

## Stabilized Corona virus Spike protein fusion proteins

The present invention relates to the field of medicine. The invention, in particular, relates to stabilized recombinant pre-fusion Corona virus spike (S) proteins, in particular to  
5 SARS CoV-2 S proteins, to nucleic acid molecules encoding said SARS CoV-2 S proteins, and uses thereof, e.g. in vaccines.

## Background of the invention

Corona viruses (CoVs) are enveloped viruses responsible for mild respiratory tract  
10 infections and atypical pneumonia in humans. CoVs are a large family of enveloped, single-stranded positive-sense RNA viruses belonging to the order Nidovirales, which can infect a broad range of mammalian and avian species, causing respiratory or enteric diseases. Corona viruses possess large, trimeric spike glycoproteins (S) that mediate binding to host cell receptors as well as fusion of viral and host cell membranes.

15 SARS-CoV-2 is a corona virus that emerged in humans from an animal reservoir in 2019 and rapidly spreads globally. SARS-CoV-2 is a beta-coronavirus, like MERS-CoV and SARS-CoV, all of which have their origin in bats. The name of the disease caused by the virus is corona virus disease 2019, abbreviated as COVID-19. Symptoms of COVID-19 range from mild symptoms to severe illness and death for confirmed COVID-19 cases. In the case  
20 of SARS-CoV-2 the S protein is the major surface protein. The S protein forms homotrimers and is composed of an N-terminal S1 subunit and a C-terminal S2 subunit, responsible for receptor binding and membrane fusion, respectively. Recent cryo-EM reconstructions of the CoV trimeric S structures of alpha-, beta-, and deltacoronaviruses revealed that the S1 subunit comprises two distinct domains: an N-terminal domain (S1 NTD) and a receptor-

binding domain (S1 RBD). SARS-CoV-2 makes use of its S1 RBD to bind to human angiotensin-converting enzyme 2 (ACE2) (Hoffmann et. al. (2020); Wrapp et. al. (2020)).

Corona viridae S proteins are classified as class I fusion proteins and are responsible for fusion. The S protein fuses the viral and host cell membranes by irreversible protein refolding from the labile pre-fusion conformation to the stable post-fusion conformation. Like many other class I fusion proteins, Corona virus S protein requires receptor binding and cleavage for the induction of conformational change that is needed for fusion and entry (Belouzard et al. (2009); Follis et al. (2006); Bosch et al. (2008), Madu et al. (2009); Walls et al. (2016)). Priming of SARS-CoV2 involves cleavage of the S protein by furin at a furin cleavage site at the boundary between the S1 and S2 subunits (S1/S2), and by TMPRSS2 at a conserved site upstream of the fusion peptide (S2') (Bestle et al. (2020); Hoffmann et. al. (2020)).

In order to refold from the pre-fusion to the post-fusion conformation, there are two regions that need to refold, which are referred to as the refolding region 1 (RR1) and refolding region 2 (RR2) (FIG. 1). For all class I fusion proteins, the RR1 includes the fusion protein (FP) and heptad repeat 1 (HR1). After cleavage and receptor binding the stretch of helices, loops and strands of all three protomers in the trimer transform to a long continuous trimeric helical coiled coil. The FP, located at the N-terminal segment of RR1, is then able to extend away from the viral membrane and inserts in the proximal membrane of the target cell. Next, the refolding region 2 (RR2), which is located C-terminal to RR1, and closer to the transmembrane region (TM) and which includes the heptad repeat 2 (HR2), relocates to the other side of the fusion protein and binds the HR1 coiled-coil trimer with the HR2 domain to form the six-helix bundle (6HB).

When viral fusion proteins, like the SARS CoV-2 S protein, are used as vaccine components, the fusogenic function of the proteins is not important. In fact, only the mimicry

of the vaccine component to the virus is important to induce reactive antibodies that can bind the virus. Therefore, for development of robust efficacious vaccine components it is desirable that the meta-stable fusion proteins are maintained in their pre-fusion conformation. It is believed that a stabilized fusion protein, such as a SARS CoV-2 S protein, in the pre-fusion  
5 conformation can induce an efficacious immune response.

In recent years several attempts have been made to stabilize various class I fusion proteins, including Corona virus S proteins. A particularly successful approach was shown to be the stabilization of the so-called hinge loop at the end of RR1 preceding the base helix (WO2017/037196, Krarup et al. (2015); Rutten et al. (2020), Hastie et al. (2017)). This  
10 approach has also proved successful for Corona virus S proteins, as shown for SARS-CoV, MERS-CoV and SARS-CoV2 (Pallesen et al. (2016); Wrapp et al. (2020)). Although the proline mutations in the hinge loop indeed increase the expression of the Corona virus S protein, the S protein may still suffer from instability. Thus, for improved vaccine design or S proteins which can for example be used as tools, e.g. as a bait for monoclonal antibody  
15 isolation, further stabilization is desired.

Since the novel SARS-CoV-2 virus was first observed in humans in late 2019, millions of people have been infected and more than hundreds of thousands have died as a result of COVID-19, in particular because SARS-CoV-2, and corona viruses more generally, lack effective treatment. In addition, there is currently no vaccine available to prevent  
20 coronavirus induced disease (COVID-19), leading to a large unmet medical need. Since emerging infectious diseases, such as COVID-19, present a major threat to public health and economic systems, there is an urgent need for novel components that can be used e.g. in vaccines to prevent coronavirus induced respiratory disease.

**Summary of the invention**

The present invention provides stabilized, recombinant, pre-fusion SARS CoV-2 S proteins, i.e. SARS CoV-2 S proteins that are stabilized in the pre-fusion conformation, and fragments thereof.

5 In certain embodiments, the pre-fusion SARS CoV-2 S proteins are soluble proteins, preferably trimeric soluble proteins.

The invention also provides nucleic acid molecules encoding the pre-fusion SARS CoV-2 S proteins and fragments thereof, as well as vectors, e.g. adenovectors, comprising such nucleic acid molecules.

10 The invention further provides methods of stabilizing SARS-CoV2 S proteins in the pre-fusion conformation, and to the pre-fusion SARS CoV-2 S proteins obtainable by said methods.

The invention moreover provides compositions, preferably immunogenic compositions, comprising a SARS-CoV-2 S protein, or a fragment thereof, a nucleic acid  
15 molecule and/or a vector, as described herein.

The invention also provides compositions for use in inducing an immune response against SARS CoV-2 S protein, and in particular to the use thereof as a vaccine against SARS-CoV-2 associated disease, such as COVID-19.

The invention also relates to methods for inducing an immune response against SARS  
20 CoV-2 in a subject, comprising administering to the subject an effective amount of a pre-fusion SARS CoV-2 S protein or a fragment thereof, a nucleic acid molecule encoding said SARS CoV-2 S protein, and/or a vector comprising said nucleic acid molecule, as described herein. Preferably, the induced immune response is characterized by the induction of neutralizing antibodies to the SARS CoV-2 virus and/or protective immunity against the  
25 SARS CoV-2 virus.

In particular aspects, the invention relates to methods for inducing anti-SARS CoV-2 S protein antibodies in a subject, comprising administering to the subject an effective amount of an immunogenic composition comprising a pre-fusion SARS CoV-2 S protein, or a fragment thereof, a nucleic acid molecule encoding said SARS CoV-2 S protein, and/or a vector comprising said nucleic acid molecule, as described herein.

The invention also relates to the use of the SARS CoV-2 S proteins or fragments thereof, as described herein, for isolating monoclonal antibodies against a SARS CoV-2 S protein from infected humans.

Also provided is the use of the pre-fusion SARS CoV-2 S proteins of the invention in methods of screening for candidate SARS CoV-2 antiviral agents, including but not limited to antibodies against SARS CoV-2.

### **Brief description of the drawings**

The foregoing summary, as well as the following detailed description of the invention, will be better understood when read in conjunction with the appended drawings. It should be understood that the invention is not limited to the precise embodiments shown in the drawings.

FIG. 1: Schematic representation of the conserved elements of the fusion domain of a SARS CoV-2 S protein. The head domain contains an N-terminal (NTD) domain, the receptor binding domain (RBD) and domains SD1 and SD2. The fusion domain contains the fusion peptide (FP), refolding region 1 (RR1), refolding region 2 (RR2), transmembrane region (TM) and cytoplasmic tail. Cleavage site between S1 and S2 and the S2' cleavage sites are indicated with arrow

FIG. 2: Analytical SEC samples of semi-stable SARS-CoV-2 S trimer proteins after freeze thaw cycles. S trimer protein according to SEQ ID NO: 3 (A) and the same protein in which the tag was replaced by a C-tag (B) after flash freezing in liquid Nitrogen and thawing 1 time (dark solid line) and 5 times (light solid line), compared with unfrozen S protein (dashed line). The peak at 5 minutes corresponds to the S trimer.

FIG. 3: Percentage of S trimer expression for S proteins with indicated mutations as measured by ACE2-Fc binding in AlphaLISA assay compared with control unstable uncleaved SARS-CoV-2 S (with furin site mutation) (SEQ ID NO: 2). The recombinant S proteins tested contain point mutations or a disulfide bridge, as indicated in the figure, introduced into the backbone of unstable uncleaved SARS-CoV2 S ectodomain (SEQ ID NO: 2)(Furin KO). Analysis was performed on crude cell culture supernatants.

FIG. 4: Analytical SEC profile showing trimer peaks of unstable uncleaved SARS-CoV-2 S (SEQ ID NO: 2) (dashed lines), compared to variants with indicated point mutations or disulfide bridge (solid lines). Analysis was performed on crude cell culture supernatants. )

### **Detailed description of the invention**

As explained above, the spike protein (S) of SARS-CoV-2 and of other Corona viruses is involved in fusion of the viral membrane with a host cell membrane, which is required for infection. SARS-CoV-2 S RNA is translated into a 1273 amino acid precursor protein, which contains a signal peptide sequence at the N-terminus (e.g. amino acid residues 1-13 of SEQ ID NO: 1) which is removed by a signal peptidase in the endoplasmic reticulum. Priming of the S protein typically involves cleavage by host proteases at the boundary

between the S1 and S2 subunits (S1/S2) in a subset of coronaviruses (including SARS CoV-2), and at a conserved site upstream of the fusion peptide (S2') in all known corona viruses. For SARS-CoV-2, furin cleaves at S1/S2 between residues 685 and 686 and subsequently within S2 at the S2' site between residues at position 815 and 816 by TMPRSS2. C-terminal  
5 to the S2' site the proposed fusion peptide is located at the N-terminus of the refolding region 1 (FIG. 1).

A vaccine against SARS-CoV-2 infection is currently not yet available. Several vaccine modalities are possible, such as genetically based or vector-based vaccines or e.g. subunit vaccines based on purified S protein. Since class I proteins are metastable proteins,  
10 increasing the stability of the pre-fusion conformation of fusion proteins increases the expression level of the protein because less protein will be misfolded and more protein will successfully transport through the secretory pathway. Therefore, if the stability of the pre-fusion conformation of the class I fusion protein, like SARS CoV-2 S protein is increased, the immunogenic properties of a vector-based vaccine will be improved since the expression of  
15 the S protein is higher and the conformation of the immunogen resembles the pre-fusion conformation that is recognized by potent neutralizing and protective antibodies. For subunit-based vaccines, stabilizing the pre-fusion S conformation is even more important. Besides the importance of high expression, which is needed to manufacture a vaccine successfully, maintenance of the pre-fusion conformation during the manufacturing process and during  
20 storage over time is critical for protein-based vaccines. In addition, for a soluble, subunit-based vaccine, the SARS CoV-2 S protein needs to be truncated by deletion of the transmembrane (TM) and the cytoplasmic region to create a soluble secreted S protein (sS). Because the TM region is responsible for membrane anchoring and increases stability, the anchorless soluble S protein is considerably more labile than the full-length protein and will  
25 even more readily refold into the post-fusion end-state. In order to obtain soluble S protein in

the stable pre-fusion conformation that shows high expression levels and high stability, the pre-fusion conformation thus needs to be stabilized. Because also the full length (membrane-bound) SARS CoV-2 S protein is metastable, the stabilization of the pre-fusion conformation is also desirable for the full-length SARS CoV-2 S protein, i.e. including the TM and cytoplasmic region, e.g. for any DNA, RNA, live attenuated or vector-based vaccine approach.

The present invention thus provides stabilized, recombinant pre-fusion SARS CoV-2 S proteins, comprising an S1 and an S2 domain, and comprising at least one mutation selected from the group consisting of a mutation of at least one amino acid in the loop region corresponding to amino acid residues 941 – 945 into G, and a disulfide bridge between residues 970 and 999, wherein the numbering of the amino acid positions is according to the numbering of the amino acid positions in SEQ ID NO: 1, and fragments thereof. According to the invention it has been demonstrated that the presence of a G in the loop region and/or a disulfide bridge at the indicated positions increases the stability of the proteins in the pre-fusion conformation. According to the invention, the glycine (G) or disulfide bridges are introduced by substitution (mutation) of the amino acid at that position into a specific amino acid according to the invention. According to the invention, the proteins thus comprise one or more mutations in their amino acid sequence, i.e. the naturally occurring amino acid at these positions has been substituted with another amino acid.

The proteins may comprise a mutation of at least one amino acid in the loop region corresponding to amino acid residues 941 – 945 G, in combination with a disulfide bridge between residues 970 and 999.

According to the invention it is to be understood that “a disulfide bridge between residues 970 and 999” means that the amino acids at the positions 970 and 999 have been mutated into C.

In certain embodiments, the at least one mutation in the loop region corresponding to amino acid residues 941 – 945 is a mutation of the amino acid at position 941 into G.

Alternatively, or in addition, the at least one mutation in the loop region corresponding to amino acid residues 941 – 945 is a mutation of the amino acid at position  
5 943 into G.

Alternatively, or in addition, the at least one mutation in the loop region corresponding to amino acid residues 941 – 945 is a mutation of the amino acid at position 944 into G.

According to the invention, thus one or more amino acids in the loop region may be  
10 mutated into G.

The proteins of the present invention may further comprise one or more additional mutations selected from the group consisting of: a mutation of at least one amino acid in the loop region corresponding to amino acid residues 941 – 945 into P, a mutation of the amino acid at position 892, a mutation of the amino acid at position 614, a mutation at position 572,  
15 a mutation at position 532, a disulfide bridge between residues 880 and 888, and a disulfide bridge between residues 884 and 893, wherein the numbering of the amino acid positions is again according to the numbering of the amino acid positions in SEQ ID NO: 1.

According to the invention, it has to be understood that the additional mutation of at least one amino acid in the loop region corresponding to amino acid residues 941 – 945 into P  
20 means the mutation of at least one amino acid in said loop region that has not been mutated into G.

In certain embodiments, the at least one mutation in the loop region corresponding to amino acid residues 941 – 945 is a mutation of the amino acid at position 942 into P.

Alternatively, or in addition, the at least one mutation in the loop region corresponding to amino acid residues 941 – 945 is a mutation of the amino acid at position 941 into P.

Alternatively, or in addition, the at least one mutation in the loop region  
5 corresponding to amino acid residues 941 – 945 is a mutation of the amino acid at position 944 into P.

