

Stabilized Coronavirus Spike protein fusion proteins

The present invention relates to the field of medicine. The invention in particular relates to stabilized recombinant pre-fusion Coronavirus 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 viruses responsible for mild respiratory tract infections and
10 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 species including cats, dogs, cows, bats, and humans, and avian species. Coronaviruses possess large, trimeric spike glycoproteins (S) that mediate binding to host cell receptors as well as fusion of viral and host cell membranes. The Coronavirus family contains
15 the genera Alphacoronavirus, Betacoronavirus, Gammacoronavirus, and Deltacoronavirus. These viruses cause a range of diseases including enteric and respiratory diseases. The host range is primarily determined by the viral spike protein (S protein), which mediates entry of the virus into host cells. Coronaviruses that can infect humans are found both in the genus Alphacoronavirus and the genus Betacoronavirus. Known coronaviruses of the genus
20 Betacoronavirus that cause respiratory disease in humans include SARS-CoV, MERS-CoV, HCoV-OC43 and HCoV-HKU1, and the currently circulating SARS-CoV-2.

SARS-CoV-2 is a coronavirus that emerged in humans from an animal reservoir in 2019 and rapidly spread globally. SARS-CoV-2 is a Betacoronavirus, like MERS-CoV and SARS-CoV, all of which have their origin in bats. The name of the disease caused by the

virus is coronavirus disease 2019, abbreviated as COVID-19. Symptoms of COVID-19 range from mild symptoms to severe illness and death for confirmed COVID-19 cases.

It is well known that viruses constantly change through mutation, and new virus variants are expected to occur over time. Sometimes new variants emerge and disappear.

- 5 Other times, new variants emerge and persist. Multiple variants of the virus that causes COVID-19 have already been identified globally during this pandemic. Scientists are continuously monitoring changes in the virus, including changes to the spike protein on the surface of the virus. In collaboration with a SARS-CoV-2 Interagency Group (SIG), CDC established 3 classifications for the SARS-CoV-2 variants being monitored: Variant of
- 10 Interest (VOI), Variant of Concern (VOC), and Variant of High Consequence (VOHC). There are currently several VOCs identified, including:

B.1.1.7: This variant was initially detected in the UK.

B.1.351: This variant was initially detected in South Africa in December 2020.

- P.1: This variant was initially identified in travelers from Brazil, who were tested
- 15 during routine screening at an airport in Japan, in early January.

B.1.427 and B.1.429: These two variants were first identified in California in February 2021 and were classified as VOCs in March 2021.

The B.1.526, B.1.526.1, B.1.525, B.1.617, B.1.617.1, B.1.617.2, B.1.617.3, and P.2 variants circulating in the United States are classified as variants of interest.”

- 20 The B.1.1.7, B.1.351, P.1, B.1.427, and B.1.429 variants circulating in the United States are classified as variants of concern.

In the case 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
5 bind to human angiotensin-converting enzyme 2 (ACE2) (Hoffmann et. al. (2020); Wrapp et. al. (2020)).

Coronaviridae 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
10 many other class I fusion proteins, Coronavirus 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
15 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
20 peptide (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
25 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
5 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 conformation can induce an efficacious immune response.

10 In recent years several attempts have been made to stabilize various class I fusion proteins, including Coronavirus 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 approach has also proved successful for Coronavirus S proteins, as shown for SARS-CoV,
15 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 Coronavirus 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 isolation, further stabilization is desired.

20 Since the novel SARS-CoV-2 virus was first observed in humans in late 2019, over 154 million people have been infected and more than 3 million 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 coronavirus induced disease (COVID-19), leading to a large unmet medical need. Since emerging
25 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

5 The invention provides recombinant SARS-CoV-2 S proteins that have improved trimer yields and/or improved (thermal) stability as compared to previously described SARS-CoV-2 S proteins.

 The present invention also 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
10 fragments thereof.

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

 The resulting stable pre-fusion SARS-CoV-2 S protein trimers are useful for immunization (vaccination) purposes, e.g. to improve chances of inducing broadly
15 neutralizing antibodies and reducing induction of non-neutralizing and weakly neutralizing antibodies upon administration of the recombinant stabilized SARS-CoV-2 S protein trimers or nucleic acid encoding the stabilized SARS-CoV-2 S protein trimers.

 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
20 such nucleic acid molecules.

 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 molecule and/or a vector, as described herein.

The invention also provides compositions for use in inducing an immune response
5 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-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
10 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 SARS-CoV-2 virus.

In particular aspects, the invention relates to methods for inducing anti-SARS-CoV-2
15 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
20 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.

In another general aspect, the invention relates to an isolated nucleic acid molecule encoding a recombinant SARS-CoV-2 S protein of the invention and vectors comprising the isolated nucleic acid molecule operably linked to a promoter. In one embodiment, the vector is a viral vector. In another embodiment, the vector is an expression vector. In one preferred
5 embodiment, the viral vector is an adenovirus vector.

Another general aspect relates to a host cell comprising the isolated nucleic acid molecule or vector encoding the recombinant SARS-CoV-2 S protein of the invention. Such host cells can be used for recombinant protein production, recombinant protein expression, or the production of viral particles.

10 Another general aspect relates to methods of producing a recombinant SARS-CoV-2 S protein, comprising growing a host cell comprising an isolated nucleic acid molecule or vector encoding the recombinant SARS-CoV-2 S protein of the invention under conditions suitable for production of the recombinant SARS-CoV-2 S protein.

15 **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.

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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

5 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.

10 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 a single amino acid substitution, as indicated in the figure, introduced into the backbone of unstable uncleaved SARS-CoV-2 S ectodomain (SEQ ID NO: 2) (Furin KO, left panel) and into the backbone of the semi-stable uncleaved SARS-CoV-2 S with the

15 double proline mutations in the hinge loop at position 986 and 987 (SEQ ID NO: 3) (Furin KO + PP, right panel). Analysis was performed on crude cell culture supernatants.

FIG. 4: Analytical SEC profile of semi-stabilized uncleaved SARS-CoV-2 S with two

20 stabilizing mutations to Proline in the hinge loop (+PP) (SEQ ID NO: 3) (A-C) and unstable uncleaved SARS-CoV-2 S protein (SEQ ID NO: 2) (D-F) (dashed lines), compared to variants with indicated point mutations (A, D) A892P, (B, E) A942P, (C, F) D614N in black, D614M in dark grey and D614L in light grey (solid lines). Analysis was performed on crude cell culture supernatants. The peak at 5 minutes corresponds to the S trimer. G) SEC-

25 MALS with purified stabilized S protein with A942P mutation (SEQ ID NO: 5). SEC signal

is shown in grey thick line and corresponding to the left axis. The black thin line shows the molar mass traces (right y axis). The dn/dc value used is 0.185.

FIG. 5: Percentage of S trimer expression for S proteins with indicated mutations as measured

5 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 single amino acid substitution 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, left panel) and into the backbone of semi-stable uncleaved SARS-CoV-2 S
10 with the double proline in the hinge loop at position 986 and 987 (SEQ ID NO: 3) (Furin KO + PP, right panel). Analysis was performed on crude cell culture supernatants.

FIG 6: Analytical SEC profile of semi-stabilized uncleaved SARS-CoV2 S + PP (SEQ ID

NO: 3) (A-D) and unstable uncleaved SARS-CoV2 S protein (SEQ ID NO: 2) (E-H) (dashed
15 lines), compared to variants with indicated point mutation or disulfide bridge (solid line). Analysis was performed on crude cell culture supernatants. The peak at 5 minutes corresponds to the S trimer.

FIG. 7: Percentage of S trimer expression for S proteins with indicated mutations as measured

20 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 single amino acid substitution as indicated in the figure, introduced into the backbone of unstable uncleaved SARS-CoV2 S ectodomain (SEQ ID NO: 2) (A). Analytical SEC profile of unstable uncleaved SARS-CoV2 S (SEQ ID NO: 2) (dashed lines), compared to
25 variants with indicated point mutation (solid line). Analysis was performed on crude cell

culture supernatants. The peak at 5 minutes corresponds to the S trimer. Analysis was performed on crude cell culture supernatants.

FIG 8: Temperature stability of purified S trimers as measured by DSC. Two melting events are indicated by Tm1 and Tm2. Uncleaved SARS2-S variants corresponding to SEQ ID NO: 2 (comprising a furin KO), with one stabilizing proline mutation in the hinge loop (furin KO K986P or furin KO V987P), and both proline mutations in the hinge loop (SEQ ID NO: 3, S-2P) (A). Uncleaved variants with indicated mutations in S1 (B) and uncleaved variants with indicated mutations in S2 (C).

FIG 9: Cell-cell fusion assay. Full-length wildtype SARS-CoV-2 spike protein and variants thereof (indicated in boxes within the images), human ACE2, human TMPRSS2 and GFP were co-expressed in HEK293 cells. Redistribution of the GFP signal was used to visualize syncytia formation. The furin KO, the PP mutations and the two cystines completely abolish fusogenicity, whereas all the individual point mutants still allow fusion to occur. This implies that the single point mutants still allow the S protein to sample all possible conformational intermediates between prefusion and postfusion states.

FIG. 10: Analytical SEC profile of uncleaved SARS-CoV2 S (SEQ ID NO: 2 (dashed lines)), compared to variants with indicated point mutations (solid lines) (A). The recombinant S proteins tested contain single amino acid substitution or multiple mutations as indicated in the figure. The peak at 5 minutes corresponds to the S trimer. Amount of ACE2-Fc binding for S proteins with indicated mutations as measured by AlphaLISA assay compared with control unstable uncleaved SARS-CoV-2 S (with furin site mutation) (SEQ ID NO: 2) (B). Analysis was performed on crude cell culture supernatants. Analytical SEC with comparison of semistabilized S trimer ((K986P+V987P, SEQ ID NO: 3) with variants containing indicated

four stabilizing mutations with or without (DF) foldon (C). Temperature stability of purified uncleaved S trimers with indicated stabilizing mutations as measured by DSC. Variants without foldon trimerization domain are indicated with no-Fd (D).

- 5 FIG. 11: Freeze-thaw stability of purified uncleaved S trimers with indicated stabilizing mutations as measured by analytical SEC. Chromatograms are shown for non-frozen 1 x frozen and 3 x frozen. Right panel is S trimer without foldon trimerization site (delta foldon).

- FIG. 12: Binding of SAD-S35, ACE2-Fc, and CR3022 to 986P+987P variants, novel single
10 point mutations and disulfide bridge, and variants with combination of mutations measured with BioLayer Interferometry, showing the initial slope at the start of binding (A-C). Binding at equilibrium of S309, ACE2 and CR3022 with the semistabilized variant (FurinKO+PP, SEQ ID NO:3) and the stabilized variant with 4 stabilizing mutations without foldon after 2 weeks of storage at 4 degrees (D).

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- FIG. 13: Western blot stained with both 1A9 (GeneTex) antibody detecting S2 of the SARS-CoV-2 spike protein and anti-Beta actin (AC-15) primary antibody (Abcam, ab6276). Since the four full length spikes 660, 662, 007 and 664 all have a furin cleavage site knock out, the intact S protein is detected. Cell culture supernatants were loaded, which could contain
20 exosomes, produced after the membranes of the Expi293F cells are saturated with incorporated spikes. A molecular weight marker was loaded in lane 1. The lane indicated with pcDNA shows supernatant of cells that were transfected with empty pcDNA vector.

- FIG. 14: Luminescence intensities measured with cell-based ELISA (CBE). Luminescence
25 was calculated as an average of a duplicate.

FIG. 15: Binding of a panel of antibodies (on X-axis) to three proteins used for immunization of mice, measured with BioLayer Interferometry, showing the initial slope V_0 at the start of binding.

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FIG 16: **A.** SARS-CoV-2 L-0008 (lineage B.1) isolate neutralizing antibody titers were measured by a wild-type VNA (wtVNA) at day 27. As the number of samples for the wtVNA was limited not all samples were measured for the 0.5 μ g COR201225 (n=5), COR200619 (n=5) and COR200627 (n=6) groups. SARS-CoV-2 B.1 Spike protein

10 neutralizing antibody titers induced by the invention as measured with a lentiviral pseudo particle neutralization assay (psVNA) at **B.** day 27 and **C.** day 41. 2 mice were excluded as there was not enough serum left to perform the psVNA at day 27 on these samples. The value above each x-axis are the group geometric mean titers. Horizontal bars per group denote group geometric means. Dashed horizontal lines denote the Lower Limit Of Detection (LLOD) and the Upper Limit of Detection.

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FIG. 17: Analytical SEC profile of semi-stabilized uncleaved SARS-CoV-2 S with two stabilizing mutations to Proline in the hinge loop (+PP) and a foldon (SEQ ID NO: 3) shown with a dashed line and a more stabilized S protein without the PP and without a foldon shown with a solid line (COR201291).

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FIG. 18: Cryo-EM data processing workflow. A typical micrograph, representing approximately 75% of 9760 micrographs is shown as well as representatives 2D classes. 3D classification was performed to distinguish heterogeneity in the sample and the classes showing the highest resolution were refined.

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FIG. 19: Resolution assessment of cryo-EM structure: A) Local resolution map for closed structure (Full map, slide through, top view) B) Local resolution map for “one up” structure (Full map, slide through, top view) C) Global resolution assessment by Fourier shell correlation at the 0.143 criterion D) Correlations of model vs map by Fourier shell correlation at the 0.5 criterion.

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 to the S2' site the proposed fusion peptide is located at the N-terminus of the refolding region 1 (FIG. 1).

Several vaccines against SARS-CoV-2 infection are currently available. Several different vaccine modalities are possible, such as RNA or vector-based vaccines, and/or subunit vaccines based on purified S protein. Since class I proteins are metastable proteins, 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 the S protein is higher and the conformation of the immunogen resembles the pre-fusion

5 conformation that is recognized by potent neutralizing and protective antibodies. For subunit-based vaccines, stabilizing the pre-fusion S conformation is even more important. In addition, it is important that the stabilized S proteins have improved trimer yields as compared to previously described SARS-CoV-2 S protein trimers. Besides the importance of high expression, which is needed to manufacture a vaccine successfully, maintenance of the

10 trimeric pre-fusion conformation during the manufacturing process and during 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

15 is considerably more labile than the full-length protein and will even more readily refold into the post-fusion end-state. In order to obtain soluble trimeric 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

20 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 provides recombinant SARS-CoV-2 S proteins that have improved trimer yields and/or improved (thermal) stability as compared to previously described SARS-CoV-2 S proteins.

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 P, a mutation of the amino acid at position 892, a mutation of the amino acid at position 614, a mutation at position 572, 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 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 specific amino acids and/or a disulfide bridge at the indicated positions increase the stability of the proteins in the pre-fusion conformation. According to the invention, the specific amino acids 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. In certain embodiments, the proteins comprise an amino acid sequences, wherein the amino acid at position 892 is not alanine (A), the amino acid at position 614 is not aspartic acid (D), the amino acid at position 532 is not Asparagine (N) and/or amino acid at position 572 is not threonine (T).

In certain embodiments, the proteins comprise at least two mutations comprising a mutation of at least one amino acid in the loop region corresponding to amino acid residues 941 – 945 into P, and a mutation selected from the group consisting of a mutation of the amino acid at position 892, a mutation of the amino acid at position 614, a mutation at position 572, a mutation at position 532, a disulfide bridge between residues 880 and 888 and a disulfide bridge between residues 884 and 893.

In certain embodiments, the proteins comprise at least two mutations comprising a mutation of at least one amino acid in the loop region corresponding to amino acid residues 941 – 945 into P, and a mutation selected from the group consisting of a mutation of the amino acid at position 892, a mutation of the amino acid at position 614, a mutations at
5 position 572 and a mutations at position 532, a disulfide bridge between residues 880 and 888 and a disulfide bridge between residues 884 and 893, provided that 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 proteins thus comprise a mutation of at least one amino in
10 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 of the amino acid at position 572, and/or a mutation at position 532, and/or either a disulfide bridge between residues 880 and 888 or a disulfide bridge between residues 884 and 893.

In a preferred embodiment, the disulfide bridge is a disulfide bridge between residues
15 880 and 888. According to the invention it is to be understood that “a disulfide bridge between residues 880 and 880” means that the amino acids at the positions 880 and 888 have been mutated into C. Similarly, it is to be understood that “a disulfide bridge between residues 884 and 893” means that the amino acids at the positions 884 and 893 have been mutated into C

20 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 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.

5 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.

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

The invention thus also provides stabilized, recombinant pre-fusion SARS-CoV-2 S proteins, comprising an S1 and an S2 domain, wherein the amino acid at position 941, 942 or
10 944 is P, the amino acid at position 892 is P, the amino acid at position 614 is N or G, the amino acid at position 572 is I, and/or the amino acid at position 532 is P, and/or comprising a disulfide bridge between residues 880 and 888, and/or a disulfide bridge between residues 884 and 893, wherein the numbering of the amino acid positions is according to the numbering of the amino acid positions in SEQ ID NO: 1.

15 In a preferred embodiment, the amino acid at position 892 is proline (P), the amino acid at position 614 is asparagine (N) or glycine (G), the amino acid at position 942 is proline (P) or the amino acid at position 944 is proline (P).

