670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
 675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
 690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
 705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
 725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
 740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
 755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
 770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
 785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
 805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
 820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Cys Val Leu Pro Pro Leu
 835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
 850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
 865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
 885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
 900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
 915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
 930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro
1190 1195 1200

Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu
1205 1210 1215

Leu Ser Thr Phe Leu Gly Leu Glu Val Leu Phe Gln Gly Pro Gly
1220 1225 1230

His His His His His His His His Ser Ala Trp Ser His Pro Gln
1235 1240 1245

Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser
1250 1255 1260

Ala Trp Ser His Pro Gln Phe Glu Lys
1265 1270

<210> 65

<211> 1272

<212> PRT

<213> Artificial Sequence

<220>

<223> COV2_S_(R682G_R683S_R685S_K41C_A520C_K986P_V987P)_trimer_tag_2

<400> 65

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Cys Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val

705		710		715		720
Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu						
	725			730		735
Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr						
	740			745		750
Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln						
	755			760		765
Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe						
	770			775		780
Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser						
	785			790		795
Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly						
	805			810		815
Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp						
	820			825		830
Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu						
	835			840		845
Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly						
	850			855		860
Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile						
	865			870		875
Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr						
	885			890		895
Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn						
	900			905		910
Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala						
	915			920		925
Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn						
	930			935		940
Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val						
	945			950		955
Leu Asn Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln						
	965			970		975
Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val						
	980			985		990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro
1190 1195 1200

Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu
1205 1210 1215

Leu Ser Thr Phe Leu Gly Leu Glu Val Leu Phe Gln Gly Pro Gly
1220 1225 1230

His His His His His His His His Ser Ala Trp Ser His Pro Gln
1235 1240 1245

Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser
1250 1255 1260

Ala Trp Ser His Pro Gln Phe Glu Lys
1265 1270

<210> 66
<211> 1272
<212> PRT
<213> Artificial Sequence

<220>
<223> COV2_S_(R682G_R683S_R685S_P225C_F562C_K986P_V987P)_trimer_tag_2

<400> 66

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Cys Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
 210 215 220
 Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
 225 230 235 240
 Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
 245 250 255
 Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
 260 265 270
 Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 275 280 285
 Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
 290 295 300
 Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
 305 310 315 320
 Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
 325 330 335
 Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 340 345 350
 Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
 355 360 365
 Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 370 375 380
 Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 385 390 395 400
 Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 405 410 415
 Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 420 425 430
 Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 435 440 445
 Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460
 Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Cys Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln

1025		1030		1035
Ser Ala Pro His Gly Val	Val Phe Leu His Val	Thr Tyr Val Pro		
1040	1045	1050		
Ala Gln Glu Lys Asn Phe	Thr Thr Ala Pro Ala	Ile Cys His Asp		
1055	1060	1065		
Gly Lys Ala His Phe Pro	Arg Glu Gly Val Phe	Val Ser Asn Gly		
1070	1075	1080		
Thr His Trp Phe Val Thr	Gln Arg Asn Phe Tyr	Glu Pro Gln Ile		
1085	1090	1095		
Ile Thr Thr Asp Asn Thr	Phe Val Ser Gly Asn	Cys Asp Val Val		
1100	1105	1110		
Ile Gly Ile Val Asn Asn	Thr Val Tyr Asp Pro	Leu Gln Pro Glu		
1115	1120	1125		
Leu Asp Ser Phe Lys Glu	Glu Leu Asp Lys Tyr	Phe Lys Asn His		
1130	1135	1140		
Thr Ser Pro Asp Val Asp	Leu Gly Asp Ile Ser	Gly Ile Asn Ala		
1145	1150	1155		
Ser Val Val Asn Ile Gln	Lys Glu Ile Asp Arg	Leu Asn Glu Val		
1160	1165	1170		
Ala Lys Asn Leu Asn Glu	Ser Leu Ile Asp Leu	Gln Glu Leu Gly		
1175	1180	1185		
Lys Tyr Glu Gln Gly Gly	Gly Ser Gly Tyr Ile	Pro Glu Ala Pro		
1190	1195	1200		
Arg Asp Gly Gln Ala Tyr	Val Arg Lys Asp Gly	Glu Trp Val Leu		
1205	1210	1215		
Leu Ser Thr Phe Leu Gly	Leu Glu Val Leu Phe	Gln Gly Pro Gly		
1220	1225	1230		
His His His His His His	His His Ser Ala Trp	Ser His Pro Gln		
1235	1240	1245		
Phe Glu Lys Gly Gly Gly	Ser Gly Gly Gly Gly	Ser Gly Gly Ser		
1250	1255	1260		
Ala Trp Ser His Pro Gln	Phe Glu Lys			
1265	1270			