Alternatively, or in addition, the mutation at position 892 is a mutation into P.

Alternatively, or in addition, the mutation at position 614 is a mutation into N or G.

Alternatively, or in addition, the mutation at position 532 is a mutation into P.

10 Alternatively, or in addition, the mutation at position 572 is a mutation into I.

In certain embodiments, the proteins do not comprise both the disulfide bridge between residues 880 and 888 and the disulfide bridge between residues 884 and 893.

In certain embodiments, the SARS CoV-2 S proteins further comprise a deletion of the furin cleavage site. A deletion of the furin cleavage, e.g. by mutation of one or more  
15 amino acids in the furin cleavage site (such that the protein is not cleaved by furin), renders the protein uncleaved, which further increases its stability. Deleting the furin cleavage site can be achieved in any suitable way that is known to the skilled person. In certain embodiments, the deletion of the furin cleavage site comprises a mutation of the amino acid at position 682 into S and/or a mutation of the amino acid at position 685 into G.

20 In certain embodiments, the proteins further comprise a mutation of the amino acids at position 986 and 987 into proline.

In certain embodiments, the SARS CoV-2 S proteins of the invention comprise at least two mutations.

In certain embodiments, the SARS CoV-2 S proteins of the invention comprise at  
25 least three mutations.

In certain embodiments, the SARS CoV-2 S proteins of the invention comprise at least four mutations.

In certain embodiments, the SARS CoV-2 S proteins of the invention comprise at least five mutations.

5 In certain embodiments, the SARS CoV-2 S proteins of the invention comprise at least six mutations.

An amino acid according to the invention can be any of the twenty naturally occurring (or 'standard' amino acids) or variants thereof, such as e.g. D-amino acids (the D-enantiomers of amino acids with a chiral center), or any variants that are not naturally found in proteins,  
10 such as e.g. norleucine. The standard amino acids can be divided into several groups based on their properties. Important factors are charge, hydrophilicity or hydrophobicity, size and functional groups. These properties are important for protein structure and protein-protein interactions. Some amino acids have special properties such as cysteine, that can form covalent disulfide bonds (or disulfide bridges) to other cysteine residues, proline that induces turns of the  
15 polypeptide backbone, and glycine that is more flexible than other amino acids. Table 1 shows the abbreviations and properties of the standard amino acids.

It will be appreciated by a skilled person that the mutations can be made to the protein by routine molecular biology procedures.

In certain embodiments, the present invention provides recombinant SARS-CoV-2 S  
20 proteins, and fragments thereof, wherein the amino acid at position 941 is G, the amino acid at position 943 is G, and/or the amino acid at position 944 is G, and/or which comprise a disulfide bridge between residues 970 and 999, wherein the numbering of the amino acid positions is according to the numbering of the amino acid positions in SEQ ID NO: 1.

In certain embodiments, the SARS CoV-2 S proteins further comprise a deletion of  
25 the furin cleavage site. A deletion of the furin cleavage, e.g. by mutation of one or more

amino acids in the furin cleavage site (such that the protein is not cleaved by furin), renders the protein uncleaved, which further increases its stability. Deleting the furin cleavage site can be achieved in any suitable way that is known to the skilled person. In certain embodiments, the deletion of the furin cleavage site comprises a mutation of the amino acid  
5 at position 682 into S and/or a mutation of the amino acid at position 685 into G.

In certain embodiments, the proteins further comprise a mutation of the amino acids at position 986 and 987 into proline.

In certain embodiments, the invention provides SARS-CoV 2 proteins comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 8-119, or fragments  
10 thereof.

In a preferred embodiment, the proteins comprise a deletion of the furin cleavage site, a mutation of the amino acid at position 614 into N or G, a mutation of the amino acid at position 892 into P, a mutation of the amino acid at position 942 into P, a mutation of the amino acid at position 943 into G and a mutation of the amino acid at position 987 into P.

15 When these mutations are introduced in the amino acid sequence of the SARS CoV-2 S ectodomain, stable soluble trimeric SARS CoV-2 S proteins are obtained without the need to add a heterologous trimerization domain.

The term "fragment" as used herein refers to a peptide that has an amino-terminal and/or carboxy-terminal and/or internal deletion, but where the remaining amino acid  
20 sequence is identical to the corresponding positions in the sequence of a SARS CoV-2 S protein, for example, the full-length sequence of a SARS CoV-2 S protein. It will be appreciated that for inducing an immune response and in general for vaccination purposes, a protein needs not to be full length nor have all its wild type functions, and fragments of the protein are equally useful. A fragment according to the invention is an immunologically  
25 active fragment, and typically comprises at least 15 amino acids, or at least 30 amino acids,

of the SARS CoV-2 S protein. In certain embodiments, it comprises at least 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, or 550 amino acids, of the SARS CoV-2 S protein. In certain embodiment, the fragment is the SARS CoV2 ectodomain.

In certain embodiments, the proteins according to the invention are soluble proteins,  
5 e.g. S protein ectodomains, and comprise a truncated S2 domain. As used herein a “truncated” S2 domain refers to a S2 domain that is not a full length S2 domain, i.e. wherein either N-terminally or C-terminally one or more amino acid residues have been deleted. According to the invention, at least the transmembrane domain and cytoplasmic domain are deleted to permit expression as a soluble ectodomain (corresponding to the amino acids 1-  
10 1208 of SEQ ID NO: 1). For the stabilization of such soluble SARS CoV-2 S protein in the pre-fusion conformation, a heterologous trimerization domain, such as a fibrin – based trimerization domain, may be fused to the C-terminus of the Corona virus S protein ectodomain. This fibrin domain or ‘Foldon’ is derived from T4 fibrin and was described earlier as an artificial natural trimerization domain (Letarov et al., (1993); S-Guthe et al.,  
15 (2004)). Thus, in certain embodiments, the transmembrane region has been replaced by a heterologous trimerization domain. In a preferred embodiment, the heterologous trimerization domain is a foldon domain comprising the amino acid sequence of SEQ ID NO:4. However, it is to be understood that according to the invention other trimerization domains are also possible. It is also possible that the proteins do not comprise a heterologous trimerization  
20 domain.

Thus, in certain preferred embodiments, the soluble SARS CoV-2 S proteins do not comprise a heterologous trimerization domain.

The pre-fusion SARS CoV-2 S proteins according to the invention are trimeric and stable, i.e. do not readily change into the post-fusion conformation upon processing of the  
25 proteins, such as e.g. upon purification, freeze-thaw cycles, and/or storage etc. In certain

embodiments, the pre-fusion SARS CoV-2 S proteins have an increased stability as compared to SARS CoV-2 S proteins without the mutations of the invention, e.g. as indicated by an increased melting temperature (measured by e.g. differential scanning fluorimetry).

The proteins according to the invention may comprise a signal peptide, also referred to as signal sequence or leader peptide, corresponding to amino acids 1-13 of SEQ ID NO: 1. Signal peptides are short (typically 5-30 amino acids long) peptides present at the N-terminus of the majority of newly synthesized proteins that are destined towards the secretory pathway. In certain embodiments, the proteins according to the invention do not comprise a signal peptide.

In certain embodiments, the proteins comprise a tag sequence, such as a HIS-Tag or C-Tag. A His-Tag (or polyhistidine-tag) is an amino acid motif in proteins that consists of at least five histidine (H) residues, preferably placed at the N- or C-terminus of the protein, which is generally used for purification purposes. In certain embodiments, the proteins according to the invention do not comprise a tag sequence. Alternatively, other tags like a C-tag can be used for these purposes.

The invention also provides methods for stabilizing a SARS CoV-2 S protein, said method comprising introducing in the amino acid sequence of a SARS CoV-2 S protein at least one mutation selected from the group consisting of a mutation of at least one amino acid in the loop region corresponding to amino acid residues 941 – 945 into G, and a disulfide bridge between residues 970 and 999, wherein the numbering of the amino acid positions is according to the numbering of the amino acid positions in SEQ ID NO: 1.

In certain embodiments, the at least one mutation in the loop region corresponding to amino acid residues 941 – 945 is a mutation of the amino acid at position 941 into G.

Alternatively, or in addition, the at least one mutation in the loop region corresponding to amino acid residues 941 – 945 is a mutation of the amino acid at position 943 into G.

Alternatively, or in addition, the at least one mutation in the loop region  
5 corresponding to amino acid residues 941 – 945 is a mutation of the amino acid at position 944 into G.

In certain embodiments, the methods further comprise deleting the furin cleavage site. Deleting the furin cleavage site may be achieved in any way known in the art. In certain embodiments, the deletion of the furin cleavage site comprises introducing a  
10 mutation of the amino acid at position 682 into S and/or a mutation of the amino acid at position 685 into G.

In certain embodiments, the methods further comprise introducing a mutation of the amino acids at position 986 and 987 into proline.

The present invention further provides nucleic acid molecules encoding the SARS  
15 CoV-2 S proteins according to the invention. The term “nucleic acid molecule” as used in the present invention refers to a polymeric form of nucleotides (i.e. polynucleotides) and includes both DNA (e.g. cDNA, genomic DNA) and RNA, and synthetic forms and mixed polymers of the above.

In preferred embodiments, the nucleic acid molecules encoding the proteins according  
20 to the invention are codon-optimized for expression in mammalian cells, preferably human cells, or insect cells. Methods of codon-optimization are known and have been described previously (e.g. WO 96/09378 for mammalian cells). A sequence is considered codon-optimized if at least one non-preferred codon as compared to a wild type sequence is replaced by a codon that is more preferred. Herein, a non-preferred codon is a codon that is used less  
25 frequently in an organism than another codon coding for the same amino acid, and a codon

that is more preferred is a codon that is used more frequently in an organism than a non-preferred codon. The frequency of codon usage for a specific organism can be found in codon frequency tables, such as in <http://www.kazusa.or.jp/codon>. Preferably more than one non-preferred codon, preferably most or all non-preferred codons, are replaced by codons that are more preferred. Preferably the most frequently used codons in an organism are used in a codon-optimized sequence. Replacement by preferred codons generally leads to higher expression.

It will be understood by a skilled person that numerous different polynucleotides and nucleic acid molecules can encode the same protein as a result of the degeneracy of the genetic code. It is also understood that skilled persons may, using routine techniques, make nucleotide substitutions that do not affect the protein sequence encoded by the nucleic acid molecules to reflect the codon usage of any particular host organism in which the proteins are to be expressed. Therefore, unless otherwise specified, a "nucleotide sequence encoding an amino acid sequence" includes all nucleotide sequences that are degenerate versions of each other and that encode the same amino acid sequence. Nucleotide sequences that encode proteins and RNA may or may not include introns.

Nucleic acid sequences can be cloned using routine molecular biology techniques, or generated de novo by DNA synthesis, which can be performed using routine procedures by service companies having business in the field of DNA synthesis and/or molecular cloning (e.g. GeneArt, GenScript, Invitrogen, Eurofins).

The invention also provides vectors comprising a nucleic acid molecule as described above. In certain embodiments, a nucleic acid molecule according to the invention thus is part of a vector. Such vectors can easily be manipulated by methods well known to the person skilled in the art and can for instance be designed for being capable of replication in prokaryotic and/or eukaryotic cells. In addition, many vectors can be used for transformation

of eukaryotic cells and will integrate in whole or in part into the genome of such cells, resulting in stable host cells comprising the desired nucleic acid in their genome. The vector used can be any vector that is suitable for cloning DNA and that can be used for transcription of a nucleic acid of interest.

5           In certain embodiments of the invention, the vector is an adenovirus vector. An adenovirus according to the invention belongs to the family of the Adenoviridae, and preferably is one that belongs to the genus Mastadenovirus. It can be a human adenovirus, but also an adenovirus that infects other species, including but not limited to a bovine adenovirus (e.g. bovine adenovirus 3, BAdV3), a canine adenovirus (e.g. CAdV2), a porcine adenovirus  
10   (e.g. PAdV3 or 5), or a simian adenovirus (which includes a monkey adenovirus and an ape adenovirus, such as a chimpanzee adenovirus or a gorilla adenovirus). Preferably, the adenovirus is a human adenovirus (HAdV, or AdHu), or a simian adenovirus such as chimpanzee or gorilla adenovirus (ChAd, AdCh, or SAdV), or a rhesus monkey adenovirus (RhAd). In the invention, a human adenovirus is meant if referred to as Ad without  
15   indication of species, e.g. the brief notation “Ad26” means the same as HAdV26, which is human adenovirus serotype 26. Also as used herein, the notation “rAd” means recombinant adenovirus, e.g., “rAd26” refers to recombinant human adenovirus 26.

Most advanced studies have been performed using human adenoviruses, and human adenoviruses are preferred according to certain aspects of the invention. In certain preferred  
20   embodiments, a recombinant adenovirus according to the invention is based upon a human adenovirus. In preferred embodiments, the recombinant adenovirus is based upon a human adenovirus serotype 5, 11, 26, 34, 35, 48, 49, 50, 52, etc. According to a particularly preferred embodiment of the invention, an adenovirus is a human adenovirus of serotype 26. Advantages of these serotypes include a low seroprevalence and/or low pre-existing

neutralizing antibody titers in the human population, and experience with use in human subjects in clinical trials.

Simian adenoviruses generally also have a low seroprevalence and/or low pre-existing neutralizing antibody titers in the human population, and a significant amount of work has been reported using chimpanzee adenovirus vectors (e.g. US6083716; WO 2005/071093; WO 2010/086189; WO 2010085984; Farina et al, 2001, J Virol 75: 11603-13; Cohen et al, 2002, J Gen Virol 83: 151-55; Kobinger et al, 2006, Virology 346: 394-401; Tatsis et al., 2007, Molecular Therapy 15: 608-17; see also review by Bangari and Mittal, 2006, Vaccine 24: 849-62; and review by Lasaro and Ertl, 2009, Mol Ther 17: 1333-39). Hence, in other embodiments, the recombinant adenovirus according to the invention is based upon a simian adenovirus, e.g. a chimpanzee adenovirus. In certain embodiments, the recombinant adenovirus is based upon simian adenovirus type 1, 7, 8, 21, 22, 23, 24, 25, 26, 27.1, 28.1, 29, 30, 31.1, 32, 33, 34, 35.1, 36, 37.2, 39, 40.1, 41.1, 42.1, 43, 44, 45, 46, 48, 49, 50 or SA7P. In certain embodiments, the recombinant adenovirus is based upon a chimpanzee adenovirus such as ChAdOx 1 (see e.g. WO 2012/172277), or ChAdOx 2 (see e.g. WO 2018/215766). In certain embodiments, the recombinant adenovirus is based upon a chimpanzee adenovirus such as BZ28 (see e.g. WO 2019/086466). In certain embodiments, the recombinant adenovirus is based upon a gorilla adenovirus such as BLY6 (see e.g. WO 2019/086456), or BZ1 (see e.g. WO 2019/086466).

Preferably, the adenovirus vector is a replication deficient recombinant viral vector, such as rAd26, rAd35, rAd48, rAd5HVR48, etc.