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
20 of amino acids with a chiral center), or any variants that are not naturally found in proteins, such as e.g. norleucine. Each known natural amino acid has a full name, an abbreviated one letter code, and an abbreviated three letter code, all of which are well known to those of ordinary skill in the art. For example, the three and one letter abbreviated codes used for the twenty naturally occurring amino acids are as follows: alanine (Ala; A), arginine (Arg; R),
25 aspartic acid (Asp; D), asparagine (Asn; N), cysteine (Cys; C), glycine (Gly; G), glutamic acid

(Glu; E), glutamine (Gln; Q), histidine (His; H), isoleucine (Ile; I), leucine (Leu; L), lysine (Lys; K), methionine (Met; M), phenylalanine (Phe; F), proline (Pro; P), serine (Ser; S), threonine (Thr; T), tryptophan (Trp; W), tyrosine (Tyr; Y) and valine (Val; V). Amino acids can be referred to by their full name, one letter abbreviated code, or three letter abbreviated code. 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 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 proteins, and fragments thereof, wherein the amino acid at position 942 is P, the amino acid at position 892 is P, the amino acid at position 614 is N or G, the amino acid at position 532 is P and/or the amino acid at position 572 is I, and/or which comprise a disulfide bridge between residues 880 and 888 or a disulfide bridge between residues 884 and 893, wherein the numbering of the amino acid positions is according to the numbering of the amino acid positions in SEQ ID NO: 1.

In a preferred embodiment, the invention provides SARS-CoV-2 proteins or fragments thereof, wherein the amino acid at position 942 is P, the amino acid at position 614 is N or G, and which comprise a disulfide bridge between residues 880 and 888, 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 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
5 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.

In certain embodiments, the proteins further comprise a mutation of the amino acids at position 986 and/or 987 into proline. In certain embodiments, the amino acid at position 986
10 is not proline. In certain embodiments, the amino acid at position 986 is K and the amino acid at position 987 is P.

In preferred embodiments, the present invention provides recombinant SARS-CoV-2 S proteins, and fragments thereof, comprising a deletion of the furin cleavage site, and wherein the amino acid at position 942 is P, the amino acid at position 892 is P, the amino
15 acid at position 987 is P, wherein the numbering of the amino acid positions is according to the numbering of the amino acid positions in SEQ ID NO: 1.

In another preferred embodiment, the present invention provides recombinant SARS-CoV-2 S proteins, and fragments thereof, comprising a deletion of the furin cleavage site and wherein the amino acid at position 942 is P, the amino acid at position 892 is P, the amino
20 acid at position 614 is N or G, the amino acid at position 987 is P, wherein the numbering of the amino acid positions is according to the numbering of the amino acid positions in SEQ ID NO: 1.

In another preferred embodiment, the SARS-CoV-2 S proteins comprise a deletion of the furin cleavage site and the amino acid at position 942 is P, the amino acid at position 892
25 is P, the amino acid at position 614 is N and the amino acid at position 987 is P.

In another preferred embodiment, the SARS-CoV-2 S proteins comprise a deletion of the furin cleavage site and the amino acid at position 944 is P, the amino acid at position 614 is G, the amino acid at position 572 is I, the amino acid at position 532 is P, and comprises a disulfide bridge between residues 880 and 888, and wherein the amino acid at position 987 is

5 P.

In certain embodiments, the invention provides SARS-CoV 2 proteins comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 5-194 and SEQ ID NO: 197-418, SEQ ID NO: 420 and SEQ ID NO: 421, or fragments thereof. In a preferred embodiment, the SARS-CoV 2 proteins comprise an amino acid sequence of SEQ ID NO: 417 or SEQ ID NO: 418. In certain embodiments, the proteins according to the invention do not comprise a signal peptide sequence or a tag sequence.

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 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 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 documents, a fragment is the SARS-CoV-2 S ectodomain.

In certain embodiments, the proteins according to the invention are soluble (trimeric) proteins, 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

25

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 (corresponding to the amino acids 1-1208 of SEQ ID NO: 1) to permit expression as a soluble ectodomain (corresponding to the amino acids 1-1208 of SEQ ID NO: 1). For the

5 stabilization of such soluble trimeric 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., (2004)). Thus, in certain
10 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 or no heterologous trimerization domain is added to the S ectodomain.

15 In a preferred embodiment, the soluble trimeric SARS-CoV2 S proteins of the invention do not comprise a heterologous trimerization domain.

In preferred embodiments, the present invention provides recombinant SARS-CoV-2 S proteins comprising a truncated S2 domain and comprising a deletion of the furin cleavage site and wherein the amino acid at position 942 is P, the amino acid at position 892 is P, the
20 amino acid at position 987 is P, wherein the protein does not comprise a heterologous trimerization domain and wherein numbering of the amino acid positions is according to the numbering of the amino acid positions in SEQ ID NO: 1.

In preferred embodiments, the present invention provides recombinant SARS-CoV-2 S proteins comprising a truncated S2 domain and comprising a deletion of the furin cleavage
25 site and wherein the amino acid at position 942 is P, the amino acid at position 892 is P, the

amino acid at position 614 is N or G, the amino acid at position 987 is P, wherein the protein does not comprise a heterologous trimerization domain and wherein numbering of the amino acid positions is according to the numbering of the amino acid positions in SEQ ID NO: 1.

The recombinant prefusion SARS-CoV-2 S proteins according to the invention
5 preferably have improved trimer yields and/or improved (thermal) stability.

Alternatively, or in addition, the prefusion SARS-CoV-2 S proteins according to the invention induce increased titers of neutralizing antibodies, as compared to SARS-CoV-2 S proteins without the stabilizing mutations of the invention.

In certain embodiment, the pre-fusion SARS-CoV-2 S proteins according to the
10 invention are stable, i.e. do not readily change into the post-fusion conformation upon processing of the 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
15 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.
20 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,
25 which is generally used for purification purposes. Alternatively, other tags like a C-tag can be

used for these purposes. In certain embodiments, the proteins according to the invention do not comprise a tag sequence.

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
5 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 P, a mutation of the amino acid at position 892, a mutation of the amino acid at position 614, a mutation at position 572, 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
10 acid positions is according to the numbering of the amino acid positions in SEQ ID NO: 1.

In certain embodiments, the methods comprise introducing at least two mutations comprising a mutation of at least one amino acid in the loop region corresponding to amino acid residues 941 – 945 into P, and a mutation selected from the group consisting of a
mutation of the amino acid at position 892, a mutation of the amino acid at position 614, a
15 mutation at position 572, a mutation at position 532, a disulfide bridge between residues 880 and 888 and a disulfide bridge between residues 884 and 893.

In certain embodiments, the methods comprise introducing at least two mutations comprising a mutation of at least one amino acid in the loop region corresponding to amino acid residues 941 – 945 into P, and a mutation selected from the group consisting of a
20 mutation of the amino acid at position 892, a mutation of the amino acid at position 614, a mutation at position 572, a mutation at position 532, a disulfide bridge between residues 880 and 888 and a disulfide bridge between residues 884 and 893, provided that 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 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
5 941 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 944 into P.

Alternatively, or in addition, the mutation at position 892 is a mutation into P.
10 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.

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

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

Alternatively, or in addition, the methods further comprise introducing a mutation of the amino acids at position 986 and/or 987 into proline. In a preferred embodiment, the
20 methods comprise introducing a mutation of the amino acid at position 987 into proline.

The present invention further provides nucleic acid molecules encoding the SARS-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
25 of the above.

In preferred embodiments, the nucleic acid molecules encoding the proteins according 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-
5 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 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
10 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.

15 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
20 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
25 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).

In certain embodiments, the nucleic acid sequences encode SARS-CoV 2 proteins comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 5-194
5 and SEQ ID NO: 197-418, SEQ ID NO: 420 and SEQ ID NO: 421, or fragments thereof.

In a preferred embodiment, the nucleic acid sequence encodes a SARS-CoV 2 protein comprising an amino acid sequence of SEQ ID NO: 417 or SEQ ID NO: 418.

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
10 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
15 used can be any vector that is suitable for cloning DNA and that can be used for transcription of a nucleic acid of interest.

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
20 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 (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
25 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 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.

5 Most advanced studies have been performed using human adenoviruses, and human adenoviruses are preferred according to certain aspects of the invention. In certain preferred 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
10 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
15 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
20 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
25 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

5 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

10 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

15 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

20 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

25 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
5 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
10 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.

15 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.

20 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
25 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 a SARS-CoV-2 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 SARS-CoV-2 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

5 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

10 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

15 can be obtained from various sources, including viruses, prokaryotic, or eukaryotic sources, 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.

20 A “heterologous nucleic acid molecule” (also referred to herein as ‘transgene’) is a 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

25 sequences may be added. Many promoters can be used for expression of a transgene(s), and

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 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 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 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 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

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

5 stabilized pre-fusion SARS-CoV-2 S protein, a nucleic acid molecule, and/or a vector, 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

10 invention. Also provided are pre-fusion SARS-CoV-2 S proteins, nucleic acid molecules, 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-

15 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.

20 As used herein SARS-CoV-2 may refer to the Wuhan-Hu-1 strain as originally identified in 2019 in Wuhan, or to variants thereof, e.g. variants comprising one or more mutations in the S protein, including but not limited to the B.1, B.1.1.7, B.1.351, P.1, B.1.427, B.1.429, B.1.526, B.1.526.1, B.1.525, B.1.617, B.1.617.1, B.1.617.2, B.1.617.3, and P.2 virus variants.

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. ≥ 50 years old, ≥ 60 years old, and preferably ≥ 65 years old), hospitalized patients and patients
5 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
10 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
15 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
20 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
25 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 5 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, 10 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.

15 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 20 US 4,372,945 or US 4,474,757.

In other embodiments, the compositions do not comprise adjuvants.

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 25 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 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

5 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 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

10 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 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

15 different forms of the same antigenic component. A combination product may also comprise immunogenic components against other infectious agents, e.g. other respiratory viruses 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

20 invention and the additional active components.

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

25 the art.

Administration of the compositions according to the invention can be performed using 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
5 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 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.

10 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 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
15 (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 invention further provides a host cell comprising the isolated nucleic acid molecule or vector encoding the recombinant SARS-CoV-2 S protein of the invention. Such host cells can be used for recombinant protein production, recombinant protein expression, or the
20 production of viral particles.

In addition, the invention relates to methods of producing a recombinant SARS-CoV-2 S protein, comprising growing a host cell comprising an isolated nucleic acid molecule or vector encoding the recombinant SARS-CoV-2 S protein of the invention under conditions suitable for production of the recombinant SARS-CoV-2 S protein.

The SARS-CoV-2 S proteins of the invention 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.

5 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
10 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.

15

Examples

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

A plasmid corresponding to the semi-stabilized SARS-CoV2 S protein described by
20 (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 (based on SEQ ID NO: 3) 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
25 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% CO₂. 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 µm 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 cComplete His-tag 5 mL (Roche). Both proteins were further purified by size-exclusion chromatography using a HiLoad Superdex 200 16/600 column (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 614, 892 and 942 (numbering according to SEQ ID NO: 1)
15 were mutated. 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 Expi293F cells, and 3 days after transfection the supernatants were tested for binding to ACE2-Fc using AlphaLISA (FIG. 3).

For the AlphaLISA assay, SARS-CoV2 S variants in the pcDNA2004 vector
20 containing a linker followed by a sortase A tag followed by a Flag- tag followed by a flexible (G₄S)₇ 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% Tween-20 + 0.5 mg/mL BSA). Then, 10 µL of each dilution were transferred to a 96-well
25 plate and mixed with 40 µL 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.

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-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) or the variant with the additional PP (SEQ ID NO:3), the S variants with stabilizing substitutions D614N, A892P and A942P showed higher ACE2-Fc binding (FIG. 3).

The cell culture supernatants of transfections with a semi-stable uncleaved SARS-CoV-2 S + PP design and with a labile uncleaved SARS-CoV-2 S protein, and of variants with a single point mutation as described above (D614N, A892P and A942P) were analyzed using analytical SEC (FIG. 4). An ultra high-performance liquid chromatography system (Vanquish, Thermo Scientific) and μ DAWN TREOS instrument (Wyatt) coupled to an Optilab μ 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 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, μ 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 using SEC-MALS, mMALS detectors were inline and data was

5 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 semi-stable soluble uncleaved S variant with a C-terminal foldon domain +PP, the variants with additional stabilizing substitutions D614N, A892P and especially A942P showed higher trimer content according to analytical SEC of culture supernatant (FIG. 4 A-C). Similarly,

10 compared with the soluble uncleaved S variant with a C-terminal foldon domain, variants with stabilizing substitutions D614N, A892P and especially A942P showed higher trimer content according to analytical SEC of culture supernatant. The A942P mutation has a stronger effect on trimer expression than the published double proline mutation in the hinge loop, reflecting higher stability during synthesis and transport (compare dashed line of FIG

15 4B with solid line of FIG 4 E). SEC-MALS analysis was performed on the purified stabilized protein according to SEQ ID NO: 5 and showed that the peak at 5 minutes corresponds to the mass of a trimeric S protein (FIG 4 G).

EXAMPLE 3: Stabilizing point mutations and disulfide bridges analyzed with AlphaLISA

20 *and analytical SEC*

In order to stabilize the labile pre-fusion conformation of SARS-CoV-2 S protein, disulfide bridges were introduced between residues 880 and 888 or between residues 884 and 893, and point mutations were introduced at position 532 and 572. Similar to EXAMPLE 2, plasmids coding for the uncleaved SARS-CoV-2 S protein with or without the double proline

25 in the hinge loop were expressed in Expi293F cells, and 3 days after transfection the

supernatants were tested for binding to ACE2-Fc using AlphaLISA as described in

EXAMPLE 2 (FIG. 5).

Compared with the soluble labile uncleaved S variant with a C-terminal foldon, the variants with stabilizing substitutions T572I, N532P and with the introduction of a disulfide
5 between residues 880 and 888 showed higher ACE2-Fc binding (FIG. 5, left panel).

In addition, compared with the soluble semi stable uncleaved S variant with a C-terminal foldon domain and the double proline, the variants with stabilizing substitutions T572I, N532P, with the introduction of a disulfide between residues 880 and 888 and with a disulfide between residues 884 and 893 showed higher ACE2-Fc binding (FIG. 5, right
10 panel).

The cell culture supernatants of transfections with a semi stable uncleaved SARS-CoV-2 S + PP design and with a labile uncleaved SARS-CoV-2 S protein, and of variants with an introduced disulfide bridge or a single point mutation as described above (T572I, N532P, CYS880-CYS888 and CYS884-CYS893) were analyzed using analytical SEC (FIG.
15 6) as described in EXAMPLE 2. Compared with the semi-stable soluble uncleaved S variant with a C-terminal foldon domain +PP, the variants with stabilizing substitutions T572I, N532P and the disulfide bridges 880C-888C and 884C-893C (FIG. 6 A-D) showed higher trimer content according to analytical SEC of culture supernatant. Similarly, compared with the soluble uncleaved S variant, the variants with stabilizing substitutions T572I, N532P and
20 the variant with disulfide bridge 880C-888C showed higher trimer content according to analytical SEC of culture supernatant (FIG 6 E-H).

EXAMPLE 4: Stabilizing point mutations analyzed with AlphaLISA and analytical SEC

In order to stabilize the labile pre-fusion conformation of SARS-CoV-2 S protein, point mutations were introduced at position 941 and 944. Similar to EXAMPLE 2, plasmids coding for the labile uncleaved SARS-CoV-2 S protein were expressed in Expi293F cells, and
5 3 days after transfection the supernatants were tested for binding to ACE2-Fc using AlphaLISA as described in EXAMPLE 2 (FIG. 7 A).

Compared with the soluble labile uncleaved S variant with a C-terminal foldon, the variants with additional stabilizing substitutions T941P and A944P showed higher ACE2-Fc binding (FIG. 7A).

10 The cell culture supernatants of transfections with a labile uncleaved SARS-CoV-2 S protein, and of variants with a single point mutation as described above (T941P and A944P) were analyzed using analytical SEC (FIG. 7B) as described in EXAMPLE 2. Compared with the labile soluble uncleaved S variant with a C-terminal foldon domain, the variants with stabilizing substitutions T941P and A944P (FIG. 7B) showed higher trimer content according
15 to analytical SEC of culture supernatant.

EXAMPLE 5: Differential scanning calorimetry (DSC)

Melting temperatures for S trimers were determined using MicroCal capillary DSC system. 400 µL of 0.5 mg/mL protein sample was used per measurement. The measurement
20 was performed with a start temperature of 20°C and a final temperature of 110°C. The scan rate 100°C/h and the feedback mode; Low (=signal amplification). The data were analyzed using the Origin J. Software (MicroCal VP-analysis tool). The purified uncleaved S trimer (SEQ ID NO: 2) showed a wide range of melting events with a major melting event (Tm2) at 64°C (FIG 8, top panel). Introduction of the mutation K986P drastically destabilized the
25 trimer since most of the trimer melted at 48 °C. The mutation V987P had relatively little

impact as the major melting event (T_{m2}) happened at 64°C and the double proline mutation (K986P + V987P) showed a slight increase of the melting event at 47 °C (FIG 8, top panel). The middle panel shows DSC thermostability data of the uncleaved semistable S trimer (Furin KO+PP, SEQ ID NO: 3, dashed line) with additional indicated point mutation in the S1 domain. N532P had no effect on the T_m and T572I and D614N showed a strong stabilizing effect (middle panel). The bottom panel shows DSC thermostability data of the uncleaved semistable S trimer (SEQ ID NO: 3, dashed line) with additional indicated mutations in the S2 domain. A942P had no effect on the T_m and A892P and disulfide F88C-G880C showed a strong stabilizing effect (bottom panel).

EXAMPLE 6: S protein fusogenicity

A cell-cell fusion assay to mimic the entry pathway of SARS-CoV-2 at the plasma membrane was developed by transiently co-expressing GFP, ACE2, TMPRSS2 and full-length S variants in HEK293 cells (see Figure 9). After 18-24 hr, cell monolayers were visualized using an EVOS microscope. All identified stabilizing mutations were tested, as well as furin KO, and the double proline mutations. The assay was performed at a saturating concentration of the S protein to obtain yes or no answers regarding fusion competence. Whereas the furin KO, the PP mutations and the two cystines completely abolished fusogenicity, the individual point mutants still allowed fusion to occur. This implies that these variants are folded correctly and are functional.