<210> 67
 <211> 1272

<212> PRT
<213> Artificial Sequence

<220>
<223> COV2_S_(R682G_R683S_R685S_P589C_F855C_K986P_V987P)_trimer_tag_2

<400> 67

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro

255

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
 530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
 545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Cys Cys Ser Phe
 565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
 580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
 595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
 610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
 625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
 645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
 660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
 675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
 690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
 705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
 725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
 740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
 755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
 770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
 785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Cys Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro
1190 1195 1200

Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu
1205 1210 1215

Leu Ser Thr Phe Leu Gly Leu Glu Val Leu Phe Gln Gly Pro Gly
1220 1225 1230

His His His His His His His His Ser Ala Trp Ser His Pro Gln
1235 1240 1245

Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser
1250 1255 1260

Ala Trp Ser His Pro Gln Phe Glu Lys
1265 1270

<210> 68

<211> 1272

<212> PRT

<213> Artificial Sequence

<220>

<223> COV2_S_(R682G_R683S_R685S_P665C_L864C_K986P_V987P)_trimer_tag_2

<400> 68

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe

565

570

575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Cys Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Cys
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro
1190 1195 1200

Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu
1205 1210 1215

Leu Ser Thr Phe Leu Gly Leu Glu Val Leu Phe Gln Gly Pro Gly
1220 1225 1230

His His His His His His His His Ser Ala Trp Ser His Pro Gln
1235 1240 1245

Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser
1250 1255 1260

Ala Trp Ser His Pro Gln Phe Glu Lys
1265 1270

<210> 69

<211> 1272

<212> PRT

<213> Artificial Sequence

<220>

<223> COV2_S_(R682G_R683S_R685S_S383C_D985C_K986P_V987P)_trimer_tag_2

<400> 69

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
 65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
 85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
 100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
 115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
 130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
 145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
 165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
 180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
 195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
 210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
 225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
 245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
 260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
 290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
 305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
 325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Cys Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr

885

890

895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
 900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
 915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
 930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
 945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Cys Pro Pro Glu Ala Glu Val Gln
 965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
 980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
 995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
 1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
 1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
 1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
 1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
 1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
 1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
 1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
 1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
 1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
 1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro
1190 1195 1200

Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu
1205 1210 1215

Leu Ser Thr Phe Leu Gly Leu Glu Val Leu Phe Gln Gly Pro Gly
1220 1225 1230

His His His His His His His His Ser Ala Trp Ser His Pro Gln
1235 1240 1245

Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser
1250 1255 1260

Ala Trp Ser His Pro Gln Phe Glu Lys
1265 1270

<210> 70

<211> 1272

<212> PRT

<213> Artificial Sequence

<220>

<223> COV2_S_(R682G_R683S_R685S_T547C_N978C_K986P_V987P)_trimer_tag_2

<400> 70

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile

100

105

110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
 115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
 130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
 145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
 165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
 180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
 195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
 210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
 225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
 245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
 260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
 290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
 305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
 325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
 355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Cys Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Cys Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro

1190	1195	1200
Arg Asp Gly Gln Ala Tyr Val	Arg Lys Asp Gly Glu Trp Val Leu	
1205	1210	1215
Leu Ser Thr Phe Leu Gly Leu	Glu Val Leu Phe Gln Gly Pro Gly	
1220	1225	1230
His His His His His His His	His Ser Ala Trp Ser His Pro Gln	
1235	1240	1245
Phe Glu Lys Gly Gly Gly Ser	Gly Gly Gly Gly Ser Gly Gly Ser	
1250	1255	1260
Ala Trp Ser His Pro Gln Phe	Glu Lys	
1265	1270	
<210> 71		
<211> 1272		
<212> PRT		
<213> Artificial Sequence		
<220>		
<223> COV2_S_(R682G_R683S_R685S_V382C_R983C_K986P_V987P)_trimer_tag_2		
<400> 71		
Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe		
1	5	10 15
Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu		
	20	25 30
His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp		
	35	40 45
Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp		
50	55	60
Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu		
65	70	75 80
Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser		
	85	90 95
Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile		
	100	105 110
Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr		
	115	120 125
Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr		
130	135	140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Cys Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn

420

425

430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
 500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
 515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
 530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
 545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
 565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
 580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
 595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
 610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
 625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
 645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
 660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
 675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
 690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
 705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
 725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
 740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
 755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
 770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
 785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
 805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
 820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
 835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
 850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
 865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
 885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
 900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
 915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
 930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
 945 950 955 960

Leu Asn Asp Ile Leu Ser Cys Leu Asp Pro Pro Glu Ala Glu Val Gln
 965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro
1190 1195 1200

Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu
1205 1210 1215

Leu Ser Thr Phe Leu Gly Leu Glu Val Leu Phe Gln Gly Pro Gly
1220 1225 1230

His His His His His His His Ser Ala Trp Ser His Pro Gln
1235 1240 1245

Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser
1250 1255 1260

Ala Trp Ser His Pro Gln Phe Glu Lys
1265 1270

<210> 72
<211> 1272
<212> PRT
<213> Artificial Sequence

<220>
<223> COV2_S_(R682G_R683S_R685S_A570C_V963C)_trimer_tag_2

<400> 72

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Cys Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr

740

745

750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
 755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
 770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
 785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
 805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
 820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
 835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
 850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
 865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
 885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
 900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
 915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
 930 935 940

Thr Leu Cys Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
 945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
 965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
 980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
 995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
 1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro
1190 1195 1200

Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu
1205 1210 1215

Leu Ser Thr Phe Leu Gly Leu Glu Val Leu Phe Gln Gly Pro Gly
1220 1225 1230

His His His His His His His His Ser Ala Trp Ser His Pro Gln
1235 1240 1245

Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser
1250 1255 1260

Ala Trp Ser His Pro Gln Phe Glu Lys
1265 1270

<210> 73
<211> 1272
<212> PRT
<213> Artificial Sequence

<220>
<223> COV2_S_(R682G_R683S_R685S_D614C_T859C)_trimer_tag_2

<400> 73

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
 245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
 260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
 290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
 305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
 325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
 355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
 500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Cys Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Cys Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp

1055														
Gly	Lys	Ala	His	Phe	Pro	Arg	Glu	Gly	Val	Phe	Val	Ser	Asn	Gly
1070						1075					1080			
Thr	His	Trp	Phe	Val	Thr	Gln	Arg	Asn	Phe	Tyr	Glu	Pro	Gln	Ile
1085						1090					1095			
Ile	Thr	Thr	Asp	Asn	Thr	Phe	Val	Ser	Gly	Asn	Cys	Asp	Val	Val
1100						1105					1110			
Ile	Gly	Ile	Val	Asn	Asn	Thr	Val	Tyr	Asp	Pro	Leu	Gln	Pro	Glu
1115						1120					1125			
Leu	Asp	Ser	Phe	Lys	Glu	Glu	Leu	Asp	Lys	Tyr	Phe	Lys	Asn	His
1130						1135					1140			
Thr	Ser	Pro	Asp	Val	Asp	Leu	Gly	Asp	Ile	Ser	Gly	Ile	Asn	Ala
1145						1150					1155			
Ser	Val	Val	Asn	Ile	Gln	Lys	Glu	Ile	Asp	Arg	Leu	Asn	Glu	Val
1160						1165					1170			
Ala	Lys	Asn	Leu	Asn	Glu	Ser	Leu	Ile	Asp	Leu	Gln	Glu	Leu	Gly
1175						1180					1185			
Lys	Tyr	Glu	Gln	Gly	Gly	Gly	Ser	Gly	Tyr	Ile	Pro	Glu	Ala	Pro
1190						1195					1200			
Arg	Asp	Gly	Gln	Ala	Tyr	Val	Arg	Lys	Asp	Gly	Glu	Trp	Val	Leu
1205						1210					1215			
Leu	Ser	Thr	Phe	Leu	Gly	Leu	Glu	Val	Leu	Phe	Gln	Gly	Pro	Gly
1220						1225					1230			
His	His	His	His	His	His	His	His	Ser	Ala	Trp	Ser	His	Pro	Gln
1235						1240					1245			
Phe	Glu	Lys	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Ser
1250						1255					1260			
Ala	Trp	Ser	His	Pro	Gln	Phe	Glu	Lys						
1265						1270								