In a preferred embodiment of the invention, the adenoviral vectors comprise capsid proteins from rare serotypes, e.g. including Ad26. In the typical embodiment, the vector is an rAd26 virus. An “adenovirus capsid protein” refers to a protein on the capsid of an adenovirus (e.g., Ad26, Ad35, rAd48, rAd5HVR48 vectors) that is involved in determining

the serotype and/or tropism of a particular adenovirus. Adenoviral capsid proteins typically include the fiber, penton and/or hexon proteins. As used herein a “capsid protein” for a particular adenovirus, such as an “Ad26 capsid protein” can be, for example, a chimeric capsid protein that includes at least a part of an Ad26 capsid protein. In certain embodiments, the capsid protein is an entire capsid protein of Ad26. In certain embodiments, the hexon, penton and fiber are of Ad26.

One of ordinary skill in the art will recognize that elements derived from multiple serotypes can be combined in a single recombinant adenovirus vector. Thus, a chimeric adenovirus that combines desirable properties from different serotypes can be produced.

Thus, in some embodiments, a chimeric adenovirus of the invention could combine the absence of pre-existing immunity of a first serotype with characteristics such as temperature stability, assembly, anchoring, production yield, redirected or improved infection, stability of the DNA in the target cell, and the like. See for example WO 2006/040330 for chimeric adenovirus Ad5HVR48, that includes an Ad5 backbone having partial capsids from Ad48, and also e.g. WO 2019/086461 for chimeric adenoviruses Ad26HVRPtr1, Ad26HVRPtr12, and Ad26HVRPtr13, that include an Ad26 virus backbone having partial capsid proteins of Ptr1, Ptr12, and Ptr13, respectively)

In certain embodiments the recombinant adenovirus vector useful in the invention is derived mainly or entirely from Ad26 (i.e., the vector is rAd26). In some embodiments, the adenovirus is replication deficient, e.g., because it contains a deletion in the E1 region of the genome. For adenoviruses being derived from non-group C adenovirus, such as Ad26 or Ad35, it is typical to exchange the E4-orf6 coding sequence of the adenovirus with the E4-orf6 of an adenovirus of human subgroup C such as Ad5. This allows propagation of such adenoviruses in well-known complementing cell lines that express the E1 genes of Ad5, such as for example 293 cells, PER.C6 cells, and the like (see, e.g. Havenga, et al., 2006, J Gen

Virol 87: 2135-43; WO 03/104467). However, such adenoviruses will not be capable of replicating in non-complementing cells that do not express the E1 genes of Ad5.

The preparation of recombinant adenoviral vectors is well known in the art. Preparation of rAd26 vectors is described, for example, in WO 2007/104792 and in Abbink et al., (2007) Virol 81(9): 4654-63. Exemplary genome sequences of Ad26 are found in GenBank Accession EF 153474 and in SEQ ID NO: 1 of WO 2007/104792. Examples of vectors useful for the invention for instance include those described in WO2012/082918, the disclosure of which is incorporated herein by reference in its entirety.

Typically, a vector useful in the invention is produced using a nucleic acid comprising the entire recombinant adenoviral genome (e.g., a plasmid, cosmid, or baculovirus vector). Thus, the invention also provides isolated nucleic acid molecules that encode the adenoviral vectors of the invention. The nucleic acid molecules of the invention can be in the form of RNA or in the form of DNA obtained by cloning or produced synthetically. The DNA can be double-stranded or single-stranded.

The adenovirus vectors useful in the invention are typically replication deficient. In these embodiments, the virus is rendered replication deficient by deletion or inactivation of regions critical to replication of the virus, such as the E1 region. The regions can be substantially deleted or inactivated by, for example, inserting a gene of interest, such as a gene encoding the SARS-CoV2 S protein (usually linked to a promoter) within the region. In some embodiments, the vectors of the invention can contain deletions in other regions, such as the E2, E3 or E4 regions, or insertions of heterologous genes linked to a promoter within one or more of these regions. For E2- and/or E4-mutated adenoviruses, generally E2- and/or E4-complementing cell lines are used to generate recombinant adenoviruses. Mutations in the E3 region of the adenovirus need not be complemented by the cell line, since E3 is not required for replication.

A packaging cell line is typically used to produce sufficient amounts of adenovirus vectors for use in the invention. A packaging cell is a cell that comprises those genes that have been deleted or inactivated in a replication deficient vector, thus allowing the virus to replicate in the cell. Suitable packaging cell lines for adenoviruses with a deletion in the E1 region include, for example, PER.C6, 911, 293, and E1 A549.

In a preferred embodiment of the invention, the vector is an adenovirus vector, and more preferably a rAd26 vector, most preferably a rAd26 vector with at least a deletion in the E1 region of the adenoviral genome, e.g. such as that described in Abbink, J Virol, 2007, 81(9): p. 4654-63, which is incorporated herein by reference. Typically, the nucleic acid sequence encoding the stabilized SARS-CoV2 S protein is cloned into the E1 and/or the E3 region of the adenoviral genome.

Host cells comprising the nucleic acid molecules encoding the pre-fusion SARS CoV-2 S proteins also form part of the invention. The pre-fusion SARS CoV-2 S proteins may be produced through recombinant DNA technology involving expression of the molecules in host cells, e.g. Chinese hamster ovary (CHO) cells, tumor cell lines, BHK cells, human cell lines such as HEK293 cells, PER.C6 cells, or yeast, fungi, insect cells, and the like, or transgenic animals or plants. In certain embodiments, the cells are from a multicellular organism, in certain embodiments they are of vertebrate or invertebrate origin. In certain embodiments, the cells are mammalian cells, such as human cells, or insect cells. In general, the production of a recombinant proteins, such the pre-fusion SARS CoV-2 S proteins of the invention, in a host cell comprises the introduction of a heterologous nucleic acid molecule encoding the protein in expressible format into the host cell, culturing the cells under conditions conducive to expression of the nucleic acid molecule and allowing expression of the protein in said cell. The nucleic acid molecule encoding a protein in expressible format may be in the form of an expression cassette, and usually requires sequences capable of

bringing about expression of the nucleic acid, such as enhancer(s), promoter, polyadenylation signal, and the like. The person skilled in the art is aware that various promoters can be used to obtain expression of a gene in host cells. Promoters can be constitutive or regulated, and can be obtained from various sources, including viruses, prokaryotic, or eukaryotic sources,  
5 or artificially designed.

Cell culture media are available from various vendors, and a suitable medium can be routinely chosen for a host cell to express the protein of interest, here the pre-fusion SARS CoV-2 S proteins. The suitable medium may or may not contain serum.

A “heterologous nucleic acid molecule” (also referred to herein as ‘transgene’) is a  
10 nucleic acid molecule that is not naturally present in the host cell. It is introduced into for instance a vector by standard molecular biology techniques. A transgene is generally operably linked to expression control sequences. This can for instance be done by placing the nucleic acid encoding the transgene(s) under the control of a promoter. Further regulatory sequences may be added. Many promoters can be used for expression of a transgene(s), and  
15 are known to the skilled person, e.g. these may comprise viral, mammalian, synthetic promoters, and the like. A non-limiting example of a suitable promoter for obtaining expression in eukaryotic cells is a CMV-promoter (US 5,385,839), e.g. the CMV immediate early promoter, for instance comprising nt. –735 to +95 from the CMV immediate early gene enhancer/promoter. A polyadenylation signal, for example the bovine growth hormone polyA  
20 signal (US 5,122,458), may be present behind the transgene(s). Alternatively, several widely used expression vectors are available in the art and from commercial sources, e.g. the pcDNA and pEF vector series of Invitrogen, pMSCV and pTK-Hyg from BD Sciences, pCMV-Script from Stratagene, etc, which can be used to recombinantly express the protein of interest, or to obtain suitable promoters and/or transcription terminator sequences, polyA sequences, and  
25 the like.

The cell culture can be any type of cell culture, including adherent cell culture, e.g. cells attached to the surface of a culture vessel or to microcarriers, as well as suspension culture. Most large-scale suspension cultures are operated as batch or fed-batch processes because they are the most straightforward to operate and scale up. Nowadays, continuous  
5 processes based on perfusion principles are becoming more common and are also suitable. Suitable culture media are also well known to the skilled person and can generally be obtained from commercial sources in large quantities, or custom-made according to standard protocols. Culturing can be done for instance in dishes, roller bottles or in bioreactors, using batch, fed-batch, continuous systems and the like. Suitable conditions for culturing cells are  
10 known (see e.g. Tissue Culture, Academic Press, Kruse and Paterson, editors (1973), and R.I. Freshney, Culture of animal cells: A manual of basic technique, fourth edition (Wiley-Liss Inc., 2000, ISBN 0-471-34889-9)).

The invention further provides compositions comprising a pre-fusion SARS CoV-2 S protein and/or a nucleic acid molecule, and/or a vector, as described above. The invention  
15 also provides compositions comprising a nucleic acid molecule and/or a vector, encoding such pre-fusion SARS CoV-2 S protein. The invention further provides immunogenic compositions comprising a pre-fusion SARS CoV-2 S protein, and/or a nucleic acid molecule, and/or a vector, as described above. The invention also provides the use of a stabilized pre-fusion SARS CoV-2 S protein, a nucleic acid molecule, and/or a vector,  
20 according to the invention, for inducing an immune response against a SARS CoV-2 S protein in a subject. Further provided are methods for inducing an immune response against SARS CoV-2 S protein in a subject, comprising administering to the subject a pre-fusion SARS CoV-2 S protein, and/or a nucleic acid molecule, and/or a vector according to the invention. Also provided are pre-fusion SARS CoV-2 S proteins, nucleic acid molecules,  
25 and/or vectors, according to the invention for use in inducing an immune response against

SARS CoV-2 S protein in a subject. Further provided is the use of the pre-fusion SARS CoV-2 S proteins, and/or nucleic acid molecules, and/or vectors according to the invention for the manufacture of a medicament for use in inducing an immune response against SARS CoV-2 S protein in a subject. In certain embodiments, the nucleic acid molecule is DNA and/or an RNA molecule.

The pre-fusion SARS CoV-2 S proteins, nucleic acid molecules, or vectors of the invention may be used for prevention (prophylaxis, including post-exposure prophylaxis) of SARS CoV-2 infections. In certain embodiments, the prevention may be targeted at patient groups that are susceptible for and/or at risk of SARS CoV-2 infection or have been diagnosed with a SARS CoV-2 infection. Such target groups include, but are not limited to e.g., the elderly (e.g.  $\geq 50$  years old,  $\geq 60$  years old, and preferably  $\geq 65$  years old), hospitalized patients and patients who have been treated with an antiviral compound but have shown an inadequate antiviral response. In certain embodiments, the target population comprises human subjects from 2 months of age.

The pre-fusion SARS CoV-2 S proteins, nucleic acid molecules and/or vectors according to the invention may be used e.g. in stand-alone treatment and/or prophylaxis of a disease or condition caused by SARS CoV-2, or in combination with other prophylactic and/or therapeutic treatments, such as (existing or future) vaccines, antiviral agents and/or monoclonal antibodies.

The invention further provides methods for preventing and/or treating SARS CoV-2 infection in a subject utilizing the pre-fusion SARS CoV-2 S proteins, nucleic acid molecules and/or vectors according to the invention. In a specific embodiment, a method for preventing and/or treating SARS CoV-2 infection in a subject comprises administering to a subject in need thereof an effective amount of a pre-fusion SARS CoV-2 S protein, nucleic acid molecule and/or a vector, as described above. A therapeutically effective amount refers to an amount of a

protein, nucleic acid molecule or vector, that is effective for preventing, ameliorating and/or treating a disease or condition resulting from infection by SARS CoV-2. Prevention encompasses inhibiting or reducing the spread of SARS CoV-2 or inhibiting or reducing the onset, development or progression of one or more of the symptoms associated with infection by SARS CoV-2. Amelioration as used in herein may refer to the reduction of visible or perceptible disease symptoms, viremia, or any other measurable manifestation of SARS CoV-2 infection.

For administering to subjects, such as humans, the invention may employ pharmaceutical compositions comprising a pre-fusion SARS CoV-2 S protein, a nucleic acid molecule and/or a vector as described herein, and a pharmaceutically acceptable carrier or excipient. In the present context, the term "pharmaceutically acceptable" means that the carrier or excipient, at the dosages and concentrations employed, will not cause any unwanted or harmful effects in the subjects to which they are administered. Such pharmaceutically acceptable carriers and excipients are well known in the art (see Remington's Pharmaceutical Sciences, 18th edition, A. R. Gennaro, Ed., Mack Publishing Company [1990]; Pharmaceutical Formulation Development of Peptides and Proteins, S. Frokjaer and L. Hovgaard, Eds., Taylor & Francis [2000]; and Handbook of Pharmaceutical Excipients, 3rd edition, A. Kibbe, Ed., Pharmaceutical Press [2000]). The CoV S proteins, or nucleic acid molecules, preferably are formulated and administered as a sterile solution although it may also be possible to utilize lyophilized preparations. Sterile solutions are prepared by sterile filtration or by other methods known per se in the art. The solutions are then lyophilized or filled into pharmaceutical dosage containers. The pH of the solution generally is in the range of pH 3.0 to 9.5, e.g. pH 5.0 to 7.5. The CoV S proteins typically are in a solution having a suitable pharmaceutically acceptable buffer, and the composition may also contain a salt. Optionally stabilizing agent may be

present, such as albumin. In certain embodiments, detergent is added. In certain embodiments, the CoV S proteins may be formulated into an injectable preparation.

In certain embodiments, a composition according to the invention further comprises one or more adjuvants. Adjuvants are known in the art to further increase the immune response to an applied antigenic determinant. The terms “adjuvant” and “immune stimulant” are used interchangeably herein and are defined as one or more substances that cause stimulation of the immune system. In this context, an adjuvant is used to enhance an immune response to the SARS CoV-2 S proteins of the invention. Examples of suitable adjuvants include aluminium salts such as aluminium hydroxide and/or aluminium phosphate; oil-emulsion compositions (or oil-in-water compositions), including squalene-water emulsions, such as MF59 (see e.g. WO 90/14837); saponin formulations, such as for example QS21 and Immunostimulating Complexes (ISCOMS) (see e.g. US 5,057,540; WO 90/03184, WO 96/11711, WO 2004/004762, WO 2005/002620); bacterial or microbial derivatives, examples of which are monophosphoryl lipid A (MPL), 3-O-deacylated MPL (3dMPL), CpG-motif containing oligonucleotides, ADP-ribosylating bacterial toxins or mutants thereof, such as *E. coli* heat labile enterotoxin LT, cholera toxin CT, and the like; eukaryotic proteins (e.g. antibodies or fragments thereof (e.g. directed against the antigen itself or CD1a, CD3, CD7, CD80) and ligands to receptors (e.g. CD40L, GMCSF, GCSF, etc), which stimulate immune response upon interaction with recipient cells. In certain embodiments the compositions of the invention comprise aluminium as an adjuvant, e.g. in the form of aluminium hydroxide, aluminium phosphate, aluminium potassium phosphate, or combinations thereof, in concentrations of 0.05 – 5 mg, e.g. from 0.075-1.0 mg, of aluminium content per dose.