EXAMPLE 7: Combination of stabilizing mutations analyzed with analytical SEC and AlphaLISA

In order to stabilize the labile pre-fusion conformation of SARS-CoV-2 S protein, a combination of indicated stabilizing point mutations from previous examples were introduced

in SEQ ID NO:2 (FIG 10). Similar to EXAMPLE 2, plasmids coding for the labile uncleaved SARS-CoV-2 S protein (dashed line) and stabilized variants were expressed in Expi293F cells, and 3 days after transfection the supernatants were analyzed for trimer content by analytical SEC as described in EXAMPLE 2. As shown in FIG 10 A, the variant with the four mutations A892P, A942P, D614N and V987P showed the highest trimer content which was much higher than the semistabilized S protein based on SEQ ID NO:3 (Furin KO+PP). FIGURE 10B shows that the trimers in the cell culture supernatants also showed higher ACE2-Fc binding using AlphaLISA as described in EXAMPLE 2 (FIG. 10 B).

In order to obtain soluble native S trimers, a C-terminal heterologous trimerization domain was added as described by Pallesen et al. (Pallesen, PNAS, 2017). To investigate whether the point mutations sufficiently stabilized the protein to trimerize without the addition of a trimerization domain, a variant was made with four stabilizing mutations without the foldon (DF) (A892P-A942P-D614N-V987P-DF). As shown in FIG 10 C and table 2, a large trimer peak was detected in analytical SEC at approximately 5.3 minutes. A slight shift to longer retention time was observed due to the lower molecular weight. The molecular weight was confirmed by MALS detection (Table 2). Subsequently, thermostability of the variants with combinations of stabilizing mutations was tested by DSC (D). Uncleaved S variants as indicated in panel D were compared with the semistabilized uncleaved variant with the double proline at position 986 and 987 (SEQ ID NO: 3, dashed line). Variants with 4 or 5 mutations with or without foldon all showed a single T_m at 66°C

EXAMPLE 8: Freeze-thaw stability of SARS-2 S variants

Purified SARS-2 S trimers with indicated mutations (FIG. 11, Table 3) were tested for freeze-thaw (F/T) stability using analytical SEC to measure the remaining amount of trimer

after each F/T step. Proteins were diluted to 0.32 mg/ml in a Tris buffer without cryoprotective excipients (20mM Tris, 150mM NaCl, pH7.4) and snap frozen using liquid Nitrogen and thawed once (1x) or repeatedly (3x, 5x). The semistabilized variant with the K986P+V987P was almost completely lost after 3 times F/T but the stabilized variants

5 survived these conditions much better (FIG 11, Table 3).

EXAMPLE 9: Antigenicity of stabilized SARS-2 S variants

RBD exposure was characterized by ACE2, by neutralizing antibody SAD-S35 and non-neutralizing antibody CR3022 (Yuan et al., (2020) that compete with ACE2. ACE2 and

10 SAD-S35 can only bind RBD in the up configuration and CR3022 can only bind when 2 RBDs are in the up configuration (Fig. 12A). The variant with K986P shows higher binding of SAD-S35, ACE2 and CR3022 than Furin KO+PP (SEQ ID NO: 3), which agrees with the results obtained with SEC and AlphaLISA in supernatants, indicating that it causes more RBD exposure and thus more opening of the trimer. D614N and T572I show very low

15 binding to SAD-S35 and ACE2 compared to S-2P and almost no CR3022 binding, indicating more closed trimers with some 1-up configurations, but hardly any 2-up or 3-up RBD up configurations. A892P improved trimer closure compared to control to a lesser extent, while A942 seemed to increase its opening. These mutants likely exhibit a mixture of closed, 1-up and 2-up structures (FIG. 12B) When the stabilizing mutations are combined, lower binding

20 is shown for ACE2-Fc and the antibodies compared to FurinKO+PP (SEQ ID NO:3) indicating that the trimer is mostly in the closed conformation (FIG 12C). Next, storage stability at 4 degrees was tested for FurinKO+PP compared with stabilized variant (A892P-A942P-D614N-V987P-DF) using BioLayer Interferometry at endpoint equilibrium. ACE2-Fc binding and CR3022 binding were comparable with freshly purified material indicating that

25 the stabilized protein was still in the closed conformation. The strongly neutralizing

monoclonal antibody S309 that binds RBD in the closed conformation shows binding with both proteins (Pinto et. al., 2020) (FIG 12D). The differential binding of CR3022 and S309 to the stabilized foldon-less S trimer indicates a well folded RBD in the down configuration.

5 EXAMPLE 10: A942P increases S expression of FL S

Different full length (FL) S proteins were produced in Expi292F cells. COR200660 (660) has a furin knock out mutation, i.e a mutation of the amino acid at position 682 into S and/or a mutation of the amino acid at position 685 into G. COR200662 (662) is the same as 660, but with an additional A942P substitution. COR200007 (007) has furin knock out
10 mutation and additional mutations K986P and V987P. COR200664 is the same as 007, but with an additional A942P substitution.

Higher amounts of spikes detected in the supernatant when A942P is present compared with when it is not present (as shown in Figure 13), indicate that A942P increases the expression of full-length (FL) S protein, whereas the amount of beta actin of the cell itself
15 is not changed by the A942P substitution. Applying whole cell lysates on SDS-PAGE followed by Western blotting, shows that A942P increases the expression of full length S protein by a factor ~1.4 (data not shown).

EXAMPLE 11: Antigenicity of membrane bound S with stabilizing substitutions

20 The antigenicity of the seven membrane bound S proteins encoded by the different DNA constructs was evaluated in cell-based ELISA (CBE) as described below. Binding was assessed to three neutralizing ligands, i.e. angiotensin-converting enzyme 2 (ACE2-Fc) (Liu et al. (2017)), and two monoclonal antibodies (mAbs), COVA1-22 and COVA2-15 (Brouwer

et al., 2020) and two non-neutralizing mAbs, i.e. CR3015 (van den Brink et al., (2005)) and CR3046 (Bos et al., (2020)). The D614N (like D614G), A892P and T572I substitutions decrease the binding of CR3015 and CR3046 compared to the wild type spike in the membrane suggesting that these substitutions stabilize the spike. A892P and T572I decrease binding of CR3015 and CR3046 with or without D614G (Figure 14).

Cell-based ELISA Method

HEK293 cells were seeded at 2×10^5 cells/mL in appropriate medium in a flat-bottomed 96-well microtiter plate (Corning). The plate was incubated overnight at 37 °C in 10% CO₂. After 24 h, transfection of the cells was performed with 300 ng DNA per well and the plate was incubated for 48 h at 37 °C in 5% CO₂. Two days post transfection, cells were washed with 100 µl/well of blocking buffer containing 1% (w/v) BSA (Sigma), 1 mM MgCl₂, 1.8 mM CaCl₂, and 5 mM Tris pH 8.0 in 1× PBS (GIBCO). After washing, nonspecific binding was blocked, using 100 µl/well of blocking solution for 20 min at 4 °C. Subsequently, cells were incubated in 50 µl/well blocking buffer containing 1 µg/ml primary antibodies ACE2-Fc, COVA1-22, COVA2-15, CR3015 and CR3046 for 1 hr at 4 °C. The plate was washed three times with 100 µl/well of the blocking buffer, three times with 100 µl/well of washing buffer containing 1 mM MgCl₂, 1.8 mM CaCl₂ in 1× PBS and then incubated with 100 µl/well of the blocking buffer for 5 min at 4 °C. After blocking, the cells were incubated with 50 µl/well of secondary antibodies HRP conjugated Mouse Anti-Human IgG (Jackson, 1:2500) or HRP Conjugated goat anti-mouse IgG (Jackson, 1:2500) then incubated 40 min at 4 °C. The plate was washed three times with 100 µl/well of the blocking buffer, three times with 100 µl/well washing buffer. 30 µl/well of BM Chemiluminescence ELISA substrate (Roche, 1:50) was added to the plate, and the luminosity was immediately measured using the Ensign Plate Reader.

EXAMPLE 12: *In vitro* antigenicity of three soluble proteins tested for immunogenicity in mice.

Antigenicity of COR200617, COR200619 and COR201225 was assessed with a panel of neutralizing antibodies against the N-terminal domain (NTD) (4A8 (Chi et. al., (2020) and
 5 several antibodies that bind either the RBD in the up and down or antibodies that only bind RBD in the up configuration. See Henderson et. al., (2020) for the definition of ‘up’ and ‘down’. The following antibodies are directed against the closed conformation of spike and recognize both the up and down state: COVA1-22 (Brouwers et. al., (2020)), against the RBD in the ‘up’ or ‘down’ position (S2M11 (Tortorice et. al., (2020)), C144 (Barnes et. al., (2020),
 10 2-43 (Liu et al, (2020)) and COVA2-15 Brouwers et. al., (2020)). The following antibodies are directed against the RBD in the open conformation of spike and recognize the up state: (ACE2-Fc and SAD-S35 (AcroBiosystems), as described below. As shown in Figure 14, the non-neutralizing antibodies CR3022 (Yuan et al., (2020)), CR3015 and CR3046 do not bind to the pre-fusion conformation. CR3022 can only bind when 2 RBDs are in the up
 15 configuration. These three antibodies bind well to COR200627, but not to COR200619 and COR201225, indicating that COR200627 lost (part) of its pre-fusion conformation, whereas COR200619 and COR201225 are in the pre-fusion conformation. The ACE2-Fc and SAD-S35, which bind to the RBD when it is in the “up” position, bind less to COR200619 and COR201225 than to COR200627 indicating that COR200619 and COR201225 have more
 20 RBDs in the down position and is thus more closed than COR200627.

Antibodies were immobilized on anti-hIgG (AHC) sensors (FortéBio, cat. #18–5060) in 1×kinetics buffer (FortéBio, cat. #18–1092) in 96-well black flat-bottom polypropylene microplates (FortéBio, cat. #3694). The experiment was performed on an Octet RED384 instrument (Pall-FortéBio) at 30 °C with a shaking speed of 1000 rpm. Activation was 600 s,
 25 immobilization of antibodies 900 s, followed by washing for 600 s, and then binding the S

proteins for 300 s. The data analysis was performed using the FortéBio Data Analysis 12.0 software (FortéBio).

EXAMPLE 13: *COR200619 and COR201225 are immunogenic in mice*

5 In this example the in vivo immunogenicity of recombinant SARS-CoV-2 Spike proteins of the invention was assessed. SARS-CoV-2 S proteins were generated that were stabilized in a predominantly closed conformation: COR201225 and COR200619. The immunogenicity was compared to a stabilized SARS-CoV-2 spike protein with an open conformation (COR200627).

10 The Spike protein variants thus were presented from most closed (top) to the most open variant (bottom). All constructs had furin knockout mutations (R682S R685G). In addition, the constructs contained the stabilizing mutations that are shown in the table below:

Structure	Construct	Conformation	Stabilizing mutations
	COR201225	Predominantly closed	N532P, T572I D614G, G880C, F888C, A944P, V987P
	COR200619	Predominantly closed	D614N, A892P, A942P, V987P
	COR200627	Open (foldon)	A942P , K986P, V987P

Groups of 7 female BALB/c mice (age 8-10 weeks at the start of the study) were intramuscularly immunized with 5 or 0.5 µg S protein with 100 µg aluminium hydroxide adjuvant on day 0 and day 28. Mice were bled on day 27 and 41 to analyze neutralizing antibody responses against SARS-CoV-2 B.1 (Wuhan-Hu-1 + D614G) Spike protein by a pseudovirion neutralization assay (psVNA) or the SARS-CoV-2 L-0008 isolate (lineage B.1) by wild-type VNA (wtVNA). See Solfrosi et al., for details on the assays used.

Results

Neutralizing antibody titers against the SARS-CoV-2 isolate L-0008 (lineage B.1) were undetectable or close to the LLOD four weeks (day 27) after immunization with one dose of COR200627 (open conformation) as measured by a wild-type virus neutralization assay (wtVNA) (Figure 16). In contrast, COR201225 and COR200619 (predominantly closed) elicited neutralizing antibodies against the SARS-CoV-2 isolate L-0008 in a dose dependent manner four weeks after immunization. This difference between COR200627 (open conformation) and COR201225 and COR200619 (predominantly closed) was also observed in a pseudovirion neutralization (psVNA) assay against the SARS-CoV-2 B.1 Spike protein. In this assay, COR200627 (open conformation) did not induce neutralizing antibody titers against SARS-CoV-2 B.1 Spike protein as measured by psVNA, while COR201225 and COR200619 (predominantly closed conformation) promoted neutralizing antibody titers in a dose-dependent manner (Figure 16). Two weeks after the second dose at week 6 (day 41) detectable neutralization titers against SARS-CoV-2 B.1 Spike protein were observed for all constructs by psVNA. However, higher neutralization titers were observed in mice immunized with COR201225 and COR200619 (predominantly closed conformation), compared to COR200627 (open conformation)

Conclusion

According to the present invention, it thus has been shown that COR201225 and COR200619 (predominantly closed and containing stabilizing mutations according to the invention) are immunogenic in mice and induce higher neutralizing antibody levels against SARS-CoV-2, compared to COR200627 (open conformation) 4 and 6 weeks after immunization.

EXAMPLE 14: Stabilization without K986P and V987P

As shown in the previous examples, the substitutions A942P, A944P, A892P and F880C-G888C increased the trimer yield of soluble S protein without the K986P and V987P substantially (Figure 4 and 6 lower panels). A892P, T572I and D614N reduced the binding substantially of non-neutralizing antibodies to membrane bound S without any further modifications, indicating more stabilized S trimers (Figure 14). Combining the substitutions N532P, T572I, D614G, F880C-G888C and A944P, but no K986P or V987P (in COR201291) resulted in much higher trimer yield than measured for the S-2P only protein (COR200017) as shown by analytical SEC with cell culture supernatant (Figure 17). The S-2P has a foldon for trimerization, whereas the COR201291 does not and therefore also produces some monomers. These examples show that the mutations of the invention that increase trimer expression or stabilize the trimer are independent of and superior to the previously described K986P and V987P substitutions.

EXAMPLE 15: Cryo-EM structure of Wuhan-Hu-01 quadruple mutant

D614N+A892P+A942P+V987P with foldon

Four stabilizing mutations D614N, A892P, A942P and V987P were introduced in the Wuhan-Hu-01 sequence. The quadruple mutant was then imaged by cryo-EM. A 2-steps 3D classification illustrates that out of 833,000 classified particles, ~80% was closed with all RBDs in the down state and 38% was categorized into a well-defined closed class while ~20% showed 1 RBD-up (Figure 18). Further processing of the 320,000 closed conformation particles allowed us to obtain a 2.8Å electron potential map for the closed conformation and a 3.0Å electron potential map for the 1 RBD-up (one up) conformation (Figure 19). An atomic model that was built into the 2.8Å electron potential map confirmed that S retains the prefusion spike conformation. The NTDs and RBDs density is less defined than for the rest of

the map, suggesting flexibility in these regions. The closed structure is highly reminiscent of the one previously solved by Walls et al. (Walls, Park et al. 2020) The two structures differ by 2.2 Å all atom RMSD and there are no significant differences in terms of relative position of domains or domain conformation. The RBD is relatively more defined and the NTD less defined compared to the closed trimer described by Walls et al. The stabilizing mutations do not significantly affect backbone conformation of the closed trimer. The viral spike is mostly closed and structurally very similar to other known closed S-2P spike conformations (Walls, Park et al. 2020, Xiong, Qu et al. 2020) and especially the closed wild-type structure of Xiong et al (Xiong, Qu et al. 2020), with all atom RMSD of 1.7Å.

Cryo-EM Grid Preparation and Data Collection

SARS-CoV-2 S protein samples were prepared in 20mM Tris, 150mM NaCl, pH7 buffer at a concentration of 0.15 mg/mL and applied to glow discharged Quantifoil R2/2 200 mesh grids before being double side blotted for 3 seconds in a Vitrobot Mark IV (Thermo Fisher Scientific and plunge frozen into liquid ethane cooled. Grids were loaded into a Titan Krios electron microscope (Thermo Fisher Scientific) operated at 300kV, equipped with a Gatan K3 BioQuantum direct electron detector. A total of 9,760 movies were collected over two microscopy sessions at The Netherlands Centre for Electron Nanoscopy (NeCEN).

Detailed data acquisition parameters are summarized in Table 1.

Cryo-EM image processing

Collected movies were imported into RELION-3.1-beta (Zivanov, Nakane et al. 2018) and subjected to beam induced drift correction using MotionCor2 (Zheng, Palovcak et al. 2017) and CTF estimation by CTFFIND-4.1.18 (Rohou and Grigorieff 2015). Detailed steps

of the image processing workflow are illustrated in Figure 17. Final reconstructions were sharpened and locally filtered in RELION post-processing.

Model building and refinement

5 The SARS-CoV-2 S PDBID 6VXX and 6VSB structures (Walls, Park et al. 2020, Wrapp, Wang et al. 2020) were used as starting models. PHENIX-1.18.261 (Liebschner, Afonine et al. 2019), Coot (Emsley, Lohkamp et al. 2010) and the Namdinator webserver (Kidmose, Juhl et al. 2019) were iteratively used to build atomic models. Geometry and statistics are given in Table 4 and 5. Final maps were displayed using UCSF ChimeraX
10 (Goddard, Huang et al. 2018).