<210> 74
 <211> 1272
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> COV2_S_(R682G_R683S_R685S_K41C_A520C)_trimer_tag_2

 <400> 74

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

275

280

285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
 290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
 305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
 325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
 355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 485 490 495

Leu Ser Phe Glu Leu Leu His Cys Pro Ala Thr Val Cys Gly Pro Lys
 500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
 515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
 530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
 545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
 1100 1105 1110

 Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
 1115 1120 1125

 Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
 1130 1135 1140

 Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
 1145 1150 1155

 Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
 1160 1165 1170

 Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
 1175 1180 1185

 Lys Tyr Glu Gln Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro
 1190 1195 1200

 Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu
 1205 1210 1215

 Leu Ser Thr Phe Leu Gly Leu Glu Val Leu Phe Gln Gly Pro Gly
 1220 1225 1230

 His His His His His His His His Ser Ala Trp Ser His Pro Gln
 1235 1240 1245

 Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser
 1250 1255 1260

 Ala Trp Ser His Pro Gln Phe Glu Lys
 1265 1270

<210> 75
 <211> 1272
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> COV2_S_(R682G_R683S_R685S_P225C_F562C)_trimer_tag_2

 <400> 75

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

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

 His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
 35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Cys Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Cys Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile

595

600

605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
 610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
 625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
 645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
 660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
 675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
 690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
 705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
 725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
 740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
 755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
 770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
 785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
 805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
 820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
 835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
 850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
 865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro
1190 1195 1200

Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu
1205 1210 1215

Leu Ser Thr Phe Leu Gly Leu Glu Val Leu Phe Gln Gly Pro Gly
1220 1225 1230

His His His His His His His His Ser Ala Trp Ser His Pro Gln
1235 1240 1245

Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser
1250 1255 1260

Ala Trp Ser His Pro Gln Phe Glu Lys
1265 1270

<210> 76
<211> 1272
<212> PRT
<213> Artificial Sequence

<220>
<223> COV2_S_(R682G_R683S_R685S_P589C_F855C)_trimer_tag_2

<400> 76

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
 100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
 115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
 130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
 145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
 165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
 180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
 195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
 210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
 225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
 245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
 260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
 290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
 305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
 325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
 355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Cys Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Cys Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala

915

920

925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
 930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
 945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
 965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
 980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
 995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
 1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
 1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
 1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
 1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
 1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
 1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
 1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
 1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
 1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
 1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
 1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
 1175 1180 1185

Lys Tyr Glu Gln Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro
1190 1195 1200

Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu
1205 1210 1215

Leu Ser Thr Phe Leu Gly Leu Glu Val Leu Phe Gln Gly Pro Gly
1220 1225 1230

His His His His His His His His Ser Ala Trp Ser His Pro Gln
1235 1240 1245

Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser
1250 1255 1260

Ala Trp Ser His Pro Gln Phe Glu Lys
1265 1270

<210> 77
<211> 1272
<212> PRT
<213> Artificial Sequence

<220>
<223> COV2_S_(R682G_R683S_R685S_P665C_L864C)_trimer_tag_2

<400> 77

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr

130	135	140														
Ser	Ser	Ala	Asn	Asn	Cys	Thr	Phe	Glu	Tyr	Val	Ser	Gln	Pro	Phe	Leu	
145					150					155					160	
Met	Asp	Leu	Glu	Gly	Lys	Gln	Gly	Asn	Phe	Lys	Asn	Leu	Arg	Glu	Phe	
				165				170						175		
Val	Phe	Lys	Asn	Ile	Asp	Gly	Tyr	Phe	Lys	Ile	Tyr	Ser	Lys	His	Thr	
			180					185					190			
Pro	Ile	Asn	Leu	Val	Arg	Asp	Leu	Pro	Gln	Gly	Phe	Ser	Ala	Leu	Glu	
		195					200					205				
Pro	Leu	Val	Asp	Leu	Pro	Ile	Gly	Ile	Asn	Ile	Thr	Arg	Phe	Gln	Thr	
	210					215					220					
Leu	Leu	Ala	Leu	His	Arg	Ser	Tyr	Leu	Thr	Pro	Gly	Asp	Ser	Ser	Ser	
225					230					235					240	
Gly	Trp	Thr	Ala	Gly	Ala	Ala	Ala	Tyr	Tyr	Val	Gly	Tyr	Leu	Gln	Pro	
				245					250					255		
Arg	Thr	Phe	Leu	Leu	Lys	Tyr	Asn	Glu	Asn	Gly	Thr	Ile	Thr	Asp	Ala	
			260					265					270			
Val	Asp	Cys	Ala	Leu	Asp	Pro	Leu	Ser	Glu	Thr	Lys	Cys	Thr	Leu	Lys	
		275					280					285				
Ser	Phe	Thr	Val	Glu	Lys	Gly	Ile	Tyr	Gln	Thr	Ser	Asn	Phe	Arg	Val	
	290					295					300					
Gln	Pro	Thr	Glu	Ser	Ile	Val	Arg	Phe	Pro	Asn	Ile	Thr	Asn	Leu	Cys	
305					310					315					320	
Pro	Phe	Gly	Glu	Val	Phe	Asn	Ala	Thr	Arg	Phe	Ala	Ser	Val	Tyr	Ala	
				325					330					335		
Trp	Asn	Arg	Lys	Arg	Ile	Ser	Asn	Cys	Val	Ala	Asp	Tyr	Ser	Val	Leu	
			340					345					350			
Tyr	Asn	Ser	Ala	Ser	Phe	Ser	Thr	Phe	Lys	Cys	Tyr	Gly	Val	Ser	Pro	
	355						360					365				
Thr	Lys	Leu	Asn	Asp	Leu	Cys	Phe	Thr	Asn	Val	Tyr	Ala	Asp	Ser	Phe	
	370					375					380					
Val	Ile	Arg	Gly	Asp	Glu	Val	Arg	Gln	Ile	Ala	Pro	Gly	Gln	Thr	Gly	
385					390					395					400	
Lys	Ile	Ala	Asp	Tyr	Asn	Tyr	Lys	Leu	Pro	Asp	Asp	Phe	Thr	Gly	Cys	
				405					410					415		

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Cys Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Cys
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro
1190 1195 1200

Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu
1205 1210 1215

Leu Ser Thr Phe Leu Gly Leu Glu Val Leu Phe Gln Gly Pro Gly

1220		1225		1230
His His His His His His His His Ser Ala Trp Ser His Pro Gln				
1235		1240		1245
Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser				
1250		1255		1260
Ala Trp Ser His Pro Gln Phe Glu Lys				
1265		1270		
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<400> 78				
Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe				
1		5	10	15
Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu				
	20	25	30	
His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp				
	35	40	45	
Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp				
50		55	60	
Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu				
65		70	75	80
Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser				
	85	90	95	
Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile				
	100	105	110	
Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr				
	115	120	125	
Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr				
130		135	140	
Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu				
145		150	155	160
Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe				
	165	170	175	

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Cys Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys

450		455		460	
Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly					
465		470		475	480
Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val					
	485		490		495
Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys					
	500		505		510
Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn					
	515		520		525
Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu					
	530		535		540
Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val					
545		550		555	560
Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe					
	565		570		575
Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val					
	580		585		590
Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile					
	595		600		605
His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser					
	610		615		620
Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val					
625		630		635	640
Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala					
	645		650		655
Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala					
	660		665		670
Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser					
	675		680		685
Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile					
	690		695		700
Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val					
705		710		715	720
Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu					
	725		730		735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Cys Lys Val Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala	Ala	Thr	Lys	Met	Ser	Glu	Cys	Val	Leu	Gly	Gln	Ser	Lys	Arg
1010						1015					1020			
Val	Asp	Phe	Cys	Gly	Lys	Gly	Tyr	His	Leu	Met	Ser	Phe	Pro	Gln
1025						1030					1035			
Ser	Ala	Pro	His	Gly	Val	Val	Phe	Leu	His	Val	Thr	Tyr	Val	Pro
1040						1045					1050			
Ala	Gln	Glu	Lys	Asn	Phe	Thr	Thr	Ala	Pro	Ala	Ile	Cys	His	Asp
1055						1060					1065			
Gly	Lys	Ala	His	Phe	Pro	Arg	Glu	Gly	Val	Phe	Val	Ser	Asn	Gly
1070						1075					1080			
Thr	His	Trp	Phe	Val	Thr	Gln	Arg	Asn	Phe	Tyr	Glu	Pro	Gln	Ile
1085						1090					1095			
Ile	Thr	Thr	Asp	Asn	Thr	Phe	Val	Ser	Gly	Asn	Cys	Asp	Val	Val
1100						1105					1110			
Ile	Gly	Ile	Val	Asn	Asn	Thr	Val	Tyr	Asp	Pro	Leu	Gln	Pro	Glu
1115						1120					1125			
Leu	Asp	Ser	Phe	Lys	Glu	Glu	Leu	Asp	Lys	Tyr	Phe	Lys	Asn	His
1130						1135					1140			
Thr	Ser	Pro	Asp	Val	Asp	Leu	Gly	Asp	Ile	Ser	Gly	Ile	Asn	Ala
1145						1150					1155			
Ser	Val	Val	Asn	Ile	Gln	Lys	Glu	Ile	Asp	Arg	Leu	Asn	Glu	Val
1160						1165					1170			
Ala	Lys	Asn	Leu	Asn	Glu	Ser	Leu	Ile	Asp	Leu	Gln	Glu	Leu	Gly
1175						1180					1185			
Lys	Tyr	Glu	Gln	Gly	Gly	Gly	Ser	Gly	Tyr	Ile	Pro	Glu	Ala	Pro
1190						1195					1200			
Arg	Asp	Gly	Gln	Ala	Tyr	Val	Arg	Lys	Asp	Gly	Glu	Trp	Val	Leu
1205						1210					1215			
Leu	Ser	Thr	Phe	Leu	Gly	Leu	Glu	Val	Leu	Phe	Gln	Gly	Pro	Gly
1220						1225					1230			
His	His	His	His	His	His	His	His	Ser	Ala	Trp	Ser	His	Pro	Gln
1235						1240					1245			
Phe	Glu	Lys	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Ser
1250						1255					1260			

Ala Trp Ser His Pro Gln Phe Glu Lys
1265 1270

<210> 79
<211> 1272
<212> PRT
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<220>
<223> COV2_S_(R682G_R683S_R685S_T547C_N978C)_trimer_tag_2

<400> 79

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Cys Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe

770	775	780
Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser 785 790 795 800		
Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly 805 810 815		
Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp 820 825 830		
Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu 835 840 845		
Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly 850 855 860		
Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile 865 870 875 880		
Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr 885 890 895		
Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn 900 905 910		
Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala 915 920 925		
Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn 930 935 940		
Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val 945 950 955 960		
Leu Cys Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln 965 970 975		
Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val 980 985 990		
Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu 995 1000 1005		
Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg 1010 1015 1020		
Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln 1025 1030 1035		
Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro 1040 1045 1050		

Ala	Gln	Glu	Lys	Asn	Phe	Thr	Thr	Ala	Pro	Ala	Ile	Cys	His	Asp	
1055						1060					1065				
Gly	Lys	Ala	His	Phe	Pro	Arg	Glu	Gly	Val	Phe	Val	Ser	Asn	Gly	
1070						1075					1080				
Thr	His	Trp	Phe	Val	Thr	Gln	Arg	Asn	Phe	Tyr	Glu	Pro	Gln	Ile	
1085						1090					1095				
Ile	Thr	Thr	Asp	Asn	Thr	Phe	Val	Ser	Gly	Asn	Cys	Asp	Val	Val	
1100						1105					1110				
Ile	Gly	Ile	Val	Asn	Asn	Thr	Val	Tyr	Asp	Pro	Leu	Gln	Pro	Glu	
1115						1120					1125				
Leu	Asp	Ser	Phe	Lys	Glu	Glu	Leu	Asp	Lys	Tyr	Phe	Lys	Asn	His	
1130						1135					1140				
Thr	Ser	Pro	Asp	Val	Asp	Leu	Gly	Asp	Ile	Ser	Gly	Ile	Asn	Ala	
1145						1150					1155				
Ser	Val	Val	Asn	Ile	Gln	Lys	Glu	Ile	Asp	Arg	Leu	Asn	Glu	Val	
1160						1165					1170				
Ala	Lys	Asn	Leu	Asn	Glu	Ser	Leu	Ile	Asp	Leu	Gln	Glu	Leu	Gly	
1175						1180					1185				
Lys	Tyr	Glu	Gln	Gly	Gly	Gly	Ser	Gly	Tyr	Ile	Pro	Glu	Ala	Pro	
1190						1195					1200				
Arg	Asp	Gly	Gln	Ala	Tyr	Val	Arg	Lys	Asp	Gly	Glu	Trp	Val	Leu	
1205						1210					1215				
Leu	Ser	Thr	Phe	Leu	Gly	Leu	Glu	Val	Leu	Phe	Gln	Gly	Pro	Gly	
1220						1225					1230				
His	His	His	His	His	His	His	His	Ser	Ala	Trp	Ser	His	Pro	Gln	
1235						1240					1245				
Phe	Glu	Lys	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Ser	
1250						1255					1260				
Ala	Trp	Ser	His	Pro	Gln	Phe	Glu	Lys							
1265						1270									