The pre-fusion SARS CoV-2 S proteins may also be administered in combination with or conjugated to nanoparticles, such as e.g. polymers, liposomes, virosomes, virus-like particles. The SARS CoV-2 S proteins may be combined with or encapsidated in or

conjugated to the nanoparticles with or without adjuvant. Encapsulation within liposomes is described, e.g. in US 4,235,877. Conjugation to macromolecules is disclosed, for example in US 4,372,945 or US 4,474,757.

In other embodiments, the compositions do not comprise adjuvants.

5 In certain embodiments, the invention provides methods for making a vaccine against a SARS CoV-2 virus, comprising providing a composition according to the invention and formulating it into a pharmaceutically acceptable composition. The term "vaccine" refers to an agent or composition containing an active component effective to induce a certain degree of immunity in a subject against a certain pathogen or disease, which will result in at least a  
10 decrease (up to complete absence) of the severity, duration or other manifestation of symptoms associated with infection by the pathogen or the disease. In the present invention, the vaccine comprises an effective amount of a pre-fusion SARS CoV-2 S protein and/or a nucleic acid molecule encoding a pre-fusion SARS CoV-2 S protein, and/or a vector comprising said nucleic acid molecule, which results in an immune response against the S  
15 protein of SARS CoV-2. This provides a method of preventing serious lower respiratory tract disease leading to hospitalization and the decrease in frequency of complications such as pneumonia and bronchiolitis due to SARS CoV-2 infection and replication in a subject. The term "vaccine" according to the invention implies that it is a pharmaceutical composition, and thus typically includes a pharmaceutically acceptable diluent, carrier or excipient. It may or  
20 may not comprise further active ingredients. In certain embodiments it may be a combination vaccine that further comprises additional components that induce an immune response against SARS CoV-2, e.g. against other antigenic proteins of SARS CoV-2, or may comprise different forms of the same antigenic component. A combination product may also comprise immunogenic components against other infectious agents, e.g. other respiratory viruses  
25 including but not limited to influenza virus or RSV. The administration of the additional

active components may for instance be done by separate, e.g. concurrent administration, or in a prime-boost setting, or by administering combination products of the vaccines of the invention and the additional active components.

Compositions may be administered to a subject, e.g. a human subject. The total dose  
5 of the SARS CoV-2 S proteins in a composition for a single administration can for instance be about 0.01  $\mu\text{g}$  to about 10 mg, e.g. 1  $\mu\text{g}$  – 1 mg, e.g. 10  $\mu\text{g}$  – 100  $\mu\text{g}$ . Determining the recommended dose will be carried out by experimentation and is routine for those skilled in the art.

Administration of the compositions according to the invention can be performed using  
10 standard routes of administration. Non-limiting embodiments include parenteral administration, such as intradermal, intramuscular, subcutaneous, transcutaneous, or mucosal administration, e.g. intranasal, oral, and the like. In one embodiment a composition is administered by intramuscular injection. The skilled person knows the various possibilities to administer a composition, e.g. a vaccine in order to induce an immune response to the  
15 antigen(s) in the vaccine.

A subject as used herein preferably is a mammal, for instance a rodent, e.g. a mouse, a cotton rat, or a non-human-primate, or a human. Preferably, the subject is a human subject.

The proteins, nucleic acid molecules, vectors, and/or compositions may also be administered, either as prime, or as boost, in a homologous or heterologous prime-boost  
20 regimen. If a boosting vaccination is performed, typically, such a boosting vaccination will be administered to the same subject at a time between one week and one year, preferably between two weeks and four months, after administering the composition to the subject for the first time (which is in such cases referred to as ‘priming vaccination’). In certain embodiments, the administration comprises at least one prime and at least one booster administration.

The SARS CoV-2 S proteins may also be used to isolate monoclonal antibodies from a biological sample, e.g. a biological sample (such as blood, plasma, or cells) obtained from an immunized animal or infected human. The invention thus also relates to the use of the SARS CoV-2 protein as bait for isolating monoclonal antibodies.

Also provided is the use of the pre-fusion SARS CoV-2 S proteins of the invention in methods of screening for candidate SARS CoV-2 antiviral agents, including but not limited to antibodies against SARS CoV-2

In addition, the proteins of the invention may be used as diagnostic tool, for example to test the immune status of an individual by establishing whether there are antibodies in the serum of such individual capable of binding to the protein of the invention. The invention thus also relates to an *in vitro* diagnostic method for detecting the presence of an ongoing or past CoV infection in a subject said method comprising the steps of a) contacting a biological sample obtained from said subject with a protein according to the invention; and b) detecting the presence of antibody-protein complexes.

## Examples

### EXAMPLE 1: Instability of semi-stabilized SARS-CoV2 S protein

A plasmid corresponding to the semi-stabilized SARS-CoV2 S protein described by (Wrapp et. al., Science 2020, FurinKO+PP according to SEQ ID NO: 3) was synthesized and codon-optimized at Gene Art (Life Technologies, Carlsbad, CA). A variant with a HIS tag and a variant with a C-tag were purified. The constructs were cloned into pCDNA2004 or generated by standard methods widely known within the field involving site-directed mutagenesis and PCR and sequenced. The expression platform used was the Expi293F cells. The cells were transiently transfected using ExpiFectamine (Life Technologies) according to the manufacturer's instructions and cultured for 6 days at 37°C and 10% CO<sub>2</sub>. The culture

supernatant was harvested and spun for 5 minutes at 300 g to remove cells and cellular debris. The spun supernatant was subsequently sterile filtered using a 0.22 um vacuum filter and stored at 4°C until use.

SARS-CoV2 S trimers were purified using a two-step purification protocol including  
5 either CaptureSelect™ C-tag affinity column for C-tagged protein, or, for HIS-tagged protein, by cOmplete His-tag 5 mL (Roche). Both proteins were further purified by size-exclusion chromatography using a HiLoad Superdex 200 16/600column (GE Healthcare). The C-tagged and HIS tagged S trimer was unstable after repeated freeze / thaw cycles FIG 2 A, B). The purified HIS-tagged S trimer and the C-tagged trimer showed decay after 1 and  
10 especially after 5 flash freezing cycles using liquid Nitrogen (FIG 2. A, B).

EXAMPLE 2: Stabilizing mutations analyzed with AlphaLISA and analytical SEC

In order to stabilize the labile pre-fusion conformation of SARS-CoV2 S protein, amino acid residues at position 941, 943 and/or 944 (numbering according to the SEQ ID  
15 NO: 1) were mutated into G and a disulfide bridge was introduced between residues 970 and 999. Plasmids coding for the recombinant SARS-CoV-2 S protein ectodomains which were C-terminally fused to a foldon (SEQ ID NO: 4) were expressed in Expi293Fcells, and 3 days after transfection the supernatants were tested for binding to ACE2-Fc using AlphaLISA (FIG. 3).

20 For the AlphaLISA assay, SARS-CoV2 S variants in the pcDNA2004 vector containing a linker followed by a sortase A tag followed by a Flag- tag followed by a flexible (G<sub>4</sub>S)<sub>7</sub> linker and ending with a His-tag, were prepared (the sequence of the tag, which was placed at the C-terminus of the S protein, is provided in SEQ ID NO: 2). Three days after transfection, crude supernatants were diluted 300 times in AlphaLISA buffer (PBS + 0.05%  
25 Tween-20 + 0.5 mg/mL BSA). Then, 10 µL of each dilution were transferred to a 96-well

plate and mixed with 40  $\mu$ L acceptor beads, donor beads and ACE2-Fc. The donor beads were conjugated to ProtA (Cat#: AS102M, Perkin Elmer), which binds to ACE2Fc. The acceptor beads were conjugated to an anti-His antibody (Cat#: AL128M, Perkin Elmer), which binds to the His-tag of the construct.

5           The mixture of the supernatant containing the expressed S protein, the ACE-2-Fc, donor beads, and acceptor beads was incubated at room temperature for 2 hours without shaking. Subsequently, the chemiluminescent signal was measured with an Ensign plate reader instrument (Perkin Elmer). The average background signal attributed to mock transfected cells was subtracted from the AlphaLISA counts measured for each of the SARS-  
10   CoV-2 S variants. Subsequently, the whole data set was divided by signal measured for the SARS CoV-2 S protein having the S backbone sequence signal to normalize the signal for each of the S variants tested to the backbone.

          Compared with the soluble uncleaved S variant with a C-terminal foldon domain (SEQ ID NO: 2), the S variants with stabilizing amino acid substitutions at position 941, 943  
15   and 944 or with a disulfide between residues 970 - 999 showed higher ACE2-Fc binding (FIG. 3).

          The cell culture supernatants of transfections with a labile uncleaved SARS-CoV-2 S protein, and of variants with amino acid substitutions at position 941, 943 and/or 944 and with a disulfide between residues 970 - 999 were analyzed using analytical SEC (FIG. 4). An  
20   ultra high-performance liquid chromatography system (Vanquish, Thermo Scientific) and  $\mu$ DAWN TREOS instrument (Wyatt) coupled to an Optilab  $\mu$ T-rEX Refractive Index Detector (Wyatt), in combination with an in-line Nanostar DLS reader (Wyatt), was used for performing the analytical SEC experiment. The cleared crude cell culture supernatants were applied to a SRT-10C SEC-500 15 cm column, (Sepax Cat# 235500-4615) with the  
25   corresponding guard column (Sepax) equilibrated in running buffer (150 mM sodium

phosphate, 50 mM NaCl, pH 7.0) at 0.35 mL/min. When analyzing supernatant samples,  $\mu$ MALS detectors were offline and analytical SEC data was analyzed using Chromeleon 7.2.8.0 software package. The signal of supernatants of non-transfected cells was subtracted from the signal of supernatants of S transfected cells. When purified proteins were analyzed

5 using SEC-MALS, mMALS detectors were inline and data was analyzed using Astra 7.3 software package. For the protein component, a  $dn/dc$  (mL/g) value of 0.1850 was used and for the glycan component a value of 0.1410. Compared with the soluble uncleaved S variant with a C-terminal foldon domain, variants with amino acid substitutions T941G, S943G, A944G and a disulfide between residues 970 - 999 showed higher trimer content according to

10 analytical SEC of culture supernatant.

**Table 1.** Standard amino acids, abbreviations and properties

| <b>Amino Acid</b> | <b>3-Letter</b> | <b>1-Letter</b> | <b>Side chain polarity</b> | <b>Side chain charge (pH 7.4)</b> |
|-------------------|-----------------|-----------------|----------------------------|-----------------------------------|
| alanine           | Ala             | A               | non-polar                  | Neutral                           |
| arginine          | Arg             | R               | Polar                      | Positive                          |
| asparagine        | Asn             | N               | Polar                      | Neutral                           |
| aspartic acid     | Asp             | D               | polar                      | Negative                          |
| cysteine          | Cys             | C               | non-polar                  | Neutral                           |
| glutamic acid     | Glu             | E               | polar                      | Negative                          |
| glutamine         | Gln             | Q               | polar                      | Neutral                           |
| glycine           | Gly             | G               | non-polar                  | Neutral                           |
| histidine         | His             | H               | polar                      | positive(10%) neutral(90%)        |
| isoleucine        | Ile             | I               | non-polar                  | Neutral                           |
| leucine           | Leu             | L               | non-polar                  | Neutral                           |
| lysine            | Lys             | K               | polar                      | Positive                          |
| methionine        | Met             | M               | non-polar                  | Neutral                           |
| phenylalanine     | Phe             | F               | non-polar                  | Neutral                           |
| proline           | Pro             | P               | non-polar                  | Neutral                           |
| serine            | Ser             | S               | polar                      | Neutral                           |
| threonine         | Thr             | T               | polar                      | Neutral                           |
| tryptophan        | Trp             | W               | non-polar                  | Neutral                           |
| tyrosine          | Tyr             | Y               | polar                      | Neutral                           |
| valine            | Val             | V               | non-polar                  | Neutral                           |

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- 30

## Sequences

- 5 SEQ ID NO 1: full length S protein (underline signal peptide, double underline TM and cytoplasmic domain that is deleted in the soluble version)

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK  
 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVVYHKNNKSWM  
 10 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG  
 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR  
 15 DISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIAYTM  
 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK  
 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF  
 20 NGTLVLPPLLTDEMQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
 GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT  
 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
 DGAHFPREGVFSVNGTHWVFTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT  
 25 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCMTT  
SCCCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

- SEQ ID NO 2: soluble S protein with furin KO, underline signal peptide, double underline linker, foldon, tags etc.)

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK  
 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVVYHKNNKSWM  
 30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG  
 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
 35 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR  
 DISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
 NGTLGTGVLTESNKKFLPFQGFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV  
 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNSPSRAGSVASQSIAYTM  
 40 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK  
 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF  
 NGTLVLPPLLTDEMQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
 GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT  
 45 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
 DGAHFPREGVFSVNGTHWVFTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT  
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 3: soluble S protein with Furin KO and double proline in the hinge loop. (underline signal peptide) double underline linker, foldon, tags etc.)