Table 1. Standard amino acids, abbreviations and properties

Amino Acid	3-Letter	1-Letter	Side chain polarity	Side chain charge (pH 7.4)
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

Table 2. SEC-MALS analysis

Mutation	Trimer peak				LMW species				Total
	Mw (kDa)	Rh (nm)	Mass fraction (%)	Retention time (min)	Mw (kDa)	Rh (nm)	Mass fraction (%)	Retention time (min)	Recovery (%)
A892P_A942P_D614N_V987P_Δfoldon	465.6	9.165	89.8	5.319	ND*	ND*	8.7	5.647	96.7*
A892P_A942P_D614N_V987P	491	9.909	100	5.08	-	-	-	-	86.6

5

Table 3. S trimer content (%) after repeated freeze-thaw steps

Mutation(s)	0x FT	1x FT	3x FT	5x FT
S-2P	100	67	8	1
S-2P-D614N	100	83	43	12
S-2P-F888C_G880C	100	75	24	4
S-2P-N532P	100	72	24	3
S-2P-A892P	100	80	21	3
S-2P-A942P	100	60	13	3
S-2P-T572I	100	81	22	3
No muts	100	73	10	1
D614G	100	72	21	3
A892P_A942P	100	82	29	4
A892P_A942P_D614N_K986P_V987P	100	77	31	11
A892P_A942P_D614N_V987P	100	74	34	8
A892P_A942P_D614N_V987P_Δfoldon	100	78	55	35

Table 4. Cryo-EM data collection

	S-closed+Fd quadruple mutant
Magnification	105,000
Data collection / Final Pixel size (Å)	0.418 / 0.836
Voltage (kV)	300
Electron exposure (e⁻/Å²)	65
Frames	50
Defocus Range (µm)	-0.6 to -2.5
Number of movies collected	9,760
Particles extracted	1,400,000
Final (closed/opened)	315,000 / 166,000
Symmetry	N/A
Masked resolution at FSC=0.143 (Å)	
(closed/opened)	2.75/2.92
Map sharpening B-factor (Å²)	
(closed/opened)	-52/-51
EMDB	EMD-11639 / EMD-11719

Table 5. Model refinement and validation statistics

		Closed trimer	One up trimer
PDB		7A4N	7AD1
Model compositions			
	Amino Acids	2889	2841
	Glycans	21	35
Mean B factors ($\text{\AA}^2$)			
	Amino Acids	94.53	107.22
	Glycans	75.34	112.75
R.m.s. deviations			
	Bond lengths ($\text{\AA}$)	0.008	0.016
	Bond angles ($^\circ$)	1.057	1.260
Validation			
	MolProbity score	1.53	1.95
	Clashscore	5.08	8.72
	Rotamers outliers (%)	0.20	0.00
	EMRinger score	3.64	3.51
Ramachandran plot			
	Favored (%)	96.14	92.15
	Allowed (%)	3.86	7.85
	Outliers (%)	0.00	0.00

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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)

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSNGTK
 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCNDPFLGVYHKNKSWM
 10 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRLPQGFSALEPLVDLPIG
 INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
 LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
 15 DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
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 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNSPRARSVASQSIIAYTM
 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK
 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
 20 NGLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
 GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSA PHGVVFLHVTYVPAQEKNTTAPAICH
 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
 25 SCCSCLKGCCSCGCKFDEDDSEPVLKGVKLHYT

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

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSNGTK
 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCNDPFLGVYHKNKSWM
 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRLPQGFSALEPLVDLPIG
 INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
 35 LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
 DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
 NGLTGTGVLTESNKKFLPFQGFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNSPRAGSVASQSIIAYTM
 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK
 40 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
 NGLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
 GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSA PHGVVFLHVTYVPAQEKNTTAPAICH
 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
 45 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLG
RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSHHHHHH

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 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
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 15 NGLTVLPPLTDEMIQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
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SEQ ID NO 4: foldon

25 GYIPEAPRDGQAYVRKDGWVLLSTFL

SEQ ID NO 5: SEQ ID NO 2 + A942P

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SEQ ID NO 6: SEQ ID NO 2 + A892P

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15 GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSR LDKVEAEVQIDRLITGRLQSLQTYVT
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SEQ ID NO 7: SEQ ID NO 2 + D614N

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IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLND
LCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP FER
30 DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVG YQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQ QFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSM TKTSDVCTMYICGDSTEC SNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQJLPDPSKPSKR SFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
35 NGLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SAI
GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSR LDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLM SFPQSAPHGVVFLHVTYVPAQEKNF TTA PAICH D
GKAHFPREGV FVSNGTHW FVTQRNFYEPQIITDNTFVSGNCDV VIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLG
40 RSLEVL FQGPGLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 8: SEQ ID NO 2 + T572I

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIK VCEFQFCNDPFLGVYYHKNNKSWM
45 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLND
50 LCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP FER
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVG YQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF

NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEV
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNPSRAGSVASQSIAYTMS
LGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKFN
5 GLTVLPPLLTDEMAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNNSAIG
KIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTVYVPAQEKNTTAPAICHG
KAHFPRGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGYIPEAPRDGQAYVRKDGGEWVLLSTFLGR
10 SLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 9: SEQ ID NO 2 + N532P

15 MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND
20 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGNGYNYLYRFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNPSRAGSVASQSIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
25 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQK
NGLTVLPPLLTDEMAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNNSAI
GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTVYVPAQEKNTTAPAICHG
GKAHFPRGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
30 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 10: SEQ ID NO 2 + G880C + F888C

35 MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
40 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGNGYNYLYRFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNPSRAGSVASQSIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
45 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQK
NGLTVLPPLLTDEMAQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNNSAI
GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTVYVPAQEKNTTAPAICHG
50 GKAHFPRGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGSYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

5 SEQ ID NO 11: SEQ ID NO 2 + S884C + A893C

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
10 INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDPDFTGCVIAWNSNNLDSKVGNGYNYLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMIQYTSALLAGTITCGWTFGAGACLPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWVFTQRFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGSYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

25
SEQ ID NO 12: SEQ ID NO 3 + A942P

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDPDFTGCVIAWNSNNLDSKVGNGYNYLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMIQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
40 GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWVFTQRFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGSYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

45
SEQ ID NO 13: SEQ ID NO 3 + A892P

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
50 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP

INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLND
LCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
5 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVS VITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGV TQNVLYENQKLIANQFN SAI
10 GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSA PHGVVFLHVTYVPAQEKNF TTAICH D
GKAHFPREGVFVSN GTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLG
RSLEVL FQGPGLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH
15

SEQ ID NO 14: SEQ ID NO 3 + D614N

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTW FHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIK VCEFQCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP IG
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLND
LCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
25 DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVS VITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
30 NGLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGV TQNVLYENQKLIANQFN SAI
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSA PHGVVFLHVTYVPAQEKNF TTAICH D
GKAHFPREGVFVSN GTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLG
35 RSLEVL FQGPGLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 15: SEQ ID NO 3 + T572I

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTW FHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIK VCEFQCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP IG
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLND
45 LCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVS VITPGTNTSNQVAVLYQDVNCTEV
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTMS
LGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDKN
50 TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF N
GLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGV TQNVLYENQKLIANQFN SAI

KIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAHPGVVFLHVTVYVPAQEKNTTAPAICHG
KAHFPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLGR
5 SLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 16: SEQ ID NO 3 + N532P

10 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIK VCEFQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLV RDLPQGFSALEPLVDLP
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENG TITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLC PFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLND
15 LCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP FER
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQ QFGRDIADTTDAVRDPQTLEILDITPCSFGGVS VITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSEYCDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSM TKTSDVCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
20 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVT LADAGFIKQYGDCLGDIAARDL ICAQKF
NGLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SAI
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAHPGVVFLHVTVYVPAQEKNTTAPAICH D
GKAHFPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
25 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 17: SEQ ID NO 3 + G880C + F888C

30 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIK VCEFQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLV RDLPQGFSALEPLVDLP
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENG TITDAVDCALDPLSETKCTLSFTVEKG
35 IYQTSNFRVQPTESIVRFPNITNLC PFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLND
LCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP FER
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQ QFGRDIADTTDAVRDPQTLEILDITPCSFGGVS VITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSEYCDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSM TKTSDVCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
40 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVT LADAGFIKQYGDCLGDIAARDL ICAQKF
NGLTVLPPLLTDEMI AQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SAI
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAHPGVVFLHVTVYVPAQEKNTTAPAICH D
45 GKAHFPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

50

SEQ ID NO 18: SEQ ID NO 3 + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIK VCEFQFCNDPFLGVYYHKNNKSWM
5 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSE TKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSNLKP
10 DISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQ QFGRDIADTTDAVRDPQTLEILDITPCSFGGVS VITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSM TKTSDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKR SFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMI AQYTSALLAGTITCGWTFGAGAC LQIPFAMQMAYRFNGIGV TQNVLYENQKLIANQFN
15 SAI
GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNF GAISSVLNDILSRDPPEAEVQIDRLITGR LQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYH LMSFPQSAPHGVVFLHVTVYVPAQEKNFTTAPAICH
D
GKAHFPREGV FVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDV VIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ GSGYIPEAPRDGQAYVRKDGEWVLLSTFLG
20 RSLEVL FQGPGLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 19: SEQ ID NO 2 + A942P + A892P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
25 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIK VCEFQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSE TKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSNLKP
30 DISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQ QFGRDIADTTDAVRDPQTLEILDITPCSFGGVS VITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSM TKTSDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKR SFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
35 NGLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGAL QIPFAMQMAYRFNGIGV TQNVLYENQKLIANQFN
SAI
GKIQDSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNF GAISSVLNDILSRDKVEAEVQIDRLITGR LQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYH LMSFPQSAPHGVVFLHVTVYVPAQEKNFTTAPAICH
D
GKAHFPREGV FVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDV VIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ GSGYIPEAPRDGQAYVRKDGEWVLLSTFLG
40 RSLEVL FQGPGLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 20: SEQ ID NO 2 + A942P + D614N

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
45 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIK VCEFQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSE TKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
50 LCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSNLKP
DISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN

NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
5 NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
GKIQDSLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLG
10 RSEVLFGQPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 21: SEQ ID NO 2 + A942P + T572I

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
15 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVN
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTMS
LGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKN
20 TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
GLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
SAIGKIQDSLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH
25 KAHPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLGR
SLEVLFGQPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 22: SEQ ID NO 2 + A942P + N532P

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
35 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVN
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
40 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
SAIGKIQDSLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH
45 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLGR
SLEVLFGQPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGSYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

5 SEQ ID NO 23: SEQ ID NO 2 + A942P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
10 INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMIQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTVVPAQEKNTTAPAICH
GKAHFPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGSYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

25
SEQ ID NO 24: SEQ ID NO 2 + A942P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMIQYTSALLAGTITCGWTFGAGACLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
40 GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTVVPAQEKNTTAPAICH
GKAHFPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGSYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

45
SEQ ID NO 25: SEQ ID NO 2 + A892P + D614N

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
50 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP

INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
5 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFN SAI
10 GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRQLSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSA PHGVVFLHVTYVPAQEKNFTTAPAICHD
GKAHFPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLG
RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH
15

SEQ ID NO 26: SEQ ID NO 2 + A892P + T572I

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTW FHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIK VCEFQCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLV RDLPQGFSALEPLVDLP IG
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
25 DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTMS
LGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF N
30 GLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFN SAI
KIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRQLSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSA PHGVVFLHVTYVPAQEKNFTTAPAICHDG
KAHFPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLGR
35 SLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 27: SEQ ID NO 2 + A892P + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTW FHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIK VCEFQCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLV RDLPQGFSALEPLVDLP IG
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLND
45 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
50 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFN SAI

GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGVVFLHVTVYVPAQEKNTTAPAICH
GKAHFPREGVFSVNGTHWFVTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYEAPRDGQAYVRKDGGEWVLLSTFLG
5 RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 28: SEQ ID NO 2 + A892P + G880C + F888C

10 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKCEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
15 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
FER DISTEIQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
20 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMIQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGVVFLHVTVYVPAQEKNTTAPAICH
GKAHFPREGVFSVNGTHWFVTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
25 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYEAPRDGQAYVRKDGGEWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 29: SEQ ID NO 2 + A892P + S884C + A893C

30 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKCEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
35 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
FER DISTEIQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
40 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMIQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGVVFLHVTVYVPAQEKNTTAPAICH
45 GKAHFPREGVFSVNGTHWFVTQRFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYEAPRDGQAYVRKDGGEWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

50

SEQ ID NO 30: SEQ ID NO 2 + D614N + T572I

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFQCNDFLGVYHKNKNSWM
5 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLTSGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRAPGQGTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
10 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNSYECDIPIGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSSTECNNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMIQYTSALLAGTITSGWTFGAGAALQIPFAMQMAVYRFGIGVTQNVLYENQKLIANQFNSAI
15 GKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
DKAHFPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH
20

SEQ ID NO 31: SEQ ID NO 2 + D614N + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFQCNDFLGVYHKNKNSWM
25 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLTSGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRAPGQGTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSNLKPFR
30 DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNSYECDIPIGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSSTECNNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
35 NGLTVLPPLLTDEMIQYTSALLAGTITSGWTFGAGAALQIPFAMQMAVYRFGIGVTQNVLYENQKLIANQFNSAI
GKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
DKAHFPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLG
40 RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 32: SEQ ID NO 2 + D614N + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFQCNDFLGVYHKNKNSWM
45 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLTSGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
50 LCFTNVYADSFVIRGDEVQRAPGQGTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN

NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQNVNCTEV
 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
 SLGAENSVAYSNNISIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
 5 NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
 GKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNFTTAPAICH
 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEVLLSTFLG
 10 RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 33: SEQ ID NO 2 + D614N + S884C + A893C

15 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKCEFCNDPFLGVYHKNKNSWM
 ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFNKLNREFVFNIDGYFKIYSKHTPINLVRDLPGGFSALEPLVDLP
 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
 20 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
 FER DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVN
 FNF NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQNVNCTEV
 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
 SLGAENSVAYSNNISIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
 25 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
 NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGACLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
 SAI GKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNFTTAPAICH
 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
 30 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEVLLSTFLG
 RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 34: SEQ ID NO 2 + T572I + N532P

35 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKCEFCNDPFLGVYHKNKNSWM
 ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFNKLNREFVFNIDGYFKIYSKHTPINLVRDLPGGFSALEPLVDLP
 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
 40 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
 D LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
 FER DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVN
 FNF NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEVP
 VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTMS
 45 LGAENSVAYSNNISIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
 TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
 N GLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
 SAI GKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVTQ
 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNFTTAPAICH
 50 D GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP

DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLGR
SLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

5 SEQ ID NO 35: SEQ ID NO 2 + T572I + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPGGSALEPLVDLP
10 INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGYNYLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVP
15 VAIHADQLTPTWRVYSTGNSVQTRAGCLIGAEHVNNSECDIPGAGICASYQTQNTSPSRAGSVASQSIIAYTMS
LGAENSVAYSNNISIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKFN
GLTVLPPLLTDEMAIQYTSALLACTITSGWTCGAGAAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIG
KIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQ
20 QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAHPGVVFLHVTVYVPAQEKNTTAPAICHG
KAHFPREGVFSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLGR
SLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

25 SEQ ID NO 36: SEQ ID NO 2 + T572I + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPGGSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGYNYLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
35 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVP
VAIHADQLTPTWRVYSTGNSVQTRAGCLIGAEHVNNSECDIPGAGICASYQTQNTSPSRAGSVASQSIIAYTMS
LGAENSVAYSNNISIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKFN
GLTVLPPLLTDEMAIQYTSALLAGTITCGWTFGAGACLIQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIG
40 KIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAHPGVVFLHVTVYVPAQEKNTTAPAICHG
KAHFPREGVFSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLGR
SLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

45 SEQ ID NO 37: SEQ ID NO 2 + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
50 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPGGSALEPLVDLP

INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGVSP TKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
5 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEMI AQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFN SAI
10 GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSA PHGVVFLHVTYVPAQEKNTTAPAICH D
GKAHFPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLG
RSLEVL FQGPGLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH
15

SEQ ID NO 38: SEQ ID NO 2 + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIK/CEFCNDPFLGVYHKNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLV RDLPQGFSALEPLVDLP IG
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGVSP TKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSNLKPFR
25 DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLCAQKF
30 NGLTVLPPLLTDEMI AQYTSALLAGTITCGWTFGAGACLQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFN SAI
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSA PHGVVFLHVTYVPAQEKNTTAPAICH D
GKAHFPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLG
35 RSLEVL FQGPGLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 39: SEQ ID NO 2 + A942P + A892P + D614N

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIK/CEFCNDPFLGVYHKNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLV RDLPQGFSALEPLVDLP IG
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGVSP TKLND
45 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK
50 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFN SAI

5 GKIQDSLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGVVFLHVTVYVPAQEKNTTAPAICH
GKAHFPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 40: SEQ ID NO 2 + A942P + A892P + T572I

10 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVS
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPLQGFS
INITRFQTLALHRSYLT
15 PGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTK
LCFTNVYADSFVIRGDEV
15 RQIAPGQTGKIADYNKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
FERDISTEIQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVN
NFGNGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTE
VVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYEC
20 DIPGAGICASYQTQTNSPSRAGSVASQSIIAYTMS
LGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALT
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVT
20 LADAGFIKQYGDCLGDIAARDLCAQKFN
GLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIG
KIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQ
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGVVFLHVTVYVPAQEKNTTAPAICH
25 DGAHFPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLGR
SLEVLFGQPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 41: SEQ ID NO 2 + A942P + A892P + N532P

30 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVS
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPLQGFS
INITRFQTLALHRSYLT
35 PGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTK
LCFTNVYADSFVIRGDEV
35 RQIAPGQTGKIADYNKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
FERDISTEIQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVN
NFGNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTE
VPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYEC
40 DIPGAGICASYQTQTNSPSRAGSVASQSIIAYTMS
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALT
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVT
40 LADAGFIKQYGDCLGDIAARDLCAQKFN
NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDSLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGVVFLHVTVYVPAQEKNTTAPAICH
45 DGAHFPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

50

SEQ ID NO 42: SEQ ID NO 2 + A942P + A892P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYHKNKNSWM
5 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVRIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
10 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNSYECDIPIGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSSTECNNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLTDEMIAQYTSALLACTITSGWTCGAGPALQIPFAMQAMAYRFNGIGVTQNVLYENQKLIANQFNSAI
15 GKIQDSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRQLSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH
20