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<211> 1272

<212> PRT

<213> Artificial Sequence

<220>

<223> COV2_S_(R682G_R683S_R685S_V382C_R983C)_trimer_tag_2

<400> 80

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

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

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
 290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
 305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
 325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Cys Ser Pro
 355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
 500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
 515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
 530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Cys Leu Asp Lys Val Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile

1085		1090		1095
Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val				
1100		1105		1110
Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu				
1115		1120		1125
Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His				
1130		1135		1140
Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala				
1145		1150		1155
Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val				
1160		1165		1170
Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly				
1175		1180		1185
Lys Tyr Glu Gln Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro				
1190		1195		1200
Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu				
1205		1210		1215
Leu Ser Thr Phe Leu Gly Leu Glu Val Leu Phe Gln Gly Pro Gly				
1220		1225		1230
His His His His His His His His Ser Ala Trp Ser His Pro Gln				
1235		1240		1245
Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser				
1250		1255		1260
Ala Trp Ser His Pro Gln Phe Glu Lys				
1265		1270		

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<210> 81
<211> 1272
<212> PRT
<213> Artificial Sequence

<220>
<223> SEQ128430_-_ prefusion-stabilized trimer_tag SARS_CoV_2_S-protein
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      3C Protease Site, G, His8, SA, Strep tag, GGGSGGGSGGSA, Strep
      tag

<400> 81
Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe
1          5          10          15

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Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu

20

25

30

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
 35 40 45

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

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
 65 70 75 80

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
 85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
 100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
 115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
 130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
 145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
 165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
 180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
 195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
 210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
 225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
 245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
 260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
 290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
 580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
 595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
 610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
 625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
 645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
 660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
 675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
 690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
 705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
 725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
 740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
 755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
 770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
 785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
 805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
 820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
 835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu

1115		1120		1125
Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His				
1130		1135		1140
Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala				
1145		1150		1155
Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val				
1160		1165		1170
Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly				
1175		1180		1185
Lys Tyr Glu Gln Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro				
1190		1195		1200
Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu				
1205		1210		1215
Leu Ser Thr Phe Leu Gly Leu Glu Val Leu Phe Gln Gly Pro Gly				
1220		1225		1230
His His His His His His His His Ser Ala Trp Ser His Pro Gln				
1235		1240		1245
Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser				
1250		1255		1260
Ala Trp Ser His Pro Gln Phe Glu Lys				
1265		1270		

<210> 82
 <211> 1272
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> SEQ128430_-_prefusion-stabilized_trimer_tag SARS_CoV_2_S-protein
 (1-1208,R682G,R683S,R685S,K986P,V987P), trimerization domain, HRV
 3C Protease Site, G, His8, SA, Strep tag, GGGSGGGSGGSA, Strep
 tag

 <400> 82

Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe
1 5 10 15
Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu
20 25 30
His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45
Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp

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

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
 355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 370 375 380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
 500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
 515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
 530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
 545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
 565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
 580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
 595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala
660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Gly Val Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala

1145		1150		1155
Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val				
1160		1165		1170
Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly				
1175		1180		1185
Lys Tyr Glu Gln Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro				
1190		1195		1200
Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu				
1205		1210		1215
Leu Ser Thr Phe Leu Gly Leu Glu Val Leu Phe Gln Gly Pro Gly				
1220		1225		1230
His His His His His His His His Ser Ala Trp Ser His Pro Gln				
1235		1240		1245
Phe Glu Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser				
1250		1255		1260
Ala Trp Ser His Pro Gln Phe Glu Lys				
1265		1270		