5 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK  
 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVVYHKNNKSWM  
 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG  
 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGYNYLYRFRKSNLKPFR  
 10 DISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV  
 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQNTSPSRAGSVASQSIAYTM  
 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF  
 15 NGTLVLPPLLTDEMQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
 GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRLQSLQTYVT  
 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
 DGAHFPREGVFSVNGTHWFTVQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYEAPRDGOAYVRKDGWVLLSTFLG  
 20 RSLEVLFQGPGLPETGGGSDYKDDDDKGGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSHHHHHH

SEQ ID NO 4: foldon

25 GYIPEAPRDGOAYVRKDGWVLLSTFL

SEQ ID NO 5: WT soluble S (ectodomain)

30 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK  
 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVVYHKNNKSWM  
 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG  
 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
 35 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGYNYLYRFRKSNLKPFR  
 DISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV  
 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQNTSPRRARSVASQSIAYTM  
 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
 40 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF  
 NGTLVLPPLLTDEMQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
 GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT  
 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
 DGAHFPREGVFSVNGTHWFTVQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
 45 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

SEQ ID NO 6: WT full length S + Furin KO

50 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK  
 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVVYHKNNKSWM  
 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG

INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVG YLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
5 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNPSRAGSVASQSIIAYTM  
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIARDLICAQKF  
NGLTVLPPLLTDEMQAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
10 GKIQDSSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH  
GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT  
SPDVLGDIDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEYKWPWYIWLGLFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

15

SEQ ID NO 7: WT soluble S + Furin KO

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKCEFCNDPFLGVYHKNKNSWM  
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVG YLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR  
25 DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNPSRAGSVASQSIIAYTM  
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIARDLICAQKF  
30 NGLTVLPPLLTDEMQAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH  
GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT  
SPDVLGDIDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEY

35

SEQ ID NO 8: SEQ ID NO 1 + T941G

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKCEFCNDPFLGVYHKNKNSWM  
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVG YLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR  
45 DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNPSRRARSVASQSIIAYTM  
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIARDLICAQKF  
50 NGLTVLPPLLTDEMQAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSSLSSGASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH  
GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

5 SEQ ID NO 9: SEQ ID NO 1 + S943G

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVVYHKNNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG  
10 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTEVK  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR  
DSTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFEGGVSVITPGTNTSNQVAVLYQDVNCTEV  
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSEYCDIPGAGICASYQTQTNSPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF  
NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSLSTAGALGLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRQLSLQTYVT  
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGTVFLHVTYVPAQEKNFHTTAPAICHD  
GKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

25 SEQ ID NO 10: SEQ ID NO 1 + D614N + A892P + A942P + T941G

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVVYHKNNKSWM  
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTEVK  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR  
DSTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFEGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSEYCDIPGAGICASYQTQTNSPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF  
NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
40 GKIQDSLSSGPSALGLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGTVFLHVTYVPAQEKNFHTTAPAICHD  
GKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

45 SEQ ID NO 11: SEQ ID NO 1 + D614N + A892P + A942P + S943G

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVVYHKNNKSWM  
50 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTEVK  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
5 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLICAQKF  
NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSLSSTPGALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRQLSLQTYVT  
10 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVLGDIDISGINASVNIQKEIDRLNEVAKNLNESLIDLQELGKYEYKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

15 SEQ ID NO 12: SEQ ID NO 1 + D614N + A892P + A942P + T941G + S943G

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFFHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFNDPFLGVYHKNKSWM  
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDLPQGFSALEPLVDLPIG  
20 INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNEGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLICAQKF  
NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSLSGPGALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRQLSLQTYVT  
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVLGDIDISGINASVNIQKEIDRLNEVAKNLNESLIDLQELGKYEYKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

35 SEQ ID NO 13: SEQ ID NO 1 + D614N + A892P + A942P + T941G + A944P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFFHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFNDPFLGVYHKNKSWM  
40 ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDLPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNEGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
45 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLICAQKF  
NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
50 GKIQDSLSGSPGLGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

5 SEQ ID NO 14: SEQ ID NO 1 + D614N + A892P + A942P + S943G + A944P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVVYHKNNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPQGFSALEPLVDLP  
10 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLKSFTEK  
YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN  
LCFTNVYADSFVIRGDEVRIAPGQGTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP  
DISTEIYQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFEGGVSVITPGTNTSNQVAVLYQNVNCTE  
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF  
NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDLSSTPGPLGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRQLSLQTYVT  
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAPHGVVFLHVTYVPAQEKNFHTTAPAICH  
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

25  
SEQ ID NO 15: SEQ ID NO 1 + T941G + K986P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVVYHKNNKSWM  
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPQGFSALEPLVDLP  
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLKSFTEK  
YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN  
LCFTNVYADSFVIRGDEVRIAPGQGTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP  
DISTEIYQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF  
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFEGGVSVITPGTNTSNQVAVLYQDVNCTE  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF  
NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
40 GKIQDLSLSSGASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPVEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAPHGVVFLHVTYVPAQEKNFHTTAPAICH  
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

45  
SEQ ID NO 16: SEQ ID NO 1 + S943G + K986P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVVYHKNNKSWM  
50 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPQGFSALEPLVDLP  
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLKSFTEK  
YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIAYTM  
5 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLICAQKF  
NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNLSAI  
GKIQDLSLSTAGALGLQDQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPVEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
10 GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT  
SPDVLGDISGINASVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

15 SEQ ID NO 17: SEQ ID NO 1 + D614N + A892P + A942P + T941G + K986P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFFHAIHVSNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFNDPFLGVYHKNKNSWM  
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDLPQGFSALEPLVDLPIG  
20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNEGTITDAVDCALDPLSEKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLICAQKF  
NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNLSAI  
GKIQDLSLSSGSPALGLQDQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPVEAEVQIDRLITGRQLSLQTYVT  
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT  
SPDVLGDISGINASVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

35 SEQ ID NO 18: SEQ ID NO 1 + D614N + A892P + A942P + S943G + K986P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFFHAIHVSNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFNDPFLGVYHKNKNSWM  
40 ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDLPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNEGTITDAVDCALDPLSEKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
45 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLICAQKF  
NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNLSAI  
GKIQDLSLSTPGALGLQDQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPVEAEVQIDRLITGRQLSLQTYVT  
50 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

5 SEQ ID NO 19: SEQ ID NO 1 + D614N + A892P + A942P + T941G + S943G + K986P

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHKNKNSWM  
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP  
10 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP  
DISTEIYQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFEGGVSVITPGTNTSNQVAVLYQNVNCTEV  
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF  
NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSLSSGPGALGLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPVEAEVQIDRLITGRLQSLQTYVT  
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTYVPAQEKNFHTTAPAICHD  
GKAHFPREGVFVSNNGTHWFTVQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

25 SEQ ID NO 20: SEQ ID NO 1 + D614N + A892P + A942P + T941G + A944P + K986P

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHKNKNSWM  
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP  
30 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP  
DISTEIYQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFEGGVSVITPGTNTSNQVAVLYQNVNCTEV  
35 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF  
NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSLSSGPGALGLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPVEAEVQIDRLITGRLQSLQTYVT  
40 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTYVPAQEKNFHTTAPAICHD  
GKAHFPREGVFVSNNGTHWFTVQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

45 SEQ ID NO 21: SEQ ID NO 1 + D614N + A892P + A942P + S943G + A944P + K986P

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHKNKNSWM  
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP  
50 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND

LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIAYTM  
5 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLICAQKF  
NGLTVLPPLLTDEMQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNLSAI  
GKIQDSLSSTPGPLGLQDQVNVQNAQALNTLVKQLSSNFGAISSVLNDILSRDPVEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH  
10 GKAHFPREGVFSNGTHWVFTQRFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT  
SPDVLGDIDISGINASVNIQKEIDRLNEVAKNLNESLIDLQELGKYEYKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

15 SEQ ID NO 22: SEQ ID NO 1 + T941G + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM  
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDLPQGFSALEPLVDLPIG  
20 INITRFQTLALHRSYLTGDSGSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV  
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLICAQKF  
NGLTVLPPLLTDEMQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNLSAI  
GKIQDSLSGASALGLQDQVNVQNAQALNTLVKQLSSNFGAISSVLNDILSRDKPEAEVQIDRLITGRQLSLQTYVT  
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFSNGTHWVFTQRFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT  
SPDVLGDIDISGINASVNIQKEIDRLNEVAKNLNESLIDLQELGKYEYKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

35  
SEQ ID NO 23: SEQ ID NO 1 + S943G + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM  
40 ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDLPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLTGDSGSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
45 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLICAQKF  
NGLTVLPPLLTDEMQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNLSAI  
50 GKIQDSLSSTAGALGLQDQVNVQNAQALNTLVKQLSSNFGAISSVLNDILSRDKPEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFSNGTHWVFTQRFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

5 SEQ ID NO 24: SEQ ID NO 1 + D614N + A892P + A942P + T941G + V987P

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYYHKNNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPQGFSALEPLVDLP  
10 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP  
DISTEIYQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFEGGVSVITPGTNTSNQVAVLYQNVNCTEV  
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSEYCDIPGAGICASYQTQTNSPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF  
NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSLSSGPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKPEAEVQIDRLITGRQLSLQTYVT  
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTYVPAQEKNFHTTAPAICH  
GKAHFPREGVVFVSNGTHWFVTQRNIFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

25

SEQ ID NO 25: SEQ ID NO 1 + D614N + A892P + A942P + S943G + V987P

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYYHKNNKSWM  
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPQGFSALEPLVDLP  
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP  
DISTEIYQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF  
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFEGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSEYCDIPGAGICASYQTQTNSPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF  
NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
40 GKIQDSLSTPGALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKPEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTYVPAQEKNFHTTAPAICH  
GKAHFPREGVVFVSNGTHWFVTQRNIFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

45

SEQ ID NO 26: SEQ ID NO 1 + D614N + A892P + A942P + T941G + S943G + V987P

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYYHKNNKSWM  
50 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPQGFSALEPLVDLP  
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
5 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLICAQKF  
NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNLSAI  
GKIQDSLSGGPGALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKPEAEVQIDRLITGRLQSLQTYVT  
10 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVLGDIDISGINASVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

15 SEQ ID NO 27: SEQ ID NO 1 + D614N + A892P + A942P + T941G + A944P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFNDPFLGVYHKNKNSWM  
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDPQGFSALEPLVDLPIG  
20 INITRFQTLALHRSYLTGDSGGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLICAQKF  
NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNLSAI  
GKIQDSLSGGPSPLGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKPEAEVQIDRLITGRLQSLQTYVT  
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVLGDIDISGINASVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

35 SEQ ID NO 28: SEQ ID NO 1 + D614N + A892P + A942P + S943G + A944P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFNDPFLGVYHKNKNSWM  
40 ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLTGDSGGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
45 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLICAQKF  
NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNLSAI  
50 GKIQDSLSSTPGPLGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKPEAEVQIDRLITGRLQSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT

SPDVDLGDISGINASVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

5 SEQ ID NO 29: SEQ ID NO 1 + T941G + K986P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHKNKNSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG  
10 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR  
DSTEIYQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFEGGVSVITPGTNTSNQVAVLYQDVNCTEV  
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQTNSPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF  
NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSLSSGASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPAEVQIDRLITGRQLSLQTYVT  
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGTVFLHVTYVPAQEKNFHTTAPAICHD  
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVDLGDISGINASVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

25 SEQ ID NO 30: SEQ ID NO 1 + S943G + K986P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHKNKNSWM  
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR  
DSTEIYQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFEGGVSVITPGTNTSNQVAVLYQDVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQTNSPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF  
NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
40 GKIQDSLSSGASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGTVFLHVTYVPAQEKNFHTTAPAICHD  
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVDLGDISGINASVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

45 SEQ ID NO 31: SEQ ID NO 1 + D614N + A892P + A942P + T941G + K986P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHKNKNSWM  
50 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND

LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIAYTM  
5 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF  
NGLTVLPPLLTDEMQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNLSAI  
GKIQDSSLSSGPGALGLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH  
10 GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT  
SPDVLGDIDISGINASVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

15 SEQ ID NO 32: SEQ ID NO 1 + D614N + A892P + A942P + S943G + K986P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFFHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFNDPFLGVYHKNKNSWM  
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDLPQGFSALEPLVDLPIG  
20 INITRFQTLALHRSYLTGDSGSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF  
NGLTVLPPLLTDEMQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNLSAI  
GKIQDSSLSTPGALGLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRQLSLQTYVT  
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT  
SPDVLGDIDISGINASVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

35 SEQ ID NO 33: SEQ ID NO 1 + D614N + A892P + A942P + T941G + S943G + K986P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFFHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFNDPFLGVYHKNKNSWM  
40 ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDLPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLTGDSGSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
45 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF  
NGLTVLPPLLTDEMQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNLSAI  
50 GKIQDSSLSSGPGALGLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

5 SEQ ID NO 34: SEQ ID NO 1 + D614N + A892P + A942P + T941G + A944P + K986P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHKNKNSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPQGFSALEPLVDLP  
10 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR  
DSTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFEGGVSVITPGTNTSNQVAVLYQNVNCTEV  
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQTNSPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF  
NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDLSLSSGSPGLKLDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPAEVQIDRLITGRLQSLQTYVT  
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTYVPAQEKNFHTTAPAICHD  
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

25

SEQ ID NO 35: SEQ ID NO 1 + D614N + A892P + A942P + S943G + A944P + K986P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHKNKNSWM  
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPQGFSALEPLVDLP  
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR  
DSTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFEGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQTNSPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF  
NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
40 GKIQDLSLSTPGPLGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPAEVQIDRLITGRLQSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTYVPAQEKNFHTTAPAICHD  
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

45

SEQ ID NO 36: SEQ ID NO 6 + T941G

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHKNKNSWM  
50 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPQGFSALEPLVDLP  
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFER  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQGFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPSRAGSVASQSIAYTM  
5 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF  
NGLTVLPPLLTDEMQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNLSAI  
GKIQDSSLSSGASALGLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH  
10 GKAHFPREGVFSNGTHWFTVQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVLGDIDISGINASVNIQKEIDRLNEVAKNLNESLIDLQELGKEYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

15 SEQ ID NO 37: SEQ ID NO 6 + S943G

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFFHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHKNKNSWM  
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDLPQGFSALEPLVDLPIG  
20 INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFER  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQGFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV  
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPSRAGSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF  
NGLTVLPPLLTDEMQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNLSAI  
GKIQDSSLSTAGALGLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRQLSLQTYVT  
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFSNGTHWFTVQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVLGDIDISGINASVNIQKEIDRLNEVAKNLNESLIDLQELGKEYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

35 SEQ ID NO 38: SEQ ID NO 6 + D614N + A892P + A942P + T941G

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFFHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHKNKNSWM  
40 ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDLPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFER  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
45 NGLTGTGVLTESNKKFLPFQGFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPSRAGSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF  
NGLTVLPPLLTDEMQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNLSAI  
50 GKIQDSSLSSGASALGLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFSNGTHWFTVQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

5 SEQ ID NO 39: SEQ ID NO 6 + D614N + A892P + A942P + S943G

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYYHKNNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG  
10 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFVTEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR  
DSTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSEGGVSVITPGTNTSNQVAVLYQNVNCTEV  
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSEYCDIPGAGICASYQTQTNPSRAGSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRLTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLICAQKF  
NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSLSTPGALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRQLSLQTYVT  
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTYVPAQEKNFHTTAPAICHD  
GKAHFPREGVVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

25

SEQ ID NO 40: SEQ ID NO 6 + D614N + A892P + A942P + T941G + S943G

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYYHKNNKSWM  
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFVTEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR  
DSTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSEGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSEYCDIPGAGICASYQTQTNPSRAGSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRLTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLICAQKF  
NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
40 GKIQDSLSSGPGALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTYVPAQEKNFHTTAPAICHD  
GKAHFPREGVVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

45

SEQ ID NO 41: SEQ ID NO 6 + D614N + A892P + A942P + T941G + A944P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYYHKNNKSWM  
50 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFVTEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQNTNSPSRAGSVASQSIAYTM  
5 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF  
NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSLSSGSPGLKLDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
10 GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVLGDIDISGINASVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

15 SEQ ID NO 42: SEQ ID NO 6 + D614N + A892P + A942P + S943G + A944P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWFAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFNDPFLGVYHKNKNSWM  
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPGGSALEPLVDLP  
20 INITRFQTLALHRSYLTGDSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQNTNSPSRAGSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF  
NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSLSSSTPGPLKLDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRQLSLQTYVT  
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVLGDIDISGINASVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

35  
SEQ ID NO 43: SEQ ID NO 6 + T941G + K986P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWFAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFNDPFLGVYHKNKNSWM  
40 ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPGGSALEPLVDLP  
INITRFQTLALHRSYLTGDSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
45 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQNTNSPSRAGSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF  
NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN  
50 GKIQDSLSSGASALGLKLDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPVEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT

SPDVDLGDISGINASVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

5 SEQ ID NO 44: SEQ ID NO 6 + S943G + K986P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYYHKNNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP  
10 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLKSFTEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR  
DSTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFEGGVSVITPGTNTSNQVAVLYQDVNCTEV  
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSEYCDIPGAGICASYQTQTNPSRAGSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCMYICGDSTECNNLLQYGSFCTQLNRLTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF  
NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGAAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDLSSTAGALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPVEAEVQIDRLITGRQLSLQTYVT  
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGTVFLHVTYVPAQEKNFHTTAPAICH  
GKAHFPREGVFVSNGTHWFVTQNRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVDLGDISGINASVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

25 SEQ ID NO 45: SEQ ID NO 6 + D614N + A892P + A942P + T941G + K986P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYYHKNNKSWM  
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP  
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLKSFTEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR  
DSTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFEGGVSVITPGTNTSNQVAVLYQDVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSEYCDIPGAGICASYQTQTNPSRAGSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCMYICGDSTECNNLLQYGSFCTQLNRLTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF  
NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
40 GKIQDLSLSSGPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPVEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGTVFLHVTYVPAQEKNFHTTAPAICH  
GKAHFPREGVFVSNGTHWFVTQNRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVDLGDISGINASVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

45 SEQ ID NO 46: SEQ ID NO 6 + D614N + A892P + A942P + S943G + K986P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYYHKNNKSWM  
50 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP  
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLKSFTEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPSRAGSVASQSIAYTM  
5 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIARDLICAQKF  
NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSLSSTPGALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPVEAEVQIDRLITGRQLSLQTYVT  
10 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
D GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVLGDIDISGINASVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

15 SEQ ID NO 47: SEQ ID NO 6 + D614N + A892P + A942P + T941G + S943G + K986P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFFHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFQNDPFLGVYYHKNNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPGGSALEPLVDLPIG  
20 INITRFQTLALHRSYLTGDSGGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPSRAGSVASQSIAYTM  
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIARDLICAQKF  
NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSLSGGPGALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPVEAEVQIDRLITGRQLSLQTYVT  
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
D GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVLGDIDISGINASVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

35 SEQ ID NO 48: SEQ ID NO 6 + D614N + A892P + A942P + T941G + A944P + K986P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFFHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFQNDPFLGVYYHKNNKSWM  
40 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPGGSALEPLVDLPIG  
INITRFQTLALHRSYLTGDSGGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
45 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPSRAGSVASQSIAYTM  
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIARDLICAQKF  
NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
50 GKIQDSLSGGPSPLGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPVEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
D GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

5 SEQ ID NO 49: SEQ ID NO 6 + D614N + A892P + A942P + S943G + A944P + K986P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPQGFSALEPLVDLPIG  
10 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLKSFTEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR  
DSTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFEGGVSVITPGTNTSNQVAVLYQNVNCTEV  
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQTNPSRAGSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF  
NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSLSTPGPLGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPVEAEVQIDRLITGRQLSLQTYVT  
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTYVPAQEKNFHTTAPAICHD  
GKAHFPREGVFVSNGTHWVFTQRNIFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

25  
SEQ ID NO 50: SEQ ID NO 6 + T941G + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM  
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLKSFTEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR  
DSTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFEGGVSVITPGTNTSNQVAVLYQDVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQTNPSRAGSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF  
NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
40 GKIQDSLSSGASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKPEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTYVPAQEKNFHTTAPAICHD  
GKAHFPREGVFVSNGTHWVFTQRNIFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

45  
SEQ ID NO 51: SEQ ID NO 6 + S943G + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM  
50 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLKSFTEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND

LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFER  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNPSRAGSVASQSIAYTM  
5 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIARDLICAQKF  
NGLTVLPPLLTDEMQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNLSAI  
GKIQDLSSTAGALGLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKPEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH  
10 GKAHFPREGVFSNGTHWVFTQRFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVLGDIDISGINASVNIQKEIDRLNEVAKNLNESLIDLQELGKYEYKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

15 SEQ ID NO 52: SEQ ID NO 6 + D614N + A892P + A942P + T941G + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFFHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFNDPFLGVYHKNKNSWM  
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDLPQGFSALEPLVDLPIG  
20 INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNEGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFER  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNPSRAGSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIARDLICAQKF  
NGLTVLPPLLTDEMQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNLSAI  
GKIQDLSGSPALGLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKPEAEVQIDRLITGRQLSLQTYVT  
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFSNGTHWVFTQRFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVLGDIDISGINASVNIQKEIDRLNEVAKNLNESLIDLQELGKYEYKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

35 SEQ ID NO 53: SEQ ID NO 6 + D614N + A892P + A942P + S943G + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFFHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFNDPFLGVYHKNKNSWM  
40 ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDLPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNEGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFER  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
45 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNPSRAGSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIARDLICAQKF  
NGLTVLPPLLTDEMQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNLSAI  
50 GKIQDLSSTPGALGLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKPEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFSNGTHWVFTQRFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT

SPDVDLGDISGINASVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

5 SEQ ID NO 54: SEQ ID NO 6 + D614N + A892P + A942P + T941G + S943G + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFQCNDFLGVVYHKNNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPPQGFSALEPLVDLP  
10 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLKSFVTEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP  
DISTEIYQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFEGGVSVITPGTNTSNQVAVLYQNVNCTEV  
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQTNPSRAGSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF  
NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN  
GKIQDSLSSGPGALGLQDQVNVNQAQALNTLVKQLSSNFGAIVSSVNDILSRDLKPEAEVQIDRLITGRQLSLQTYVT  
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTYVPAQEKNFHTTAPAICHD  
GKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVDLGDISGINASVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

25 SEQ ID NO 55: SEQ ID NO 6 + D614N + A892P + A942P + T941G + A944P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFQCNDFLGVVYHKNNKSWM  
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPPQGFSALEPLVDLP  
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLKSFVTEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP  
DISTEIYQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF  
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFEGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQTNPSRAGSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF  
NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN  
40 GKIQDSLSSGPGALGLQDQVNVNQAQALNTLVKQLSSNFGAIVSSVNDILSRDLKPEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTYVPAQEKNFHTTAPAICHD  
GKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVDLGDISGINASVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

45 SEQ ID NO 56: SEQ ID NO 6 + D614N + A892P + A942P + S943G + A944P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFQCNDFLGVVYHKNNKSWM  
50 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPPQGFSALEPLVDLP  
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLKSFVTEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQGFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPSRAGSVASQSIAYTM  
5 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIARDLICAQKF  
NGLTVLPPLLTDEMQIYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNLSAI  
GKIQDSLSSTPGPLGLQDQVNVQNAQALNTLVKQLSSNFGAISSVLNDILSRDKPEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH  
10 GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVLGDISGINASVNIQKEIDRLNEVAKNLNESLIDLQELGKYEYKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

15 SEQ ID NO 57: SEQ ID NO 6 + T941G + K986P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFFHAIHVSNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYHKNKNSWM  
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDLPQGFSALEPLVDLPIG  
20 INITRFQTLALHRSYLTGDSGSGWTAGAAAYVGYLQPRTFLLKYNEGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN  
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQGFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV  
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPSRAGSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIARDLICAQKF  
NGLTVLPPLLTDEMQIYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNLSAI  
GKIQDSLSGASALGLQDQVNVQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRQLSLQTYVT  
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVLGDISGINASVNIQKEIDRLNEVAKNLNESLIDLQELGKYEYKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

35 SEQ ID NO 58: SEQ ID NO 6 + S943G + K986P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFFHAIHVSNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYHKNKNSWM  
40 ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDLPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLTGDSGSGWTAGAAAYVGYLQPRTFLLKYNEGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN  
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
45 NGLTGTGVLTESNKKFLPFQGFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPSRAGSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIARDLICAQKF  
NGLTVLPPLLTDEMQIYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNLSAI  
50 GKIQDSLSSTAGALGLQDQVNVQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

5 SEQ ID NO 59: SEQ ID NO 6 + D614N + A892P + A942P + T941G + K986P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVVYHKNNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPPQGFSALEPLVDLP  
10 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTEK  
YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP  
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFEGGVSVITPGTNTSNQVAVLYQNVNCTEV  
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQTNPSRAGSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF  
NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSLSSGPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPAEVQIDRLITGRQLSQTYYVT  
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGTVFLHVTYVPAQEKNFHTTAPAICHD  
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

25 SEQ ID NO 60: SEQ ID NO 6 + D614N + A892P + A942P + S943G + K986P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVVYHKNNKSWM  
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPPQGFSALEPLVDLP  
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTEK  
YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP  
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF  
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFEGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQTNPSRAGSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF  
NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
40 GKIQDSLSTPGALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPAEVQIDRLITGRQLSQTYYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGTVFLHVTYVPAQEKNFHTTAPAICHD  
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

45 SEQ ID NO 61: SEQ ID NO 6 + D614N + A892P + A942P + T941G + S943G + K986P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVVYHKNNKSWM  
50 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPPQGFSALEPLVDLP  
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTEK  
YQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQNTNSPSRAGSVASQSIAYTM  
5 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIARDLICAQKF  
NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNLSAI  
GKIQDSLSSGPGALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT  
10 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT  
SPDVLGDISGINASVNIQKEIDRLNEVAKNLNESLIDLQELGKEYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

15 SEQ ID NO 62: SEQ ID NO 6 + D614N + A892P + A942P + T941G + A944P + K986P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFFHAIHVSNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFNDPFLGVYHKNKNSWM  
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDLPQGFSALEPLVDLP  
20 INITRFQTLALHRSYLTGDSGSGWTAGAAAYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKISNCVADYSVLNNSASFSTFKCYGVSPKLN  
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQNTNSPSRAGSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIARDLICAQKF  
NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNLSAI  
GKIQDSLSSGPGALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT  
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT  
SPDVLGDISGINASVNIQKEIDRLNEVAKNLNESLIDLQELGKEYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

35 SEQ ID NO 63: SEQ ID NO 6 + D614N + A892P + A942P + S943G + A944P + K986P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFFHAIHVSNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFNDPFLGVYHKNKNSWM  
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDLPQGFSALEPLVDLP  
40 INITRFQTLALHRSYLTGDSGSGWTAGAAAYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKISNCVADYSVLNNSASFSTFKCYGVSPKLN  
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
45 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQNTNSPSRAGSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIARDLICAQKF  
NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNLSAI  
GKIQDSLSTPGPLGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT  
50 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT  
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

## 5 SEQ ID NO 64: SEQ ID NO 5 + T941G

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFQCNDFPLGVVYHKNNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPGGFSALEPLVDLPIG  
10 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYYLYRFRKSNLKPFR  
DSTEIYQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV  
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQNTSPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF  
NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSLSSGASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRQLSLQTYVT  
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGVVFLHVTYVPAQEKNFHTTAPAICHD  
GKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

## 25 SEQ ID NO 65: SEQ ID NO 5 + S943G

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFQCNDFPLGVVYHKNNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPGGFSALEPLVDLPIG  
30 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYYLYRFRKSNLKPFR  
DSTEIYQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV  
35 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQNTSPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF  
NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSLSTAGALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRQLSLQTYVT  
40 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGVVFLHVTYVPAQEKNFHTTAPAICHD  
GKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

## 45 SEQ ID NO 66: SEQ ID NO 5 + D614N + A892P + A942P + T941G

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFQCNDFPLGVVYHKNNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPGGFSALEPLVDLPIG  
50 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYYLYRFRKSNLKPFR  
DSTEIYQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN

5 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQNTSPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF  
10 NGLTVLPPLLTDEMQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNDAI  
GKIQDLSLSSGSPALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVVFVSNTHWVFTQRFYEPQIITDNTFVSGNCDVVIGVNNNTVYDPLQPELDSFKEELDKYFNHT  
SPDVLGDIGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

SEQ ID NO 67: SEQ ID NO 5 + D614N + A892P + A942P + S943G

15 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM  
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPQGFSALEPLVDLP  
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSNLKP  
20 DISTEIQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQNTSPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF  
25 NGLTVLPPLLTDEMQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNDAI  
GKIQDLSLSTPGALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVVFVSNTHWVFTQRFYEPQIITDNTFVSGNCDVVIGVNNNTVYDPLQPELDSFKEELDKYFNHT  
SPDVLGDIGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

SEQ ID NO 68: SEQ ID NO 5 + D614N + A892P + A942P + T941G + S943G

35 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM  
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPQGFSALEPLVDLP  
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSNLKP  
40 DISTEIQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQNTSPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF  
45 NGLTVLPPLLTDEMQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNDAI  
GKIQDLSLSSGPGALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVVFVSNTHWVFTQRFYEPQIITDNTFVSGNCDVVIGVNNNTVYDPLQPELDSFKEELDKYFNHT  
SPDVLGDIGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

SEQ ID NO 69: SEQ ID NO 5 + D614N + A892P + A942P + T941G + A944P

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVVYHKNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNENGITDAVDCALDPLSETKCTLSFTVEKG  
5 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQNTSPRRARSVASQSIIAYTM  
10 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF  
NGLTVLPPLLTDEMIQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSLSSGSPGLGLQDVVNQNAQALNTLVKQLSSNFGAIVSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKYHLSFQSPHGVVFLHVTYVPAQEKNFTTAPAICH  
15 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGVNNTVYDPLQPELDSFKEELDKYFNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

SEQ ID NO 70: SEQ ID NO 5 + D614N + A892P + A942P + S943G + A944P

20 MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVVYHKNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNENGITDAVDCALDPLSETKCTLSFTVEKG  
25 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQNTSPRRARSVASQSIIAYTM  
30 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF  
NGLTVLPPLLTDEMIQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSLSTPGPLGLQDVVNQNAQALNTLVKQLSSNFGAIVSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKYHLSFQSPHGVVFLHVTYVPAQEKNFTTAPAICH  
35 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGVNNTVYDPLQPELDSFKEELDKYFNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

SEQ ID NO 71: SEQ ID NO 5 + T941G + K986P

40 MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVVYHKNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNENGITDAVDCALDPLSETKCTLSFTVEKG  
45 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQNTSPRRARSVASQSIIAYTM  
50 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF  
NGLTVLPPLLTDEMIQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSLSSGASALGLQDVVNQNAQALNTLVKQLSSNFGAIVSVLNDILSRDPVEAEVQIDRLITGRLQSLQTYVT

QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGHYHLMSPQSAHPGVVFLHVTYVPAQEKNFHTTAPAICH  
D  
GKAHFPREGVVFVSNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

5

SEQ ID NO 72: SEQ ID NO 5 + S943G + K986P

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVYHKNKNSWM  
10 ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGSFALEPLVDLP  
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGITDAVDCALDPLSEKCTLKSFTEK  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTK  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYYLYRFRKSNLKP  
15 DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF  
NGLTGTGVLTESNKKFLPFQGFGRDIADTTDAVRDPQTLEILDITPCSFEGGVSVITPGTNTSNQVAVLYQDVNCTE  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSEYCDIPGAGICASYQTQNTSPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF  
20 NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGAAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSLSSSTAGALGLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPVEAEVQIDRLITGRQLQSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGHYHLMSPQSAHPGVVFLHVTYVPAQEKNFHTTAPAICH  
D  
GKAHFPREGVVFVSNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