SEQ ID NO 43: SEQ ID NO 2 + A942P + A892P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYHKNKNSWM
25 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVRIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
30 DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNSYECDIPIGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSSTECNNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
35 NGLTVLPPLTDEMIAQYTSALLAGTITCGWTFGAGPCLQIPFAMQAMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRQLSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLG
40 RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 44: SEQ ID NO 2 + A942P + D614N + T572I

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYHKNKNSWM
45 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
50 LCFTNVYADSFVIRGDEVRIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN

NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
5 NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
GKIQDSLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEVLLSTFLG
10 RSLEVLFGPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 45: SEQ ID NO 2 + A942P + D614N + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVECFQFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
15 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTK
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGNGYNYLYRFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
25 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
GKIQDSLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
30 SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 46: SEQ ID NO 2 + A942P + D614N + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVECFQFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
40 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTK
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGNGYNYLYRFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
45 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
GKIQDSLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH
50 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT

SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGSYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

5 SEQ ID NO 47: SEQ ID NO 2 + A942P + D614N + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPGGSALEPLVDLP
10 INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMAIQYTSALLAGTITCGWTFGAGACQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGVNNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGSYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

25
SEQ ID NO 48: SEQ ID NO 2 + A942P + T572I + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYHKNKNSWM
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPGGSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVP
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTMS
LGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
GLTVLPPLLTDEMAIQYTSALLAGTITSGWTFGAGAAQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
40 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTVPAQEKNTTAPAICH
KAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGVNNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGSYIPEAPRDGQAYVRKDGWVLLSTFLG
SLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

45
SEQ ID NO 49: SEQ ID NO 2 + A942P + T572I + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
50 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPGGSALEPLVDLP

INITRFQTLALHRSYLT PGDSSSGW TAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
5 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVS VITPGTNTSNQVAVLYQDVNCTEVP
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSEYCDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTMS
LGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKFN
GLTVLPPLLTDEMAIQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFN SAIG
10 KIQDSLSTSPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRQLSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSA PHGVVFLHVTVYVPAQEKNFTTAPAICHDG
KAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLGR
SLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH
15

SEQ ID NO 50: SEQ ID NO 2 + A942P + T572I + S884C + A893C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIKVECFQFCNDPFLGVYHKNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP IG
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
25 DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVS VITPGTNTSNQVAVLYQDVNCTEVP
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSEYCDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTMS
LGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKFN
30 GLTVLPPLLTDEMAIQYTSALLAGTITCGWTFGAGACQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFN SAIG
KIQDSLSTSPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRQLSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSA PHGVVFLHVTVYVPAQEKNFTTAPAICHDG
KAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLGR
35 SLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 51: SEQ ID NO 2 + A942P + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIKVECFQFCNDPFLGVYHKNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP IG
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND
45 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVS VITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSEYCDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTMS
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
50 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKFI
NGLTVLPPLLTDEMAIQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFN SAIF

GKIQDSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGVVFLHVTVYVPAQEKNFHTTAPAICH
GKAHFPREGVFVSNGTWHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
5 RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 52: SEQ ID NO 2 + A942P + N532P + S884C + A893C

10 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSNGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVFCEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLTGDDSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKTLND
15 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK
20 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEMIQYTSALLAGTITCGWTFGAGACLPFAMQAMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGVVFLHVTVYVPAQEKNFHTTAPAICH
GKAHFPREGVFVSNGTWHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
25 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 53: SEQ ID NO 2 + A892P + D614N + T572I

30 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSNGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVFCEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLTGDDSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
35 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKTLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
40 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEMIQYTSALLAGTITSGWTFGAGPALQIPFAMQAMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGVVFLHVTVYVPAQEKNFHTTAPAICH
45 GKAHFPREGVFVSNGTWHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

50

SEQ ID NO 54: SEQ ID NO 2 + A892P + D614N + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM
5 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRAPGQGTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
10 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSFECNSNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLTDEMIQAQYTSALLAGTITSGWTFGAGPALQIPFAMQAMAYRFNGIGVTQNVLYENQKLIANQFNSAI
15 GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGSYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH
20

SEQ ID NO 55: SEQ ID NO 2 + A892P + D614N + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM
25 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRAPGQGTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSNLKPFR
30 DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSFECNSNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
35 NGLTVLPPLTDEMIQAQYTSALLACTITSGWTCGAGPALQIPFAMQAMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGSYIPEAPRDGQAYVRKDGWVLLSTFLG
40 RSLEVLFGPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 56: SEQ ID NO 2 + A892P + D614N + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM
45 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRAPGQGTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSNLKPFR
50 DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN

NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
5 NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLG
10 RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 57: SEQ ID NO 2 + A892P + T572I + N532P

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKCEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDDSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
15 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTK
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVN
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTE
20 VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYT
LGAENSVAYSNNISIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQK
25 GLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
KIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNFTTAPAICH
KAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
30 DVDLGDIGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLGR
SLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 58: SEQ ID NO 2 + A892P + T572I + G880C + F888C

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKCEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDDSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
35 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTK
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVN
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTE
40 VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYT
LGAENSVAYSNNISIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQK
45 GLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
KIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNFTTAPAICH
KAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
50 SP

DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLGR
SLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

5 SEQ ID NO 59: SEQ ID NO 2 + A892P + T572I + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPGGFSALEPLVDLP
10 INITRFQTLALHRSYLTGDSGSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEVP
15 VAIHADQLTPTWRVYSTGNSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTMS
LGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
GLTVLPPLLTDEMIQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
KIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAIVSSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQ
20 QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTVYVPAQEKNTTAPAICH
KAHFPREGVFSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLGR
SLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

25
SEQ ID NO 60: SEQ ID NO 2 + A892P + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPGGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
35 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEVP
PVAIHADQLTPTWRVYSTGNSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMIQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
40 GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAIVSSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTVYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLGR
45 RSLVLFQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 61: SEQ ID NO 2 + A892P + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
50 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPGGFSALEPLVDLP

INITRFQTLALHRSYLT PGDSSSGW TAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLND
LCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
5 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMI AQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGV TQNVLYENQKLIANQFN SAI
10 GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSA PHGVVFLHVTYVPAQEKNTTAPAICH D
GKAHFPREGVFVSN GTHWFVTQRNFYEPQIITDNTFVSGNCDV VIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLG
RSLEVL FQGPGLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH
15

SEQ ID NO 62: SEQ ID NO 2 + D614N + T572I + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIK VCEFQCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLV RDLPQGFSALEPLVDLP IG
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLND
LCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
25 DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
30 NGLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGV TQNVLYENQKLIANQFN SAI
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSA PHGVVFLHVTYVPAQEKNTTAPAICH D
GKAHFPREGVFVSN GTHWFVTQRNFYEPQIITDNTFVSGNCDV VIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLG
35 RSLEVL FQGPGLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 63: SEQ ID NO 2 + D614N + T572I + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIK VCEFQCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLV RDLPQGFSALEPLVDLP IG
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLND
45 LCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
50 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMI AQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGV TQNVLYENQKLIANQFN SAI

GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYEAPRDGQAYVRKDGGEWVLLSTFLG
5 RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 64: SEQ ID NO 2 + D614N + T572I + S884C + A893C

10 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLPIG
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKTLND
15 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
20 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGACLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
25 SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYEAPRDGQAYVRKDGGEWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 65: SEQ ID NO 2 + D614N + N532P + G880C + F888C

30 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLPIG
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
35 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKTLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
40 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH
45 GKAHFPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYEAPRDGQAYVRKDGGEWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

50

SEQ ID NO 66: SEQ ID NO 2 + D614N + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYHKNKNSWM
5 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVN
10 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEMAIAQYTSALLAGTITCGWTFGAGACLQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
15 KIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
DKAHPREGVVFVSNQTHWVFTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH
20

SEQ ID NO 67: SEQ ID NO 2 + T572I + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYHKNKNSWM
25 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSNLKPFR
30 DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVN
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIAYTMS
LGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
35 GLTVLPPLLTDEMAIAQYTSALLACTITSGWTCGAGALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAIG
KIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
DKAHPREGVVFVSNQTHWVFTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
40 DVDLGDIGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLGR
SLEVLFGPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 68: SEQ ID NO 2 + T572I + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYHKNKNSWM
45 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
50 LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVN

NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEV
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNPSRAGSVASQSIAYTMS
LGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKFN
5 GLTVLPPLLTDEMAQYTSALLAGTITCGWTFGAGACLPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNNSAIG
KIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICHDG
KAHFPPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGYIPEAPRDGQAYVRKDGGEWVLLSTFLGR
10 SLEVLFGPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 69: SEQ ID NO 2 + A942P + A892P + D614N + T572I

15 MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKCEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
20 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVN
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNPSRAGSVASQSIAYTM
25 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQK
NGLTVLPPLLTDEMAQYTSALLAGTITSGWTFGAGPALQPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH
30 GKAHFPPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 70: SEQ ID NO 2 + A942P + A892P + D614N + N532P

35 MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKCEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
40 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVN
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNPSRAGSVASQSIAYTM
45 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQK
NGLTVLPPLLTDEMAQYTSALLAGTITSGWTFGAGPALQPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH
50 GKAHFPPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT

SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGSYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

5 SEQ ID NO 71: SEQ ID NO 2 + A942P + A892P + D614N + G880C + F888C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYHKNKSWM
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
10 INITRFQTLALHRSYLTGDSGSGWTAGAAAYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGNYLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVTPTNTSNQVAVLYQNVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMIQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAIVSSVNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGSYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

25

SEQ ID NO 72: SEQ ID NO 2 + A942P + A892P + D614N + S884C + A893C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYHKNKSWM
30 ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGNYLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVTPTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMIQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
40 GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAIVSSVNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGSYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

45

SEQ ID NO 73: SEQ ID NO 2 + A942P + A892P + T572I + N532P

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYHKNKSWM
50 ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG

INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG
 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
 5 DISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEVP
 VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIAYTMS
 LGAENSVAYSNNIAIPTNFTISVTTEILPVSMKTSTVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
 TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKFN
 GLTVLPPLLTDEMAIQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
 10 KIAQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRQLSLQTYVTQ
 QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAHPGVVFLHVTVYPAQEKNFTTAPAICHG
 KAHFPREGVVFVSNQTHWVFTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
 DVDLGDISGINASVNNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLGR
 SLEVLFGQPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH
 15

SEQ ID NO 74: SEQ ID NO 2 + A942P + A892P + T572I + G880C + F888C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS
 20 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLVNNATNVVIKVEFCNDPFLGVYHKNKNSWM
 ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPPQGSALPLVDLP
 INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG
 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
 25 DISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEVP
 VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIAYTMS
 LGAENSVAYSNNIAIPTNFTISVTTEILPVSMKTSTVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
 TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKFN
 30 GLTVLPPLLTDEMAIQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
 KIAQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRQLSLQTYVTQ
 QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAHPGVVFLHVTVYPAQEKNFTTAPAICHG
 KAHFPREGVVFVSNQTHWVFTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
 DVDLGDISGINASVNNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLGR
 35 SLEVLFGQPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 75: SEQ ID NO 2 + A942P + A892P + T572I + S884C + A893C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS
 40 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLVNNATNVVIKVEFCNDPFLGVYHKNKNSWM
 ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPPQGSALPLVDLP
 INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG
 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
 45 DISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEVP
 VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIAYTMS
 LGAENSVAYSNNIAIPTNFTISVTTEILPVSMKTSTVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
 TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKFN
 50 GLTVLPPLLTDEMAIQYTSALLAGTITCGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
 KIAQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRQLSLQTYVTQ
 QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAHPGVVFLHVTVYPAQEKNFTTAPAICHG
 KAHFPREGVVFVSNQTHWVFTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
 DVDLGDISGINASVNNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLGR
 SLEVLFGQPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

KIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTVYVPAQEKNTTAPAICHG
KAHFPREGVFVSNQTHWVFTQRFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGYIPEAPRDGQAYVRKDGGEWVLLSTFLGR
5 SLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 76: SEQ ID NO 2 + A942P + A892P + N532P + G880C + F888C

10 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSQNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKCEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFKIDGYFKIYSKHTPINLVRLDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
15 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
FER DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
20 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMIQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTVYVPAQEKNTTAPAICHG
GKAHFPREGVFVSNQTHWVFTQRFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
25 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 77: SEQ ID NO 2 + A942P + A892P + N532P + S884C + A893C

30 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSQNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKCEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFKIDGYFKIYSKHTPINLVRLDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
35 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
FER DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
40 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMIQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTVYVPAQEKNTTAPAICHG
45 GKAHFPREGVFVSNQTHWVFTQRFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

50

SEQ ID NO 78: SEQ ID NO 2 + A942P + D614N + T572I + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYHKNKNSWM
5 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
10 DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVTPTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNSYECDIPIGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSSTECNNLLQYGSFCTQLNRALT
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDL
15 NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGAAALQIPFAMQMAFRNGIGVGTQNVLYENQKLIANQFNSAI
QKIQDSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAIVSSVNDILSRDLKVEAEVQIDRLITGRQLS
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
20 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 79: SEQ ID NO 2 + A942P + D614N + T572I + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYHKNKNSWM
25 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
30 DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVTPTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNSYECDIPIGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSSTECNNLLQYGSFCTQLNRALT
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDL
35 NGLTVLPPLTDEMIAQYTSALLACTITSGWTCGAGAAALQIPFAMQMAFRNGIGVGTQNVLYENQKLIANQFNSAI
GKIQDSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAIVSSVNDILSRDLKVEAEVQIDRLITGRQLS
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
40 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 80: SEQ ID NO 2 + A942P + D614N + T572I + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYHKNKNSWM
45 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
50 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF

NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQNVNCTEV
 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
 SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
 5 NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGACLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
 GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH
 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLG
 10 RSLEVLFGPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 81: SEQ ID NO 2 + A942P + D614N + N532P + G880C + F888C

15 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVECFQFCNDPFLGVYHKNKNSWM
 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
 20 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGNGYNYLYRFRKSNLKP
 FER DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVN
 FNF NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQNVNCTEV
 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
 SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
 25 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
 NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
 GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH
 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
 30 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLG
 RSLEVLFGPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 82: SEQ ID NO 2 + A942P + D614N + N532P + S884C + A893C

35 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVECFQFCNDPFLGVYHKNKNSWM
 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
 40 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
 D LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGNGYNYLYRFRKSNLKP
 FER DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVN
 FNF NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQNVNCTEV
 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
 SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
 45 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
 NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGACLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
 GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH
 50 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT

SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGGSGYIPEAPRDGQAYVRKDG EWVLLSTFLG
RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

5 SEQ ID NO 83: SEQ ID NO 2 + A942P + T572I + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
10 INITRFQTLALHRSYLTGDSGSGWTAGAAAYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVP
15 VAIHADQLTPTWVYSTGSGNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTMS
LGAENSVAYSNNISIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKFN
GLTVLPPLLTDEMIQYTSALLACTITSGWTCGAGAAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
KIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQ
20 QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAHPGVVFLHVTVYVPAQEKNTTAPAICHG
KAHFPREGVFSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGGSGYIPEAPRDGQAYVRKDG EWVLLSTFLGR
SLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

25 SEQ ID NO 84: SEQ ID NO 2 + A942P + T572I + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
35 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVP
VAIHADQLTPTWVYSTGSGNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTMS
LGAENSVAYSNNISIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKFN
GLTVLPPLLTDEMIQYTSALLAGTITCGWTFGAGACLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
40 KIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAHPGVVFLHVTVYVPAQEKNTTAPAICHG
KAHFPREGVFSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGGSGYIPEAPRDGQAYVRKDG EWVLLSTFLGR
SLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

45 SEQ ID NO 85: SEQ ID NO 2 + A892P + D614N + T572I + N532P

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
50 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP

INITRFQTLALHRSYLT PGDSSSGW TAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
5 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVS VITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSEYECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSM TKTSDVCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKR SFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGV TQNVLYENQKLIANQFN SAI
10 GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNF GAISSVLNDILSRDKVEAEVQIDRLITGRQLSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLM SFPQSAPHGVVFLHVTYVPAQEKNF TTAICH D
GKAHFPREGVFVSN GTHWFVTQRNFYEPQIITDNTFVSGNCDV VIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLG
RSLEVL FQGPGLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH
15

SEQ ID NO 86: SEQ ID NO 2 + A892P + D614N + T572I + G880C + F888C

MFVFLVLLPLVSSQCVNL TTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTW FHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIK VCEFQCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNL REFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP IG
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
25 DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVS VITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSEYECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSM TKTSDVCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKR SFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
30 NGLTVLPPLLTDEMI AQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGV TQNVLYENQKLIANQFN SAI
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNF GAISSVLNDILSRDKVEAEVQIDRLITGRQLSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLM SFPQSAPHGVVFLHVTYVPAQEKNF TTAICH D
GKAHFPREGVFVSN GTHWFVTQRNFYEPQIITDNTFVSGNCDV VIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLG
35 RSLEVL FQGPGLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 87: SEQ ID NO 2 + A892P + D614N + T572I + S884C + A893C

MFVFLVLLPLVSSQCVNL TTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTW FHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIK VCEFQCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNL REFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP IG
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLND
45 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVS VITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSEYECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSM TKTSDVCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
50 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKR SFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMI AQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGV TQNVLYENQKLIANQFN SAI

GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
5 RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 88: SEQ ID NO 2 + A892P + D614N + N532P + G880C + F888C

10 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCNDPFLGVYYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLPQGFSALEPLVDLP
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
15 LCFTNVYADSFVIRGDEVVRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
FER DISTEIQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
20 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEMI AQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
25 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 89: SEQ ID NO 2 + A892P + D614N + N532P + S884C + A893C