<210> 83
 <211> 1192
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> COV2_S_(K986P_V987P)_trimer_tag_2

<400> 83

Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe
1 5 10 15
Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu
20 25 30
His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
35 40 45
Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp
50 55 60
Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
65 70 75 80
Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
85 90 95

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
100 105 110

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
115 120 125

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
130 135 140

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
145 150 155 160

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
165 170 175

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
180 185 190

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
195 200 205

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
210 215 220

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
225 230 235 240

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
245 250 255

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
260 265 270

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
275 280 285

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
290 295 300

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
305 310 315 320

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
325 330 335

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
340 345 350

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
355 360 365

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe

370

375

380

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 385 390 395 400

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 405 410 415

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 420 425 430

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 435 440 445

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 450 455 460

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 465 470 475 480

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 485 490 495

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
 500 505 510

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
 515 520 525

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
 530 535 540

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
 545 550 555 560

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
 565 570 575

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
 580 585 590

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
 595 600 605

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
 610 615 620

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
 625 630 635 640

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
 645 650 655

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
 660 665 670

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
 675 680 685

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
 690 695 700

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
 705 710 715 720

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
 725 730 735

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
 740 745 750

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
 755 760 765

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
 770 775 780

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
 785 790 795 800

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
 805 810 815

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
 820 825 830

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
 835 840 845

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
 850 855 860

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
 865 870 875 880

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
 885 890 895

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
 900 905 910

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
 915 920 925

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
930 935 940

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
945 950 955 960

Leu Asn Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln
965 970 975

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
980 985 990

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
995 1000 1005

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
1010 1015 1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln
1025 1030 1035

Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro
1040 1045 1050

Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp
1055 1060 1065

Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly
1070 1075 1080

Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile
1085 1090 1095

Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val
1100 1105 1110

Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu
1115 1120 1125

Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His
1130 1135 1140

Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala
1145 1150 1155

Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val
1160 1165 1170

Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly
1175 1180 1185

Lys Tyr Glu Gln
1190

<210> 84
<211> 27
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<213> Escherichia virus T4

<400> 84

Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys
1 5 10 15

Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
20 25

<210> 85
<211> 80
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<220>
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<400> 85

Gly Gly Gly Ser Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala
1 5 10 15

Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu Gly
20 25 30

Leu Glu Val Leu Phe Gln Gly Pro Gly His His His His His His His
35 40 45

His Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser Gly
50 55 60

Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
65 70 75 80

<210> 86
<211> 16
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<400> 86

Met Phe Val Phe Leu Val Leu Leu Pro Leu Val Ser Ser Gln Cys Val
1 5 10 15

<210> 87
<211> 22
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<223> Signal peptide

<400> 87

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Arg Gly Ala Arg Cys
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<210> 88

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Signal peptide

<400> 88

Met Ala Trp Ala Leu Leu Leu Leu Thr Leu Leu Thr Gln Gly Thr Gly
1 5 10 15

Ser Trp Ala

<210> 89

<211> 19

<212> PRT

<213> Artificial Sequence

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<400> 89

Met Thr Cys Ser Pro Leu Leu Leu Thr Leu Leu Ile His Cys Thr Gly
1 5 10 15

Ser Trp Ala

<210> 90

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Signal peptide

<400> 90

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly
20

<210> 91

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Signal peptide

<400> 91

Met Glu Trp Thr Trp Arg Val Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Ala His Ser

<210> 92

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Signal peptide

<400> 92

Met Glu Thr Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly
20

<210> 93

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Signal peptide

<400> 93

Met Glu Thr Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly
20

<210> 94

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Signal peptide

<400> 94

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser

<210> 95
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Signal peptide

<400> 95

Met Glu Trp Ser Trp Val Phe Leu Phe Phe Leu Ser Val Thr Thr Gly
1 5 10 15

Val His Ser

<210> 96
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
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<400> 96

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

Ser Leu Leu Ser Val Leu Leu Met Gly Cys Val Ala Glu Thr Gly Thr
20 25 30

Gln Cys

<210> 97
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker Sequence

<400> 97

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser Ala
1 5 10