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SEQ ID NO 73: SEQ ID NO 5 + D614N + A892P + A942P + T941G + K986P

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVYHKNKNSWM  
30 ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGSFALEPLVDLP  
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGITDAVDCALDPLSEKCTLKSFTEK  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTK  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYYLYRFRKSNLKP  
35 DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF  
NGLTGTGVLTESNKKFLPFQGFGRDIADTTDAVRDPQTLEILDITPCSFEGGVSVITPGTNTSNQVAVLYQNVNCTE  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSEYCDIPGAGICASYQTQNTSPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF  
40 NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSLSSGPSALGLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPVEAEVQIDRLITGRQLQSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGHYHLMSPQSAHPGVVFLHVTYVPAQEKNFHTTAPAICH  
D  
GKAHFPREGVVFVSNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

45

SEQ ID NO 74: SEQ ID NO 5 + D614N + A892P + A942P + S943G + K986P

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVYHKNKNSWM  
50 ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGSFALEPLVDLP  
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGITDAVDCALDPLSEKCTLKSFTEK  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTK  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYYLYRFRKSNLKP

DISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
 NGLTGTGVLTESNKKFLPFQGFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVTGTNTSNQVAVLYQNVNCTEV  
 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQNTSPRRARSVASQSIIAYTM  
 SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
 5 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF  
 NGLTVLPPLLTDEMQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNQSAI  
 GKIQDSLSTPGALGLQDVVNQNAQALNTLVKQLSSNFGAIVSSVNDILSRDPVEAEVQIDRLITGRLQSLQTYVT  
 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH  
 10 GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

SEQ ID NO 75: SEQ ID NO 5 + D614N + A892P + A942P + T941G + S943G + K986P

15 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVVYHKNNKSWM  
 ESEFRVYSSANNCTFEYVSQPFLLMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRDLPGGFSALEPLVDLP  
 INITRFQTLALHRSYLTGDDSSSGWTAGAAAYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN  
 20 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGNYLYRLFRKSNLKPFR  
 DISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
 NGLTGTGVLTESNKKFLPFQGFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVTGTNTSNQVAVLYQNVNCTEV  
 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQNTSPRRARSVASQSIIAYTM  
 SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
 25 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF  
 NGLTVLPPLLTDEMQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNQSAI  
 GKIQDSLSSGPGALGLQDVVNQNAQALNTLVKQLSSNFGAIVSSVNDILSRDPVEAEVQIDRLITGRLQSLQTYVT  
 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH  
 30 GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

SEQ ID NO 76: SEQ ID NO 5 + D614N + A892P + A942P + T941G + A944P + K986P

35 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVVYHKNNKSWM  
 ESEFRVYSSANNCTFEYVSQPFLLMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRDLPGGFSALEPLVDLP  
 INITRFQTLALHRSYLTGDDSSSGWTAGAAAYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN  
 40 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGNYLYRLFRKSNLKPFR  
 DISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
 NGLTGTGVLTESNKKFLPFQGFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVTGTNTSNQVAVLYQNVNCTEV  
 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQNTSPRRARSVASQSIIAYTM  
 SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
 45 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF  
 NGLTVLPPLLTDEMQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNQSAI  
 GKIQDSLSSGPGALGLQDVVNQNAQALNTLVKQLSSNFGAIVSSVNDILSRDPVEAEVQIDRLITGRLQSLQTYVT  
 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH  
 50 GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

SEQ ID NO 77: SEQ ID NO 5 + D614N + A892P + A942P + S943G + A944P + K986P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK  
 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVVYHKNKSWM  
 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG  
 5 INITRFQTLALHRSYLTGDSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG  
 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN  
 LCFTNVYADSFVIRGEVRQIAPGQTGKIADYNYKLDDFTGCVIWNNSNLDKVGNGYNYLYRLFRKSNLKPFR  
 DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN  
 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
 10 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTM  
 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLQYGSFCTQLNRALTGIAVEQDK  
 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSPKSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF  
 NGTLVLPPLLTDEMIQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI  
 GKIQDSLSTPGPLGLQDVVNQNAQALNTLVKQLSSNFGAIVSVLNDILSRDLPVEAEVQIDRLITGRQLSLQTYVT  
 15 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKYHLMSPQSPHGVVFLHVTYVPAQEKNFHTTAPAICH  
 GKAHFPREGVFSNGTHWFTVQRNFYEPQIITDNTFVSGNCDVVIGVNNNTVYDPLQPELDSFKEELDKYFNHT  
 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

20 SEQ ID NO 78: SEQ ID NO 5 + T941G + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK  
 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVVYHKNKSWM  
 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG  
 25 INITRFQTLALHRSYLTGDSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG  
 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN  
 LCFTNVYADSFVIRGEVRQIAPGQTGKIADYNYKLDDFTGCVIWNNSNLDKVGNGYNYLYRLFRKSNLKPFR  
 DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN  
 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV  
 30 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTM  
 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLQYGSFCTQLNRALTGIAVEQDK  
 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSPKSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF  
 NGTLVLPPLLTDEMIQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI  
 GKIQDSLSSGASALGLQDVVNQNAQALNTLVKQLSSNFGAIVSVLNDILSRDLPKPEAEVQIDRLITGRQLSLQTYVT  
 35 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKYHLMSPQSPHGVVFLHVTYVPAQEKNFHTTAPAICH  
 GKAHFPREGVFSNGTHWFTVQRNFYEPQIITDNTFVSGNCDVVIGVNNNTVYDPLQPELDSFKEELDKYFNHT  
 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

40 SEQ ID NO 79: SEQ ID NO 5 + S943G + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK  
 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVVYHKNKSWM  
 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG  
 45 INITRFQTLALHRSYLTGDSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG  
 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN  
 LCFTNVYADSFVIRGEVRQIAPGQTGKIADYNYKLDDFTGCVIWNNSNLDKVGNGYNYLYRLFRKSNLKPFR  
 DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN  
 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV  
 50 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTM  
 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLQYGSFCTQLNRALTGIAVEQDK  
 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSPKSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF  
 NGTLVLPPLLTDEMIQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI

GKIQDSLSTAGALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKPEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFVSNGTHWFTVQRNFYEPQIITDNTFVSGNCDVVIGVNNNTVYDPLQPELDSFKEELDKYFNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

5

SEQ ID NO 80: SEQ ID NO 5 + D614N + A892P + A942P + T941G + V987P

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
10 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVVYHKNNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG  
INITRQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTEVEG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVRIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGYNYLYRFRKSNLKPFR  
15 DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN  
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQNTSPRRARSVASQSIIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLDAGFIKQYGDCLGDIARDLCAQKF  
20 NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSLSSGSPALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKPEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFVSNGTHWFTVQRNFYEPQIITDNTFVSGNCDVVIGVNNNTVYDPLQPELDSFKEELDKYFNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

25

SEQ ID NO 81: SEQ ID NO 5 + D614N + A892P + A942P + S943G + V987P

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
30 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVVYHKNNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG  
INITRQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTEVEG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND  
LCFTNVYADSFVIRGDEVRIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGYNYLYRFRKSNLKPFR  
35 DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN  
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQNTSPRRARSVASQSIIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLDAGFIKQYGDCLGDIARDLCAQKF  
40 NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSLSTPGALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKPEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFVSNGTHWFTVQRNFYEPQIITDNTFVSGNCDVVIGVNNNTVYDPLQPELDSFKEELDKYFNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

45

SEQ ID NO 82: SEQ ID NO 5 + D614N + A892P + A942P + T941G + S943G + V987P

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
50 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVVYHKNNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG  
INITRQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTEVEG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGNGYNYLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQGFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQNTSPRRARSVASQSIAYTM  
5 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF  
NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSLSSGPGALGKLQDVVNQNAQALNTLVKQLSSNFGAIVSVLNDILSRDLKPEAEVQIDRLITGRLQSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
10 GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

SEQ ID NO 83: SEQ ID NO 5 + D614N + A892P + A942P + T941G + A944P + V987P

15 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVVYHKNNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPOGFSALEPLVDLP  
INITRFQTLALHRSYLTGDSGSGWTAGAAAYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLKSFTEV  
20 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSP  
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGNGYNYLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQGFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQNTSPRRARSVASQSIAYTM  
25 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF  
NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSLSSGSPGLGKLQDVVNQNAQALNTLVKQLSSNFGAIVSVLNDILSRDLKPEAEVQIDRLITGRLQSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
30 GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

SEQ ID NO 84: SEQ ID NO 5 + D614N + A892P + A942P + S943G + A944P + V987P

35 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVVYHKNNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPOGFSALEPLVDLP  
INITRFQTLALHRSYLTGDSGSGWTAGAAAYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLKSFTEV  
40 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSP  
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGNGYNYLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQGFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQNTSPRRARSVASQSIAYTM  
45 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF  
NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSLSTPGPLGKLQDVVNQNAQALNTLVKQLSSNFGAIVSVLNDILSRDLKPEAEVQIDRLITGRLQSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
50 GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

SEQ ID NO 85: SEQ ID NO 5 + T941G + K986P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVVYHKNKNSWM  
5 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSEKTKLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN  
LCFTNVYADSFVIRGDEVQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
10 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF  
NGLTVLPPLLTDEMIQAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTVQNVLYENQKLIANQFNSAI  
15 GKIQDSLSSGASALGLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAPHGVVFLHVTYVPAQEKNFHTTAPAICH  
GKAHFPREGVFSVNGTHWFTVQRNFYEPQIITDNTFVSGNCDVVIGVNNTVYDPLQPELDSFKEELDKYFNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

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SEQ ID NO 86: SEQ ID NO 5 + S943G + K986P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVVYHKNKNSWM  
25 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSEKTKLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN  
LCFTNVYADSFVIRGDEVQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
30 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF  
NGLTVLPPLLTDEMIQAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTVQNVLYENQKLIANQFNSAI  
35 GKIQDSLSTAGALGLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAPHGVVFLHVTYVPAQEKNFHTTAPAICH  
GKAHFPREGVFSVNGTHWFTVQRNFYEPQIITDNTFVSGNCDVVIGVNNTVYDPLQPELDSFKEELDKYFNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

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SEQ ID NO 87: SEQ ID NO 5 + D614N + A892P + A942P + T941G + K986P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVVYHKNKNSWM  
45 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSEKTKLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN  
LCFTNVYADSFVIRGDEVQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
50 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPRRARSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF

5 NGLTVLPPLLTDEMQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN  
GKIQDLSLSSGPGALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFVSNHGWFTVQRNFYEPQIITDNTFVSGNCDVVIGVNNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

SEQ ID NO 88: SEQ ID NO 5 + D614N + A892P + A942P + S943G + K986P + V987P

10 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTESNIIRGWIFGTTLDSKTQSLIVNNATNVVIVKCEFCNDPFLGVYVYHKNKNSWM  
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
15 IQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN  
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGYNYLYRFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN  
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQNTSPRRARSVASQSIIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK  
20 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLDAGFIKQYGDCLGDIARDLCAQKF  
NGLTVLPPLLTDEMQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN  
GKIQDLSLSTPGALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
25 GKAHFPREGVFVSNHGWFTVQRNFYEPQIITDNTFVSGNCDVVIGVNNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

SEQ ID NO 89: SEQ ID NO 5 + D614N + A892P + A942P + T941G + S943G + K986P + V987P

30 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTESNIIRGWIFGTTLDSKTQSLIVNNATNVVIVKCEFCNDPFLGVYVYHKNKNSWM  
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
35 IQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN  
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGYNYLYRFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN  
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQNTSPRRARSVASQSIIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK  
40 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLDAGFIKQYGDCLGDIARDLCAQKF  
NGLTVLPPLLTDEMQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN  
GKIQDLSLSSGPGALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
45 GKAHFPREGVFVSNHGWFTVQRNFYEPQIITDNTFVSGNCDVVIGVNNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

SEQ ID NO 90: SEQ ID NO 5 + D614N + A892P + A942P + T941G + A944P + K986P + V987P

50 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTESNIIRGWIFGTTLDSKTQSLIVNNATNVVIVKCEFCNDPFLGVYVYHKNKNSWM  
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG

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IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLND  
LCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVG GNYNYLRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSEYCDIPGAGICASYQTQTN SPRRARSVASQSI IAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSM TKTSDVCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVT LADAGFIKQYGDCLG DIAARDLICAQKF  
NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SAI  
GKIQDSLSSGSPGLKQLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSR LDPPEAEVQIDRLITGR LQSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSF PQSAPHGVVFLHVTYVPAQEKNF TTA PAICH D  
GKAHFPREGV FVSNGTHW FVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

15 SEQ ID NO 91: SEQ ID NO 5 + D614N + A892P + A942P + S943G + A944P + K986P + V987P

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MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTW FHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIKVCEFCNDPFLGVVYHKNNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLV RDLPQGFSALEPLVDLP I G  
INITRFQTL LALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLND  
LCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVG GNYNYLRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSEYCDIPGAGICASYQTQTN SPRRARSVASQSI IAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSM TKTSDVCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVT LADAGFIKQYGDCLG DIAARDLICAQKF  
NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SAI  
GKIQDSLSSSTPGPLKQLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSR LDPPEAEVQIDRLITGR LQSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSF PQSAPHGVVFLHVTYVPAQEKNF TTA PAICH D  
GKAHFPREGV FVSNGTHW FVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

35 SEQ ID NO 92: SEQ ID NO 7 + T941G

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MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTW FHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIKVCEFCNDPFLGVVYHKNNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLV RDLPQGFSALEPLVDLP I G  
INITRFQTL LALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLND  
LCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVG GNYNYLRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSEYCDIPGAGICASYQTQTN SPRAGSVASQSI IAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSM TKTSDVCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVT LADAGFIKQYGDCLG DIAARDLICAQKF  
NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SAI  
GKIQDSLSSGASALGKQLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSR LDKVEAEVQIDRLITGR LQSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSF PQSAPHGVVFLHVTYVPAQEKNF TTA PAICH D  
GKAHFPREGV FVSNGTHW FVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

SEQ ID NO 93: SEQ ID NO 7 + S943G

5 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVVYHKNNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP  
10 INITRFQTLALHRSYLTGDSGSGWTAGAAAYVGYLQPRTFLLKYNENGITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP  
15 DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQTNSPSRAGSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRLTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF  
20 NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSLSTAGALGLQDVVNQNAQALNTLVKQLSSNFGAIVSVLNDILSRDKVEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFHTAPAICH  
GKAHFPREGVFSNGTHWFTQRNFYEPQIITDNTFVSGNCDVVIGVNNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

SEQ ID NO 94: SEQ ID NO 7 + D614N + A892P + A942P + T941G

25 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVVYHKNNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP  
INITRFQTLALHRSYLTGDSGSGWTAGAAAYVGYLQPRTFLLKYNENGITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN  
30 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP  
DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQTNSPSRAGSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRLTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF  
35 NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSLSSGPSALGLQDVVNQNAQALNTLVKQLSSNFGAIVSVLNDILSRDKVEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFHTAPAICH  
GKAHFPREGVFSNGTHWFTQRNFYEPQIITDNTFVSGNCDVVIGVNNNTVYDPLQPELDSFKEELDKYFKNHT  
40 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