30 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCNDPFLGVYYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLPQGFSALEPLVDLP
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
35 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVVRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
FER DISTEIQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
40 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEMI AQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
45 GKAHFPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

50

SEQ ID NO 90: SEQ ID NO 2 + A892P + T572I + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHKNKSWM
5 ESEFRVYSSANNCTFEYVSPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSEKCTLKSTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVRIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
10 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVTGTNTSNQVAVLYQDVNCTEVP
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNSYECDIPIGAGICASYQTQNTSPSRAGSVASQSIIAYTMS
LGAENSVAYSNNISIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKFN
GLTVLPPLLTDEMAIYQTSALLACTITSGWTGAGPALQIPFAMQMAYRFNGIGVTVQNVLYENQKLIANQFN
15 QIQLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAIVSSVNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTVYVPAQEKNTTAPAICHG
KAHFPREGVFSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVIGVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGYIPEAPRDGQAYVRKDGWVLLSTFLGR
SLEVLFGPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHH
20

SEQ ID NO 91: SEQ ID NO 2 + A892P + T572I + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHKNKSWM
25 ESEFRVYSSANNCTFEYVSPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSEKCTLKSTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVRIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSNLKPFR
30 DISTEIYQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVTGTNTSNQVAVLYQDVNCTEVP
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNSYECDIPIGAGICASYQTQNTSPSRAGSVASQSIIAYTMS
LGAENSVAYSNNISIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKFN
35 GLTVLPPLLTDEMAIYQTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTVQNVLYENQKLIANQFN
QIQLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAIVSSVNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTVYVPAQEKNTTAPAICHG
KAHFPREGVFSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVIGVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGYIPEAPRDGQAYVRKDGWVLLSTFLGR
40 SLEVLFGPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHH

SEQ ID NO 92: SEQ ID NO 2 + D614N + T572I + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHKNKSWM
45 ESEFRVYSSANNCTFEYVSPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSEKCTLKSTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVRIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSNLKPFR
50 DISTEIYQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN

NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQNVNCTEV
 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNPSRAGSVASQSIIAYTM
 SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
 5 NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
 GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH
 GKAHFPREGVFVSNQTHWFTVQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEVLLSTFLG
 10 RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 93: SEQ ID NO 2 + D614N + T572I + N532P + S884C + A893C

15 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVECFQFCNDPFLGVYHKNKNSWM
 ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
 20 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLYRFRKSNLKP
 FER DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVN
 FNF NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQNVNCTEV
 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNPSRAGSVASQSIIAYTM
 SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
 25 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
 NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGACLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
 SAI GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH
 GKAHFPREGVFVSNQTHWFTVQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
 30 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEVLLSTFLG
 RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 94: SEQ ID NO 2 + A942P + A892P + D614N + T572I + N532P

35 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVECFQFCNDPFLGVYHKNKNSWM
 ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
 40 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
 D LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLYRFRKSNLKP
 FER DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVN
 FNF NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQNVNCTEV
 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNPSRAGSVASQSIIAYTM
 SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
 45 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
 NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
 SAI GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH
 50 GKAHFPREGVFVSNQTHWFTVQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGSYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

5 SEQ ID NO 95: SEQ ID NO 2 + A942P + A892P + D614N + T572I + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
10 INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNNSYECDIPIGAGICASYQTQTNPSRAGSVASQSIAYTM
SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMIQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTVVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGSYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

25

SEQ ID NO 96: SEQ ID NO 2 + A942P + A892P + D614N + T572I + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCNDPFLGVYHKNKNSWM
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
35 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNNSYECDIPIGAGICASYQTQTNPSRAGSVASQSIAYTM
SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMIQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
40 GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTVVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGSYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

45

SEQ ID NO 97: SEQ ID NO 2 + A942P + A892P + D614N + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
50 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP

INITRFQTLALHRSYLT PGDSSSGW TAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGVSP TKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
5 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNSYECDIPIGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMI AQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SAI
10 GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSA PHGVVFLHVTYVPAQEKNTTAPAICH D
GKAHFPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLG
RSLEVLFGPGGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH
15

SEQ ID NO 98: SEQ ID NO 2 + A942P + A892P + D614N + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIKVECFQCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP IG
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGVSP TKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
25 DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNSYECDIPIGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
30 NGLTVLPPLLTDEMI AQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SAI
GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSA PHGVVFLHVTYVPAQEKNTTAPAICH D
GKAHFPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLG
35 RSLEVLFGPGGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 99: SEQ ID NO 2 + A942P + A892P + T572I + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIKVECFQCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP IG
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGVSP TKLND
45 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV P
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNSYECDIPIGAGICASYQTQTNPSRAGSVASQSIIAYTMS
LGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDKN
50 TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF N
GLTVLPPLLTDEMI AQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SAI

KIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTVYVPAQEKNFTTAPAICHG
KAHFPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLGR
5 SLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 100: SEQ ID NO 2 + A942P + A892P + T572I + N532P + S884C + A893C

10 MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKCEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPLQGFSALEPLVDLP
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
15 LCFTNVYADSFVIRGDEVQRJAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
FER DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVN
FNF NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTE
VP VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTMS
LGAENSVAYSNNISIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQ
20 DKN TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDL
ICAQKFN GLTVLPPLLTDEMQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQ
FNSAIG KIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQ
SLQTYVTQ QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTVYVPAQEKN
FTTAPAICHG KAHPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKE
ELDKYFKNHTSP 25 DVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAY
VRKDGGEWVLLSTFLGR SLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 101: SEQ ID NO 2 + A942P + D614N + T572I + N532P + G880C + F888C

30 MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKCEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPLQGFSALEPLVDLP
IG INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
35 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
D LCFTNVYADSFVIRGDEVQRJAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
FER DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVN
FNF NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTE
V PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTM
40 SLGAENSVAYSNNISIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQ
DK NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDL
ICAQKF NGLTVLPPLLTDEMQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQ
FNSAI GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
45 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTVYVPAQEKNFTTAPAICH
D GKAHFPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

50 SEQ ID NO 102: SEQ ID NO 2 + A942P + D614N + T572I + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLVNNATNVVIKVCFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
5 INITRFQTLALHRSYLT PGDSSSGW TAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVRIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVN
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
10 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMI AQYTSALLAGTITCGWTFGAGACQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
GKIQDSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAPHGVVFLHVTYVPAQEKNF TTAICH
15 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

20 SEQ ID NO 103: SEQ ID NO 2 + A892P + D614N + T572I + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLVNNATNVVIKVCFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
25 INITRFQTLALHRSYLT PGDSSSGW TAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVRIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVN
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQNVNCTEV
30 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMI AQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
35 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAPHGVVFLHVTYVPAQEKNF TTAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

40 SEQ ID NO 104: SEQ ID NO 2 + A892P + D614N + T572I + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLVNNATNVVIKVCFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
45 INITRFQTLALHRSYLT PGDSSSGW TAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVRIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVN
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQNVNCTEV
50 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM

SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
5 GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFVSNGTWHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

10

SEQ ID NO 105: SEQ ID NO 2 + A942P + A892P + D614N + T572I + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVS
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVECFQFCNDPFLGVYHKNKSWM
15 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGGWTAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEK
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTK
LCFTNVYADSFVIRGDEVQRJAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGNGYNYLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVN
20 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVTGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
25 GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFVSNGTWHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

30

SEQ ID NO 106: SEQ ID NO 2 + A942P + A892P + D614N + T572I + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVS
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVECFQFCNDPFLGVYHKNKSWM
35 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGGWTAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEK
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTK
LCFTNVYADSFVIRGDEVQRJAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGNGYNYLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVN
40 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVTGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
45 GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFVSNGTWHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

50

SEQ ID NO 107: SEQ ID NO 3 + A942P + A892P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
5 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
10 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSSTECNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
15 NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQAMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGSYIPEAPRDGQAYVRKDGWVLLSTFLG
20 RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 108: SEQ ID NO 3 + A942P + D614N

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
30 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSSTECNLLQYGSFCTQLNRALTGIAVEQDK
35 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQAMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
40 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGSYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 109: SEQ ID NO 3 + A942P + T572I

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
50 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP

DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEV
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNPSRAGSVASQSIAYTMS
LGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
5 TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKFN
GLTVLPPLLTDEMAIQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNNSAI
KIQDSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICHG
KAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
10 DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLGR
SLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 110: SEQ ID NO 3 + A942P + N532P

15 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKCEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
20 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGNGYNYLYRFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNPSRAGSVASQSIAYTM
25 SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQK
NGLTVLPPLLTDEMAIQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
GKIQDSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH
30 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

35 SEQ ID NO 111: SEQ ID NO 3 + A942P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKCEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
40 INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGNGYNYLYRFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNPSRAGSVASQSIAYTM
45 SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQK
NGLTVLPPLLTDEMAIQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
GKIQDSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
50 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGSYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

5 SEQ ID NO 112: SEQ ID NO 3 + A942P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
10 INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLG DIAARDLCAQKF
NGLTVLPPLLTDEMI AQYTSALLAGTITCGWTFGAGACLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
SAI
20 GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLM SFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
D
GKAHFPREGV FVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGSYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

25
SEQ ID NO 113: SEQ ID NO 3 + A892P + D614N

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYHKNKNSWM
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLG DIAARDLCAQKF
NGLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
40 SAI
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLM SFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
D
GKAHFPREGV FVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGSYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

45
SEQ ID NO 114: SEQ ID NO 3 + A892P + T572I

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
50 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
IG

INITRFQTLALHRSYLT PGDSSSGW TAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
5 DISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEVP
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTMS
LGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKFN
GLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
10 KIAQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSA PHGVVFLHVTYVPAQEKNTTAPAICH
KAHFPREGV FVSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLGR
SLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH
15

SEQ ID NO 115: SEQ ID NO 3 + A892P + N532P

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTW FHAHVS GTNGTK
20 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIK VCEFQFCNDPFLGVYHKNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
25 DISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEVP
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYT
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
30 NGLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSA PHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGV FVSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLG
35 RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 116: SEQ ID NO 3 + A892P + G880C + F888C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTW FHAHVS GTNGTK
40 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIK VCEFQFCNDPFLGVYHKNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
45 DISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEVP
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYT
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
50 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEMI AQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
NSAI

GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGVVFLHVTVYVPAQEKNTTAPAICH
GKAHFPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
5 RSLEVLFGPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 117: SEQ ID NO 3 + A892P + S884C + A893C

10 MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRLDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTSGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
15 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNKLPDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSNLKP
FER DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
20 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMIQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGVVFLHVTVYVPAQEKNTTAPAICH
GKAHFPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
25 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 118: SEQ ID NO 3 + D614N + T572I

30 MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRLDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTSGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
35 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNKLPDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSNLKP
FER DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTM
40 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMIQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGVVFLHVTVYVPAQEKNTTAPAICH
45 GKAHFPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

50 SEQ ID NO 119: SEQ ID NO 3 + D614N + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLVNNATNVVIKVEFCQFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLTGDSGSGWTAGAAAYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
5 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSNLKPFR
DSTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNPSRAGSVASQSIIAYTM
10 SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
15 QKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

20 SEQ ID NO 120: SEQ ID NO 3 + D614N + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLVNNATNVVIKVEFCQFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
25 INITRFQTLALHRSYLTGDSGSGWTAGAAAYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSNLKPFR
DSTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
30 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMIAQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
35 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

40 SEQ ID NO 121: SEQ ID NO 3 + D614N + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLVNNATNVVIKVEFCQFCNDPFLGVYHKNKNSWM
45 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLTGDSGSGWTAGAAAYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSNLKPFR
DSTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
50 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNPSRAGSVASQSIIAYTM

SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMAIAQYTSALLAGTITCGWTFGAGACLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
5 GKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEVLLSTFLG
RSLVLFQGPGLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

10

SEQ ID NO 122: SEQ ID NO 3 + T572I + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKCEFCNDPFLGVYHKNKNSWM
15 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNF
20 NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTE
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIAYTMS
LGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
GLTVLPPLLTDEMAIAQYTSALLAGTITSGWTFGAGAAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
25 KIAQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTYVPAQEKNFTTAPAICH
KAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEVLLSTFLGR
SLEVLQGPGLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

30

SEQ ID NO 123: SEQ ID NO 3 + T572I + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKCEFCNDPFLGVYHKNKNSWM
35 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
40 NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTE
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIAYTMS
LGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
GLTVLPPLLTDEMAIAQYTSALLACTITSGWTCGAGAAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
45 KIAQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTYVPAQEKNFTTAPAICH
KAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEVLLSTFLGR
SLEVLQGPGLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

50

SEQ ID NO 124: SEQ ID NO 3 + T572I + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
5 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDPDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
10 DISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVP
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNPSRAGSVASQSIIAYTMS
LGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRLTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKFN
15 GLTVLPPLLTDEMIAQYTSALLAGTITCGWTFGAGACLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIG
KIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTVYVPAQEKNTTAPAICHDG
KAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGSYIPEAPRDGQAYVRKDGWVLLSTFLGR
20 SLEVLFGQPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 125: SEQ ID NO 3 + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND
30 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDPDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRLTGIAVEQDK
35 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMIAQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTVYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
40 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGSYIPEAPRDGQAYVRKDGWVLLSTFLGR
RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 126: SEQ ID NO 3 + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
50 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDPDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR

DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
5 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGACLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
10 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 127: SEQ ID NO 3 + A942P + A892P + D614N

15 MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFNKLNREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLP
INITRFQTLALHRSYLTSGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
20 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKTLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
25 SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
GKIQDSLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTYVPAQEKNFTTAPAICH
30 GKAHFPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

35 SEQ ID NO 128: SEQ ID NO 3 + A942P + A892P + T572I

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFNKLNREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLP
40 INITRFQTLALHRSYLTSGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKTLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEV
45 VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTMS
LGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
GLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
KIQDSLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVTQ
50 QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTYVPAQEKNFTTAPAICH
KAHFPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP

DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLGR
SLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

5 SEQ ID NO 129: SEQ ID NO 3 + A942P + A892P + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
10 INITRFQTLALHRSYLTGDSGSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVRIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMIQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
20 GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAIVSSVNDILSRDPPAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKEYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

25 SEQ ID NO 130: SEQ ID NO 3 + A942P + A892P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLTGDSGSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVRIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
35 NGLTGTGVLTESNKKFLPFQFGRIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
40 NGLTVLPPLLTDEMIQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAIVSSVNDILSRDPPAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSVNGTHWVFTQRFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKEYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
45 RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 131: SEQ ID NO 3 + A942P + A892P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
50 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG

INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
5 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMI AQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFN SAI
10 GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSA PHGVVFLHVTYVPAQEKNTTAPAICH D
GKAHFPREGVFVSNGT HWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLG
RSLEVL FQGPGLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH
15

SEQ ID NO 132: SEQ ID NO 3 + A942P + D614N + T572I

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIKVC EFQFCNDPFLGVYHKNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLV RDLPQGFSALEPLVDLP IG
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
25 DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
30 NGLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFN SAI
GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSA PHGVVFLHVTYVPAQEKNTTAPAICH D
GKAHFPREGVFVSNGT HWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLG
35 RSLEVL FQGPGLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 133: SEQ ID NO 3 + A942P + D614N + N532P

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIKVC EFQFCNDPFLGVYHKNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLV RDLPQGFSALEPLVDLP IG
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND
45 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
50 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFN SAI

GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
5 RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 134: SEQ ID NO 3 + A942P + D614N + G880C + F888C

10 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVFCEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKINIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
15 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
FER DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
20 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMI AQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
25 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 135: SEQ ID NO 3 + A942P + D614N + S884C + A893C

30 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVFCEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKINIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
35 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
FER DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
40 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMI AQYTSALLAGTITCGWTFGAGACLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
45 GKAHFPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

50

SEQ ID NO 136: SEQ ID NO 3 + A942P + T572I + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYHKNKSWM
5 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRAPGQGTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
10 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVP
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQNTSPSRAGSVASQSIIAYTMS
LGAENSVAYSNNISIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKFN
GLTVLPPLLTDEMAIYQTSALLAGTITSGWTGAGAAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIG
15 QIQDSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRQLSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTYVPAQEKNFTTAPAICHG
KAHFPREGVFSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLGR
SLEVLFGQPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH
20

SEQ ID NO 137: SEQ ID NO 3 + A942P + T572I + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYHKNKSWM
25 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRAPGQGTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYLYRLFRKSNLKPFR
30 DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVP
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQNTSPSRAGSVASQSIIAYTMS
LGAENSVAYSNNISIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKFN
35 GLTVLPPLLTDEMAIYQTSALLACTITSGWTCGAGAAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIG
KIQDSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRQLSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTYVPAQEKNFTTAPAICHG
KAHFPREGVFSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
40 DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLGR
SLEVLFGQPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 138: SEQ ID NO 3 + A942P + T572I + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYHKNKSWM
45 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
50 LCFTNVYADSFVIRGDEVQRAPGQGTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN

NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEV
 VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNPSRAGSVASQSIAYTMS
 LGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
 TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKFN
 5 GLTVLPPLLTDEMAQYTSALLAGTITCGWTFGAGACLPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNNSAIG
 KIQDSLSTSPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVTQ
 QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGHYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICHDG
 KAHFPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
 DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGYIPEAPRDGQAYVRKDGGEWVLLSTFLGR
 10 SLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 139: SEQ ID NO 3 + A942P + N532P + G880C + F888C

15 MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKCEFCNDPFLGVYHKNKNSWM
 ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETCKTLKSFTVEKG
 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND
 20 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLYRFRKSNLKPFR
 DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEV
 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNPSRAGSVASQSIAYTM
 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
 25 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
 NGLTVLPPLLTDEMAQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNNSAI
 GKIQDSLSTSPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGHYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
 GKAHFPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
 30 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
 RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 140: SEQ ID NO 3 + A942P + N532P + S884C + A893C

35 MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKCEFCNDPFLGVYHKNKNSWM
 ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETCKTLKSFTVEKG
 40 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND
 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLYRFRKSNLKPFR
 DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEV
 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNPSRAGSVASQSIAYTM
 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
 45 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
 NGLTVLPPLLTDEMAQYTSALLAGTITCGWTFGAGACLPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNNSAI
 GKIQDSLSTSPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGHYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
 50 GKAHFPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGSYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

5 SEQ ID NO 141: SEQ ID NO 3 + A892P + D614N + T572I

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
10 INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQNVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
SAI
20 GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTVVPAQEKNTTAPAICH
D
GKAHFPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGSYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

25
SEQ ID NO 142: SEQ ID NO 3 + A892P + D614N + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNF
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
40 SAI
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTVVPAQEKNTTAPAICH
D
GKAHFPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGSYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

45
SEQ ID NO 143: SEQ ID NO 3 + A892P + D614N + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVS GTNGTK
50 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
IG

INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
5 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNSYECDIPIGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMI AQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SAI
10 GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSA PHGVVFLHVTYVPAQEKNF TTAICH D
GKAHFPREGVFVSN GTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLG
RSLEVL FQGPGLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH
15

SEQ ID NO 144: SEQ ID NO 3 + A892P + D614N + S884C + A893C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTW FHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIK VCEFQFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLV RDLPQGFSALEPLVDLP IG
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
25 DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNSYECDIPIGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
30 NGLTVLPPLLTDEMI AQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SAI
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSA PHGVVFLHVTYVPAQEKNF TTAICH D
GKAHFPREGVFVSN GTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLG
35 RSLEVL FQGPGLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 145: SEQ ID NO 3 + A892P + T572I + N532P

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTW FHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIK VCEFQFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLV RDLPQGFSALEPLVDLP IG
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND
45 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVP
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNSYECDIPIGAGICASYQTQTNPSRAGSVASQSIIAYTMS
LGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDKN
50 TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF N
GLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SAI

KIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAHGCVVFLHVTVYVPAQEKNTTAPAICHDG
KAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLGR
5 SLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 146: SEQ ID NO 3 + A892P + T572I + G880C + F888C

10 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKCEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
15 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
FER DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVP
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIAYTMS
LGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
20 TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKFN
GLTVLPPLLTDEMAIQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIG
KIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAHGCVVFLHVTVYVPAQEKNTTAPAICHDG
KAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
25 DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLGR
SLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 147: SEQ ID NO 3 + A892P + T572I + S884C + A893C

30 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKCEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
35 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
FER DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVP
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIAYTMS
40 LGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKFN
GLTVLPPLLTDEMAIQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIG
KIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAHGCVVFLHVTVYVPAQEKNTTAPAICHDG
45 KAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLGR
SLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

50

SEQ ID NO 148: SEQ ID NO 3 + A892P + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIK VCEFQFCNDPFLGVVYHKNNKSWM
5 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVN
10 NGLTGTGVLTESNKKFLPFQ QFGRDIADTTDAVRDPQTLEILDITPCSFGGVS VITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSEYECDIPIGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSM TKTSDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKR SFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMI AQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
15 SAI GKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGR LQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLM SFPQSAPHGVVFLHVTVYVPAQEKNTTAPAICH
D GKAHFPREGV FVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDV VIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGS GYIPEAPRDGQAYVRKDG EWVLLSTFLG
RSLEVL FQGPGLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH
20

SEQ ID NO 149: SEQ ID NO 3 + A892P + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIK VCEFQFCNDPFLGVVYHKNNKSWM
25 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
30 DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVN
NGLTGTGVLTESNKKFLPFQ QFGRDIADTTDAVRDPQTLEILDITPCSFGGVS VITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSEYECDIPIGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSM TKTSDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKR SFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
35 NGLTVLPPLLTDEMI AQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
SAI GKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGR LQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLM SFPQSAPHGVVFLHVTVYVPAQEKNTTAPAICH
D GKAHFPREGV FVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDV VIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGS GYIPEAPRDGQAYVRKDG EWVLLSTFLG
40 RSLEVL FQGPGLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 150: SEQ ID NO 3 + D614N + T572I + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIK VCEFQFCNDPFLGVVYHKNNKSWM
45 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
50 DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVN
FNF

NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQNVNCTEV
 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
 SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
 5 NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
 GKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH
 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEVLLSTFLG
 10 RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 151: SEQ ID NO 3 + D614N + T572I + G880C + F888C

15 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVECFQFCNDPFLGVYHKNKNSWM
 ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLP
 INITRFQTLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
 20 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
 DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
 NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQNVNCTEV
 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
 SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
 25 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
 NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
 GKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH
 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
 30 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEVLLSTFLG
 RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 152: SEQ ID NO 3 + D614N + T572I + S884C + A893C

35 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVECFQFCNDPFLGVYHKNKNSWM
 ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLP
 INITRFQTLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
 40 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
 DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
 NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQNVNCTEV
 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
 SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
 45 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
 NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGACQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
 GKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH
 50 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

5 SEQ ID NO 153: SEQ ID NO 3 + D614N + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
10 INITRFQTLALHRSYLTGDSGSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMIQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTVVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

25 SEQ ID NO 154: SEQ ID NO 3 + D614N + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYHKNKNSWM
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMIQYTSALLAGTITCGWTFGAGACLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
40 GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTVVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

45 SEQ ID NO 155: SEQ ID NO 3 + T572I + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
50 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP

INITRFQTLALHRSYLT PGDSSSGW TAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
5 NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVS VITPGTNTSNQVAVLYQDVNCTEVP
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTMS
LGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKFN
GLTVLPPLLTDEMAIQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFN SAIG
10 KIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRQLSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSA PHGVVFLHVTVYVPAQEKNFTTAPAICHDG
KAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLGR
SLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH
15

SEQ ID NO 156: SEQ ID NO 3 + T572I + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIKVECFQCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP IG
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
25 DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVS VITPGTNTSNQVAVLYQDVNCTEVP
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTMS
LGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKFN
30 GLTVLPPLLTDEMAIQYTSALLAGTITCGWTFGAGACQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFN SAIG
KIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRQLSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSA PHGVVFLHVTVYVPAQEKNFTTAPAICHDG
KAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLGR
35 SLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 157: SEQ ID NO 3 + A942P + A892P + D614N + T572I

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIKVECFQCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP IG
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND
45 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVS VITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTMS
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
50 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMAIQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFN SAIG

GKIQDSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTVYVPAQEKNTTAPAICH
GKAHFPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
5 RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 158: SEQ ID NO 3 + A942P + A892P + D614N + N532P

10 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPPQGS
INITRFQTLALHRSYLTSGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCT
15 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYG
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRK
DISTEIYQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNK
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQ
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSI
20 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALT
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDI
NGLTVLPPLLTDEMIQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIAN
GKIQDSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQ
25 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTVYVPAQEKNTT
GKAHFPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEEL
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 159: SEQ ID NO 3 + A942P + A892P + D614N + G880C + F888C

30 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPPQGS
INITRFQTLALHRSYLTSGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCT
35 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYG
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRK
DISTEIYQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNK
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQ
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSI
40 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALT
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDI
NGLTVLPPLLTDEMIQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIAN
GKIQDSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQ
45 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTVYVPAQEKNTT
GKAHFPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEEL
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

50

SEQ ID NO 160: SEQ ID NO 3 + A942P + A892P + D614N + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVVYHKNNKSWM
5 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLTGDDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
10 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSSTECNNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMIQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
15 KIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPAEVQIDRLITGRQLSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
DKAHPREGVVFVSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVIGVNNVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH
20

SEQ ID NO 161: SEQ ID NO 3 + A942P + A892P + T572I + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVVYHKNNKSWM
25 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLTGDDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSNLKPFR
30 DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVP
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTMS
LGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSSTECNNLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
35 GLTVLPPLLTDEMIQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIG
KIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPAEVQIDRLITGRQLSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
DKAHPREGVVFVSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVIGVNNVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLGR
40 SLEVLFGPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 162: SEQ ID NO 3 + A942P + A892P + T572I + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVVYHKNNKSWM
45 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLTGDDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSNLKPFR
50 DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN

NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEV
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNPSRAGSVASQSIAYTMS
LGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKFN
5 GLTVLPPLLTDEMAIQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
KIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHG
KAHFPREGVVFVSNGTHWFVTQNRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVLGDISGINASVNNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLGR
10 SLEVLFGQPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 163: SEQ ID NO 3 + A942P + A892P + T572I + S884C + A893C

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLKSFTEK
15 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTK
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVN
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEV
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNPSRAGSVASQSIAYTMS
LGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
25 TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKFN
GLTVLPPLLTDEMAIQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
KIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHG
KAHFPREGVVFVSNGTHWFVTQNRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
30 DVLGDISGINASVNNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLGR
SLEVLFGQPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 164: SEQ ID NO 3 + A942P + A892P + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLKSFTEK
40 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTK
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVN
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNPSRAGSVASQSIAYT
45 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQK
NGLTVLPPLLTDEMAIQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
50 GKAHFPREGVVFVSNGTHWFVTQNRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

5 SEQ ID NO 165: SEQ ID NO 3 + A942P + A892P + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPGGSALEPLVDLP
10 INITRFQTLALHRSYLTGDSGSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPDFTGCVIAWNSNNLDSKVGNGYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVN
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPSRAGSVASQSIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMIQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAIVSSVNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTVVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWVFTQRFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

25

SEQ ID NO 166: SEQ ID NO 3 + A942P + D614N + T572I + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPGGSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPDFTGCVIAWNSNNLDSKVGNGYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVN
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPSRAGSVASQSIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMIQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
40 GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAIVSSVNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTVVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWVFTQRFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

45

SEQ ID NO 167: SEQ ID NO 3 + A942P + D614N + T572I + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
50 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPGGSALEPLVDLP

INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
5 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVS VITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMI AQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGV TQNVLYENQKLIANQFN SAI
10 GKIQDLSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSA PHGVVFLHVTYVPAQEKNTTAPAICH D
GKAHFPREGVFVSN GTHWFVTQRNFYEPQIITDNTFVSGNCDV VIGIVNNTVYDPLQPELDSFKEELD KYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLG
RSLEVL FQGPGLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH
15

SEQ ID NO 168: SEQ ID NO 3 + A942P + D614N + T572I + S884C + A893C

MFVFLVLLPLVSSQCVNL TTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTW FHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIK VCEFQFCNDPFLGVY YHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLV RDLPQGFSALEPLVDLP IG
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSNLKPFR
25 DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVS VITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
30 NGLTVLPPLLTDEMI AQYTSALLAGTITCGWTFGAGACLQIPFAMQMAYRFNGIGV TQNVLYENQKLIANQFN SAI
GKIQDLSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSA PHGVVFLHVTYVPAQEKNTTAPAICH D
GKAHFPREGVFVSN GTHWFVTQRNFYEPQIITDNTFVSGNCDV VIGIVNNTVYDPLQPELDSFKEELD KYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLG
35 RSLEVL FQGPGLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 169: SEQ ID NO 3 + A942P + D614N + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNL TTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTW FHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIK VCEFQFCNDPFLGVY YHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLV RDLPQGFSALEPLVDLP IG
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND
45 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVS VITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
50 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMI AQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGV TQNVLYENQKLIANQFN SAI

GKIQDSLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGVVFLHVTVYVPAQEKNTTAPAICH
 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
 5 RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 170: SEQ ID NO 3 + A942P + D614N + N532P + S884C + A893C

10 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYHKNKNSWM
 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGSFALEPLVDLP
 INITRFQTLALHRSYLTGDSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
 15 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
 FER DISTEIQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNF
 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPSRAGSVASQSIAYTM
 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
 20 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQK
 F NGLTVLPLLTDEMAQYTSALLAGTITCGWTFGAGACLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
 GKIQDSLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGVVFLHVTVYVPAQEKNTTAPAICH
 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
 25 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
 RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 171: SEQ ID NO 3 + A942P + T572I + N532P + G880C + F888C

30 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYHKNKNSWM
 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGSFALEPLVDLP
 INITRFQTLALHRSYLTGDSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
 35 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
 D LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
 FER DISTEIQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNF
 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
 VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPSRAGSVASQSIAYTMS
 40 LGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
 N TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQK
 FN GLTVLPLLTDEMAQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIG
 KIQDSLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVTQ
 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGVVFLHVTVYVPAQEKNTTAPAICH
 45 KAHPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
 DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLGR
 SLEVLFGQPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

50

SEQ ID NO 172: SEQ ID NO 3 + A942P + T572I + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYHKNKNSWM
5 ESEFRVYSSANNCTFEYVSPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRAPGQGTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVN
10 NGLTGTGVLTESNKKFLPFQGFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEVP
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTMS
LGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRLTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKFN
GLTVLPPLLTDEMIAQYTSALLAGTITCGWTFGAGACLPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
15 QIQDSLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTVYVPAQEKNTTAPAICHG
KAHFPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGSYIPEAPRDGQAYVRKDGWVLLSTFLGR
SLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH
20

SEQ ID NO 173: SEQ ID NO 3 + A892P + D614N + T572I + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYHKNKNSWM
25 ESEFRVYSSANNCTFEYVSPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRAPGQGTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSNLKPFR
30 DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVN
NGLTGTGVLTESNKKFLPFQGFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEVP
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTMS
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRLTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKFN
35 NGLTVPPLLTDEMIAQYTSALLAGTITSGWTFGAGALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTVYVPAQEKNTTAPAICHG
GKAHFPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGSYIPEAPRDGQAYVRKDGWVLLSTFLGR
40 RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 174: SEQ ID NO 3 + A892P + D614N + T572I + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYHKNKNSWM
45 ESEFRVYSSANNCTFEYVSPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRAPGQGTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSNLKPFR
50 DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVN

NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQNVNCTEV
 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSEYCDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
 SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
 5 NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
 GKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH
 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
 10 RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 175: SEQ ID NO 3 + A892P + D614N + T572I + S884C + A893C

15 MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYYHKNNKSWM
 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
 20 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGNGYNYLYRLFRKSNLKP
 FER DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVN
 FNF NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQNVNCTEV
 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSEYCDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
 SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
 25 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
 NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
 SAI GKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH
 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
 30 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
 RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 176: SEQ ID NO 3 + A892P + D614N + N532P + G880C + F888C

35 MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYYHKNNKSWM
 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
 40 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
 D LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGNGYNYLYRLFRKSNLKP
 FER DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVN
 FNF NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQNVNCTEV
 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSEYCDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
 SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
 45 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
 NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
 SAI GKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH
 50 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT

SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

5 SEQ ID NO 177: SEQ ID NO 3 + A892P + D614N + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPGGSALEPLVDLP
10 INITRFQTLALHRSYLTGDDSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPSRAGSVASQSIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMAIQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

25

SEQ ID NO 178: SEQ ID NO 3 + A892P + T572I + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYHKNKNSWM
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPGGSALEPLVDLP
INITRFQTLALHRSYLTGDDSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNF
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVP
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPSRAGSVASQSIAYTMS
LGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
GLTVLPPLLTDEMAIQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIG
40 KIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTVPAQEKNTTAPAICH
KAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLGR
SLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

45

SEQ ID NO 179: SEQ ID NO 3 + A892P + T572I + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
50 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPGGSALEPLVDLP

INITRFQTLALHRSYLT PGDSSSGW TAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLND
 LCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
 DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
 5 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVS VITPGTNTSNQVAVLYQDVNCTEVP
 VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTMS
 LGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKN
 TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVT LADAGFIKQYGDCLGDIAARDLICAQKFN
 GLTVLPPLLTDEMI AQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SAIG
 10 KIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSR LDPPEAEVQIDRLITGRLQSLQTYVTQ
 QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKG YHLMSPFQPSAPHGVVFLHVTYVPAQEKNF TTAICHHDG
 KAHFPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDV VIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
 DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLGR
 SLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH
 15

SEQ ID NO 180: SEQ ID NO 3 + D614N + T572I + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTW FHAIHVS GTNGTK
 20 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIK VCEFQCNDPFLGVY YHKNNKSWM
 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP IG
 INITRFQTLALHRSYLT PGDSSSGW TAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLND
 LCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
 25 DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVS VITPGTNTSNQVAVLYQNVNCTEV
 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTMS
 SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVT LADAGFIKQYGDCLGDIAARDLICAQKF
 30 NGLTVLPPLLTDEMI AQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SAI
 GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSR LDPPEAEVQIDRLITGRLQSLQTYVT
 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKG YHLMSPFQPSAPHGVVFLHVTYVPAQEKNF TTAICHHDG
 GKAHFPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDV VIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLG
 35 RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 181: SEQ ID NO 3 + D614N + T572I + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTW FHAIHVS GTNGTK
 40 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIK VCEFQCNDPFLGVY YHKNNKSWM
 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP IG
 INITRFQTLALHRSYLT PGDSSSGW TAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLND
 45 LCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
 DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVS VITPGTNTSNQVAVLYQNVNCTEV
 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTMS
 SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
 50 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVT LADAGFIKQYGDCLGDIAARDLICAQKF
 NGLTVLPPLLTDEMI AQYTSALLAGTITCGWTFGAGACLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SAI

GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFVSNQTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
5 RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 182: SEQ ID NO 3 + A942P + A892P + D614N + T572I + N532P

10 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVFCEQFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGSFALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
15 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
FERDISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVN
NFGNGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK
20 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEMIQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
SAIGKIQDSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFVSNQTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
25 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 183: SEQ ID NO 3 + A942P + A892P + D614N + T572I + G880C + F888C

30 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVFCEQFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGSFALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
35 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
DLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
FERDISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVN
NFGNGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTM
40 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEMIQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
SAIGKIQDSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
45 GKAHFPREGVFVSNQTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
RSLEVLFGPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