SEQ ID NO 95: SEQ ID NO 7 + D614N + A892P + A942P + S943G

45 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVVYHKNNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP  
INITRFQTLALHRSYLTGDSGSGWTAGAAAYVGYLQPRTFLLKYNENGITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP  
50 DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQTNSPSRAGSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRLTGIAVEQDK

NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF  
NGLTVLPPLLTDEMQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSSLSTPGALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRQLSLQTYVT  
5 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFVSNNGTHWFTVQRNFYEPQIITDNTFVSGNCDVVIGVNNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

SEQ ID NO 96: SEQ ID NO 7 + D614N + A892P + A942P + T941G + S943G

10

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTLLDSKTQSLIVNNATNVVIVKVEFCQFNDPFLGVYHKNKNSWM  
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP  
15 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGNYLYRFRKSNLKP  
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF  
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM  
20 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF  
NGLTVLPPLLTDEMQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSSLSSGPGALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
25 GKAHFPREGVFVSNNGTHWFTVQRNFYEPQIITDNTFVSGNCDVVIGVNNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

SEQ ID NO 97: SEQ ID NO 7 + D614N + A892P + A942P + T941G + A944P

30

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTLLDSKTQSLIVNNATNVVIVKVEFCQFNDPFLGVYHKNKNSWM  
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP  
35 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGNYLYRFRKSNLKP  
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF  
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM  
40 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF  
NGLTVLPPLLTDEMQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSSLSSGPGALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRQLSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
45 GKAHFPREGVFVSNNGTHWFTVQRNFYEPQIITDNTFVSGNCDVVIGVNNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

SEQ ID NO 98: SEQ ID NO 7 + D614N + A892P + A942P + S943G + A944P

50

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTLLDSKTQSLIVNNATNVVIVKVEFCQFNDPFLGVYHKNKNSWM  
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP  
50 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG

INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSEKCTLKSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN  
5 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMKTSDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF  
NGLTVLPPLLTDEMQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN  
10 GKIQDLSSTPGPLGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRQLSQTYYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGGYHLMSPQSPHGVVFLHVTYVPAQEKNFPTAPACHD  
GKAHFPREGVFSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

15

SEQ ID NO 99: SEQ ID NO 7 + T941G + K986P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFFHAIHVS  
RFDNPVLPFNDGVYFASTSEKSNIRGWIFGTTLDSTQSLIVNNATNVVIVCEFCNDPFLGVYHKNKNSWM  
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDPQGFSALEPLVDLP  
20 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSEKCTLKSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN  
25 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMKTSDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF  
NGLTVLPPLLTDEMQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN  
30 GKIQDLSSTGASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPVEAEVQIDRLITGRQLSQTYYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGGYHLMSPQSPHGVVFLHVTYVPAQEKNFPTAPACHD  
GKAHFPREGVFSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

35

SEQ ID NO 100: SEQ ID NO 7 + S943G + K986P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFFHAIHVS  
RFDNPVLPFNDGVYFASTSEKSNIRGWIFGTTLDSTQSLIVNNATNVVIVCEFCNDPFLGVYHKNKNSWM  
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDPQGFSALEPLVDLP  
40 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSEKCTLKSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN  
45 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMKTSDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF  
NGLTVLPPLLTDEMQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN  
50 GKIQDLSSTAGALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPVEAEVQIDRLITGRQLSQTYYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGGYHLMSPQSPHGVVFLHVTYVPAQEKNFPTAPACHD  
GKAHFPREGVFSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

SEQ ID NO 101: SEQ ID NO 7 + D614N + A892P + A942P + T941G + K986P

5 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKCEFCNDPFLGVVYHKNNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPGGFSALEPLVDLP  
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
10 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKTLND  
LCFTNVYADSFVIRGDEVRIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKP  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF  
NGLTGTGVLTESNKKFLPFQGFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQNTNSPSRAGSVASQSIAYTM  
15 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF  
NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN  
GKIQDSLSSGPSALGKLQDVVNQNAQALNTLVKQLSSNFGAIVSSVNDILSRDPVEAEVQIDRLITGRQLSQT  
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFSVNGTHWFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

SEQ ID NO 102: SEQ ID NO 7 + D614N + A892P + A942P + S943G + K986P

25 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKCEFCNDPFLGVVYHKNNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPGGFSALEPLVDLP  
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
30 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKTLND  
LCFTNVYADSFVIRGDEVRIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKP  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF  
NGLTGTGVLTESNKKFLPFQGFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQNTNSPSRAGSVASQSIAYTM  
35 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF  
NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN  
GKIQDSLSTPGALGKLQDVVNQNAQALNTLVKQLSSNFGAIVSSVNDILSRDPVEAEVQIDRLITGRQLSQT  
40 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFSVNGTHWFTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

SEQ ID NO 103: SEQ ID NO 7 + D614N + A892P + A942P + T941G + S943G + K986P

45 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKCEFCNDPFLGVVYHKNNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPGGFSALEPLVDLP  
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
50 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKTLND  
LCFTNVYADSFVIRGDEVRIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKP  
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF  
NGLTGTGVLTESNKKFLPFQGFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQNTNSPSRAGSVASQSIAYTM

- 5 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF  
NGLTVLPPLLTDEMQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDLSLSSGPGALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPVEAEVQIDRLITGRQLSLQTYVT  
5 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFVSNNGTHWFTVQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ
- 10 SEQ ID NO 104: SEQ ID NO 7 + D614N + A892P + A942P + T941G + A944P + K986P
- 15 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAHIVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVVYHKNKNSWM  
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRDLPPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGVLQPRFTLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN  
LCFTNVYADSFVIRGDEVQIAPGQGTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
20 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPIGAGICASYQTQTNPSRAGSVASQSIIAYTM  
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF  
NGLTVLPPLLTDEMQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDLSLSSGPGALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPVEAEVQIDRLITGRQLSLQTYVT  
25 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFVSNNGTHWFTVQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ
- 30 SEQ ID NO 105: SEQ ID NO 7 + D614N + A892P + A942P + S943G + A944P + K986P
- 35 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAHIVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVVYHKNKNSWM  
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRDLPPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGVLQPRFTLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN  
LCFTNVYADSFVIRGDEVQIAPGQGTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
40 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPIGAGICASYQTQTNPSRAGSVASQSIIAYTM  
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF  
NGLTVLPPLLTDEMQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDLSLSTPGPLGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPVEAEVQIDRLITGRQLSLQTYVT  
45 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFVSNNGTHWFTVQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ
- 50 SEQ ID NO 106: SEQ ID NO 7 + T941G + V987P
- MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAHIVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVVYHKNKNSWM

ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKP  
5 DISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN  
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQNTNSPSRAGSVASQSIIAYTM  
SLGAENSVAYSNNISIAIPTNFTISVTTEILPVSMKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF  
10 NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN  
GKIQDSSLSSGASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKPEAEVQIDRLITGRLQSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH  
GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGVNNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

15

SEQ ID NO 107: SEQ ID NO 7 + S943G + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAHIVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKCEFCNDPFLGVYHKNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKP  
25 DISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN  
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQNTNSPSRAGSVASQSIIAYTM  
SLGAENSVAYSNNISIAIPTNFTISVTTEILPVSMKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF  
30 NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN  
GKIQDSSLSTAGALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKPEAEVQIDRLITGRLQSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH  
GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGVNNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

35

SEQ ID NO 108: SEQ ID NO 7 + D614N + A892P + A942P + T941G + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAHIVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKCEFCNDPFLGVYHKNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKP  
45 DISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN  
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQNTNSPSRAGSVASQSIIAYTM  
SLGAENSVAYSNNISIAIPTNFTISVTTEILPVSMKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF  
50 NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN  
GKIQDSSLSSGASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKPEAEVQIDRLITGRLQSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH

GKAHFPREGVFVSNGTHWVFTQQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

5 SEQ ID NO 109: SEQ ID NO 7 + D614N + A892P + A942P + S943G + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFQCNDFLGVVYHKNNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPGGFSALEPLVDLP  
10 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP  
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLICAQKF  
NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSLSTPGALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKPEAEVQIDRLITGRQLSLQTYVT  
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGVVFLHVTYVPAQEKNTTAPAICHD  
GKAHFPREGVFVSNGTHWVFTQQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

25 SEQ ID NO 110: SEQ ID NO 7 + D614N + A892P + A942P + T941G + S943G + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFQCNDFLGVVYHKNNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPGGFSALEPLVDLP  
30 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP  
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
35 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLICAQKF  
NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSLSSGPGALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKPEAEVQIDRLITGRQLSLQTYVT  
40 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGVVFLHVTYVPAQEKNTTAPAICHD  
GKAHFPREGVFVSNGTHWVFTQQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

45 SEQ ID NO 111: SEQ ID NO 7 + D614N + A892P + A942P + T941G + A944P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFQCNDFLGVVYHKNNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPGGFSALEPLVDLP  
50 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP  
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF

NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGNSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQTNSPSRAGSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF  
5 NGLTVLPPLLTDEMQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSSLSSGSPGLKLDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKPEAEVQIDRLITGRLQSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFSNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGVNNNTVYDPLQPELDSFKEELDKYFNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

10

SEQ ID NO 112: SEQ ID NO 7 + D614N + A892P + A942P + S943G + A944P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK  
15 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM  
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPQGFSALEPLVDLP  
INITRFQTLALHRSYLTGDDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSNLKP  
20 DISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGNSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQTNSPSRAGSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF  
25 NGLTVLPPLLTDEMQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSSLSTPGPLKLDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKPEAEVQIDRLITGRLQSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFSNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGVNNNTVYDPLQPELDSFKEELDKYFNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

30

SEQ ID NO 113: SEQ ID NO 7 + T941G + K986P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK  
35 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM  
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPQGFSALEPLVDLP  
INITRFQTLALHRSYLTGDDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSNLKP  
40 DISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGNSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQTNSPSRAGSVASQSIAYTM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF  
45 NGLTVLPPLLTDEMQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDSSLSSGASALGKLDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH  
GKAHFPREGVFSNGTHWVFTQRFYEPQIITDNTFVSGNCDVVIGVNNNTVYDPLQPELDSFKEELDKYFNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

50

SEQ ID NO 114: SEQ ID NO 7 + S943G + K986P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYPDKVFRSSVLHSTQDLFLPFFSNVTFHAIHVSNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVVYHKNNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLTGDSGGWTAGAAAYYVGYLQPRFTLLKYNENGITDAVDCALDPLSEKCTLSFTVEKG  
5 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQNTSPSRAGSVASQSIIAYTM  
10 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF  
NGLTVLPPLLTDEMIQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN  
GKIQDSLSTAGALGLQDVVNQNAQALNTLVKQLSSNFGAIVSVLNDILSRDLPPEAEVQIDRLITGRLQSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPACHD  
15 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGVNNNTVYDPLQPELDSFKEELDKYFNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

SEQ ID NO 115: SEQ ID NO 7 + D614N + A892P + A942P + T941G + K986P + V987P

20 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYPDKVFRSSVLHSTQDLFLPFFSNVTFHAIHVSNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVVYHKNNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLTGDSGGWTAGAAAYYVGYLQPRFTLLKYNENGITDAVDCALDPLSEKCTLSFTVEKG  
25 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQNTSPSRAGSVASQSIIAYTM  
30 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF  
NGLTVLPPLLTDEMIQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN  
GKIQDSLSSGPSALGLQDVVNQNAQALNTLVKQLSSNFGAIVSVLNDILSRDLPPEAEVQIDRLITGRLQSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPACHD  
35 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGVNNNTVYDPLQPELDSFKEELDKYFNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

SEQ ID NO 116: SEQ ID NO 7 + D614N + A892P + A942P + S943G + K986P + V987P

40 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYPDKVFRSSVLHSTQDLFLPFFSNVTFHAIHVSNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVVYHKNNKSWM  
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG  
INITRFQTLALHRSYLTGDSGGWTAGAAAYYVGYLQPRFTLLKYNENGITDAVDCALDPLSEKCTLSFTVEKG  
45 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSNLKPFR  
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN  
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQNTSPSRAGSVASQSIIAYTM  
50 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF  
NGLTVLPPLLTDEMIQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN  
GKIQDSLSTPGALGLQDVVNQNAQALNTLVKQLSSNFGAIVSVLNDILSRDLPPEAEVQIDRLITGRLQSLQTYVT

QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFHTTAPAICH  
D  
GKAHFPREGV FVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

5

SEQ ID NO 117: SEQ ID NO 7 + D614N + A892P + A942P + T941G + S943G + K986P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVS  
GTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFQCNDFPLGVYHKNKNSW  
M  
10 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFS  
ALEPLVDLP  
IG  
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGITITDAVDCALDPLSE  
TKCTLKSF  
TVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFK  
CYGVSPTK  
LND  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRL  
FRKSNLKP  
FER  
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTN  
LVKNKCVN  
FNF  
15 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFEGGVSVITPGTNTSNQ  
VAVLYQN  
VNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSEYCDIPGAGICASYQTQTNSPSRAGS  
VASQSIIAY  
TM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLN  
RALTGIAVE  
QDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGD  
CLGDIAARD  
LICAQKF  
NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVGTQNVLYEN  
QKLIANQFN  
SAI  
20 GKIQDSLSSGPGALGLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLIT  
GRLQSLQT  
YVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEK  
NFHTTAPAICH  
D  
GKAHFPREGV FVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

25

SEQ ID NO 118: SEQ ID NO 7 + D614N + A892P + A942P + T941G + A944P + K986P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVS  
GTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFQCNDFPLGVYHKNKNSW  
M  
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFS  
ALEPLVDLP  
IG  
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGITITDAVDCALDPLSE  
TKCTLKSF  
TVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFK  
CYGVSPTK  
LND  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRL  
FRKSNLKP  
FER  
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTN  
LVKNKCVN  
FNF  
35 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFEGGVSVITPGTNTSNQ  
VAVLYQN  
VNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSEYCDIPGAGICASYQTQTNSPSRAGS  
VASQSIIAY  
TM  
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLN  
RALTGIAVE  
QDK  
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGD  
CLGDIAARD  
LICAQKF  
NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVGTQNVLYEN  
QKLIANQFN  
SAI  
40 GKIQDSLSSGPGALGLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLIT  
GRLQSLQT  
YVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEK  
NFHTTAPAICH  
D  
GKAHFPREGV FVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

45

SEQ ID NO 119: SEQ ID NO 7 + D614N + A892P + A942P + S943G + A944P + K986P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVS  
GTNGTK  
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFQCNDFPLGVYHKNKNSW  
M  
50 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFS  
ALEPLVDLP  
IG  
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGITITDAVDCALDPLSE  
TKCTLKSF  
TVEKG  
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFK  
CYGVSPTK  
LND  
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRL  
FRKSNLKP  
FER

5 DISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF  
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV  
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTM  
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK  
10 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF  
NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI  
GKIQDLSSTPGPLGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT  
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH  
10 GKAHFPREGVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT  
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