50

SEQ ID NO 184: SEQ ID NO 3 + A942P + A892P + D614N + T572I + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVVYHKNNKSWM
5 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
10 DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVTPTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSSTECNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLTDEMIAQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
15 GKIQDSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
DKAHPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLG
RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH
20

SEQ ID NO 185: SEQ ID NO 3 + A942P + A892P + D614N + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVVYHKNNKSWM
25 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
30 DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVTPTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSSTECNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
35 NGLTVLPPLTDEMIAQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
GKIQDSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
DKAHPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLG
40 RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 186: SEQ ID NO 3 + A942P + A892P + D614N + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVVYHKNNKSWM
45 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
50 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN

NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
5 NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
GKIQDSLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLG
10 RSEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 187: SEQ ID NO 3 + A942P + A892P + T572I + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPGGSALEPLVDLP
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
15 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTK
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVN
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEVP
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTMS
LGAENSVAYSNNISIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
20 TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
GLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
KIQDSLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNFTTAPAICH
25 KAHPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGWVLLSTFLGR
30 SLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 188: SEQ ID NO 3 + A942P + A892P + T572I + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPGGSALEPLVDLP
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
35 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTK
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVN
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEVP
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTMS
LGAENSVAYSNNISIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
40 TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
GLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
KIQDSLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNFTTAPAICH
45 KAHPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP

DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLGR
SLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

5 SEQ ID NO 189: SEQ ID NO 3 + A942P + D614N + T572I + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPGGSALEPLVDLP
10 INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMIQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPPEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

25

SEQ ID NO 190: SEQ ID NO 3 + A942P + D614N + T572I + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPGGSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
35 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNPSRAGSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMIQYTSALLAGTITCGWTFGAGACLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
40 GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

45

SEQ ID NO 191: SEQ ID NO 3 + A892P + D614N + T572I + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
50 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPGGSALEPLVDLP

INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
5 NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMI AQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
10 GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSA PHGVVFLHVTYVPAQEKNTTAPAICH
DKAHPREGVFVSNGTWHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLG
RSLEVLFGPGGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH
15

SEQ ID NO 192: SEQ ID NO 3 + A892P + D614N + T572I + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTW FHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIK VCEFQCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLV RDLPQGFSALEPLVDLP
IGINITRFQTLALHRSYLT PGDSSSGW TAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
25 DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
30 NGLTVLPPLLTDEMI AQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSA PHGVVFLHVTYVPAQEKNTTAPAICH
DKAHPREGVFVSNGTWHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGGYIPEAPRDGQAYVRKDG EWVLLSTFLG
35 RSLEVLFGPGGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 193: SEQ ID NO 3 + A942P + A892P + D614N + T572I + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTW FHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIK VCEFQCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLV RDLPQGFSALEPLVDLP
IGINITRFQTLALHRSYLT PGDSSSGW TAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND
45 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
50 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMI AQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI

5 GKIQDSLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGVVFLHVTVYVPAQEKNTTAPAICH
GKAHFPREGVFSVNGTHWFVTQRFNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 194: SEQ ID NO 3 + A942P + A892P + D614N + T572I + N532P + S884C + A893C

10 MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPPQGS
INITRFTLLALHRSYLTDPGSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCT
15 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTK
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSNL
DISTEIYQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVN
20 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNSPRAGSVASQSIIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALT
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDI
25 AARDLICAQKF
NGLTVLPPLLTDEMIQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDSLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGVVFLHVTVYVPAQEKNTTAPAICH
30 GKAHFPREGVFSVNGTHWFVTQRFNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGYIPEAPRDGQAYVRKDGGEWVLLSTFLG
RSLEVLFGQPGSLPETGGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH

SEQ ID NO 195: full length S protein with double proline in the hinge loop

30 MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPPQGS
INITRFTLLALHRSYLTDPGSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCT
35 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTK
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGNNYNYLRLFRKSNL
DISTEIYQAGSTPCNGVEGFNCFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVN
40 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALT
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDI
45 AARDLICAQKF
NGLTVLPPLLTDEMIQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQPSAPHGVVFLHVTVYVPAQEKNTTAPAICH
50 GKAHFPREGVFSVNGTHWFVTQRFNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCMT
SCCCLKGCCSCGCKFDEDDSEPVLGKVKLHYT

SEQ ID NO 196: full length S protein with furin KO

50 MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYHKNKNSWM

ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKPFR
5 DISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
10 NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFN
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKEYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
15 SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

SEQ ID NO 197: SEQ ID NO 196 + D614N + A892P + A942P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVS
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLNINATNVVIVCEFCNDPFLGVYHKNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND
25 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKPFR
DSTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
30 NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFN
GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
35 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKEYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

SEQ ID NO 198: SEQ ID NO 196 + D614N + A892P + A942P + T941P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVS
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLNINATNVVIVCEFCNDPFLGVYHKNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
45 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKPFR
DSTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTM
50 SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFN
GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT

QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNFHTTAPAICH
GKAHFPREGVFVSNQTHWVFTQRFNFEYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

5

SEQ ID NO 199: SEQ ID NO 196 + D614N + A892P + A942P + A944P

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVVYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS
10 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVVYHKNNKSWM
ESEFRVYSSANNCTFEYVVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFTLLALHRSYLTGDSGSGWTAGAAAYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEK
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTK
LCFTNVYADSFVIRGDEVRIAPGQTGKIADYNYKLDPDFTGCVIAWNSNNLDSKVGNGYNYLYRLFRKSNLKP
15 DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTE
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPGAGICASYQTQTNSPSRAGSVASQSIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQD
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDL
20 NGTLVLPPLTDEMIQAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDSLSTPSPLGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNFHTTAPAICH
GKAHFPREGVFVSNQTHWVFTQRFNFEYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
25 SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

SEQ ID NO 200: SEQ ID NO 196 + D614N + A892P + T941P

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVVYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS
30 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVVYHKNNKSWM
ESEFRVYSSANNCTFEYVVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFTLLALHRSYLTGDSGSGWTAGAAAYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEK
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTK
35 LCFTNVYADSFVIRGDEVRIAPGQTGKIADYNYKLDPDFTGCVIAWNSNNLDSKVGNGYNYLYRLFRKSNLKP
DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTE
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPGAGICASYQTQTNSPSRAGSVASQSIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQD
40 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDL
NGTLVLPPLTDEMIQAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDSLSTPASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNFHTTAPAICH
GKAHFPREGVFVSNQTHWVFTQRFNFEYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
45 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

SEQ ID NO 201: SEQ ID NO 196 + D614N + A892P + A944P

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MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVVYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVVYHKNNKSWM
ESEFRVYSSANNCTFEYVVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP

INITRFQTLALHRSYLT PGDSSSGW TAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DSTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
5 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTL EILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWVRVYSTGSNVFQTRAGCLIGA EHVNNSEYCDIPGAGICASYQTQTNSPSRAGSVASQSIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSM TKTSDVCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKR SFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTVQNVLYENQKLIANQFN SAI
10 GKIQDLSSTASPLGKLQDVVNQNAQALNTLVKQLSSNF GAISSVLNDILSRDLKPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLM SFPQSAPHGVVFLHVTYVPAQEKNF TTA PAICH D
GKAHFPREGVFVSNGTWHWFVTQRNFYEPQIITDNTFVSGNCDV VIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLKGVLHYT

15

SEQ ID NO 202: SEQ ID NO 196 + D614N + A892P + A942P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTW FHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSL LIVN NATNVVIK VCEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNL REFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP IG
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
25 DSTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTL EILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWVRVYSTGSNVFQTRAGCLIGA EHVNNSEYCDIPGAGICASYQTQTNSPSRAGSVASQSIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSM TKTSDVCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKR SFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
30 NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTVQNVLYENQKLIANQFN SAI
GKIQDLSSTSPSALGKLQDVVNQNAQALNTLVKQLSSNF GAISSVLNDILSRDLKPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLM SFPQSAPHGVVFLHVTYVPAQEKNF TTA PAICH D
GKAHFPREGVFVSNGTWHWFVTQRNFYEPQIITDNTFVSGNCDV VIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
35 SCCSCLKGCCSCGSCCKFDEDDSEPVLKGVLHYT

SEQ ID NO 203: SEQ ID NO 196 + D614N + A892P + A942P + T941P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTW FHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSL LIVN NATNVVIK VCEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNL REFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP IG
INITRFQTLALHRSYLT PGDSSSGW TAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLND
45 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DSTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTL EILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWVRVYSTGSNVFQTRAGCLIGA EHVNNSEYCDIPGAGICASYQTQTNSPSRAGSVASQSIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSM TKTSDVCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
50 NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKR SFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTVQNVLYENQKLIANQFN SAI
GKIQDLSLSPSALGKLQDVVNQNAQALNTLVKQLSSNF GAISSVLNDILSRDLKPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLM SFPQSAPHGVVFLHVTYVPAQEKNF TTA PAICH D

GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

5

SEQ ID NO 204: SEQ ID NO 196 + D614N + A892P + A942P + A944P + V987P

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVCFCNDPFLGVYHKNKNSWM
10 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSEKTKLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQGTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGYNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
15 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQJLPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMIAYQTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
20 GKIQDSLSTSPSLGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

25

SEQ ID NO 205: SEQ ID NO 196 + D614N + A892P + T941P + V987P

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVCFCNDPFLGVYHKNKNSWM
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSEKTKLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQGTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGYNYLYRLFRKSNLKPFR
35 DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSEYCDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQJLPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
40 NGLTVLPPLLTDEMIAYQTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
GKIQDSLSPASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
45 SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

SEQ ID NO 206: SEQ ID NO 196 + D614N + A892P + A944P + V987P

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVCFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSEKTKLSFTVEKG

5 IYQTSNFRVQPTESIVRFPNITNLCPPGEVFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
DSTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
10 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNLSAI
GKIQDLSLSTASPLGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKPEAEVQIDRLITGRLQSLQTYVT
15 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH
DKAHPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

15

SEQ ID NO 207: SEQ ID NO 196 + D614N + A892P + A942P + K986P + V987P

20 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSNGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLLMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRDLPPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPPGEVFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
DSTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
25 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNLSAI
30 GKIQDLSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH
DKAHPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

35

SEQ ID NO 208: SEQ ID NO 196 + D614N + A892P + A942P + T941P + K986P + V987P

40 MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSNGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLLMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRDLPPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPPGEVFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
45 DSTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
50 NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNLSAI
GKIQDLSLSPPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH
DKAHPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

5 SEQ ID NO 209: SEQ ID NO 196 + D614N + A892P + A942P + A944P + K986P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLP
10 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKR SFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFRNGIGVTQNVLYENQKLIANQFN
GKIQDSLSTSPSLGKLQDVVNQNAQALNTLVKQLSSNF GAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGVVFVSNGTWHFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

25

SEQ ID NO 210: SEQ ID NO 196 + D614N + A892P + T941P + K986P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLP
30 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
35 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKR SFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFRNGIGVTQNVLYENQKLIANQFN
GKIQDSLSPASALGKLQDVVNQNAQALNTLVKQLSSNF GAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
40 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGVVFVSNGTWHFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

45

SEQ ID NO 211: SEQ ID NO 196 + D614N + A892P + A944P + K986P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLP
50 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPSRAGSVASQSIIAYTM
5 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
GKIQDLSLSTASPLGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
10 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

15 SEQ ID NO 212: SEQ ID NO 1 + D614N + A892P + A942P

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
GKIQDLSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLDKVEAEVQIDRLITGRLQSLQTYVT
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

35 SEQ ID NO 213: SEQ ID NO 1 + D614N + A892P + A942P + T941P

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
40 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
45 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
50 GKIQDLSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

5 SEQ ID NO 214: SEQ ID NO 1 + D614N + A892P + A942P + A944P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIK/CEFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLPIG
10 INITRFQTLALHRSYLTSGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRAPGQGTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGYNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVTGTNTSNQVAVLYQNVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNLSAI
GKIQDSLSTSPPLGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

25
SEQ ID NO 215: SEQ ID NO 1 + D614N + A892P + T941P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIK/CEFCNDPFLGVYYHKNNKSWM
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLPIG
INITRFQTLALHRSYLTSGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRAPGQGTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGYNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVTGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNLSAI
40 GKIQDSLSPASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

45
SEQ ID NO 216: SEQ ID NO 1 + D614N + A892P + A944P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
50 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIK/CEFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLPIG
INITRFQTLALHRSYLTSGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
5 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSLSTASPLGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
10 GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

15 SEQ ID NO 217: SEQ ID NO 1 + D614N + A892P + A942P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKPEAEVQIDRLITGRLQSLQTYVT
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

35 SEQ ID NO 218: SEQ ID NO 1 + D614N + A892P + A942P + T941P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
40 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
45 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
50 GKIQDLSLSPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

5 SEQ ID NO 219: SEQ ID NO 1 + D614N + A892P + A942P + A944P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYHKNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
10 INITRFQTLALHRSYLTGDSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKLDDFTGCVIWNNSNLDKVGNGNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMIQAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFRNGIGVTQNVLYENQKLIANQFNSAI
GKIQDSLSTSPGLKLDVVNQNAQALNTLVKQLSSNFGAIVSSVNDILSRDKPEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

25
SEQ ID NO 220: SEQ ID NO 1 + D614N + A892P + T941P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYHKNKSWM
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKLDDFTGCVIWNNSNLDKVGNGNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMIQAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFRNGIGVTQNVLYENQKLIANQFNSAI
40 GKIQDSLSPASALGKLDVVNQNAQALNTLVKQLSSNFGAIVSSVNDILSRDKPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

45
SEQ ID NO 221: SEQ ID NO 1 + D614N + A892P + A944P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
50 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYHKNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
5 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSLSTASPLGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGHYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
10 GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVLHYT

15 SEQ ID NO 222: SEQ ID NO 1 + D614N + A892P + A942P + K986P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPGGSALEPLVDLP
20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPAEVQIDRLITGRLQSLQTYVT
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGHYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVLHYT

35 SEQ ID NO 223: SEQ ID NO 1 + D614N + A892P + A942P + T941P + K986P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPGGSALEPLVDLP
40 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
45 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
50 GKIQDLSLSTPPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGHYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

5 SEQ ID NO 224: SEQ ID NO 1 + D614N + A892P + A942P + A944P + K986P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLPIG
10 INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNLSAI
GKIQDSLSTSPPLGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

25
SEQ ID NO 225: SEQ ID NO 1 + D614N + A892P + T941P + K986P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLPIG
INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNLSAI
40 GKIQDSLSPASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

45
SEQ ID NO 226: SEQ ID NO 1 + D614N + A892P + A944P + K986P + V987P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
50 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLPIG
INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND

LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
5 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
GKIQDLSLSTASPLGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
10 GKAHFPREGVFVSNGTWHFVFTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLGCCSCGSCCKFDEDDSEPVLGKVLHYT

15 SEQ ID NO 227: SEQ ID NO 1 + A942P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIK/CEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
GKIQDLSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKEAEVQIDRLITGRLQSLQTYVT
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFVSNGTWHFVFTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLGCCSCGSCCKFDEDDSEPVLGKVLHYT

35
SEQ ID NO 228: SEQ ID NO 1 + A892P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIK/CEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
40 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
45 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
50 GKIQDLSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFVSNGTWHFVFTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT

SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

5 SEQ ID NO 229: SEQ ID NO 1 + D614N

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
10 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNGNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSM TKTSDCTMYICGDSTEC SNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKR SFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SA
GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGA ISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLM SFPQSAPHGVVFLHVTVYVPAQEKNFTTAPAICH
DKAHFPREGV FVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

25
SEQ ID NO 230: SEQ ID NO 1 + T572I

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNGNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
35 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVP
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNISAIPTNFTISVTTEILPVSM TKTSDCTMYICGDSTEC SNLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKR SFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
GLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SAIG
40 KIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGA ISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLM SFPQSAPHGVVFLHVTVYVPAQEKNFTTAPAICH
DKAHFPREGV FVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

45
SEQ ID NO 231: SEQ ID NO 1 + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
50 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
5 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
GKIQDLSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
10 GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLGCCSCGSCCKFDEDDSEPVLGKVLHYT

15 SEQ ID NO 232: SEQ ID NO 1 + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
GKIQDLSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLGCCSCGSCCKFDEDDSEPVLGKVLHYT

35
SEQ ID NO 233: SEQ ID NO 1 + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
40 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
45 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGACLQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
50 GKIQDLSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

5 SEQ ID NO 234: SEQ ID NO 1 + A942P + A892P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIK/CEFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
10 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTL EILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSYECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSM TKTSDCTMYICGDSTEC SNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKR SFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTD EMI AQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SAI
GKIQDSLSTSPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGVFVSNGTWHFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

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SEQ ID NO 235: SEQ ID NO 1 + A942P + D614N

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIK/CEFCNDPFLGVYYHKNNKSWM
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTL EILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSYECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSM TKTSDCTMYICGDSTEC SNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKR SFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTD EMI AQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SAI
40 GKIQDSLSTSPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGVFVSNGTWHFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

45
SEQ ID NO 236: SEQ ID NO 1 + A942P + T572I

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
50 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIK/CEFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEVP
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTMS
5 LGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGNFSQLPDPSPKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKFN
GLTVLPPLLTDEMIQAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNLSAIG
KIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICHDG
10 KAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

15 SEQ ID NO 237: SEQ ID NO 1 + A942P + N532P

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVCFCQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLLMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEVP
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTMS
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGNFSQLPDPSPKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKFN
NGLTVLPPLLTDEMIQAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNLSAIG
GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

35 SEQ ID NO 238: SEQ ID NO 1 + A942P + G880C + F888C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVCFCQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLLMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
40 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
45 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEVP
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTMS
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGNFSQLPDPSPKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKFN
NGLTVLPPLLTDEMIQAQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNLSAIG
50 GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

5 SEQ ID NO 239: SEQ ID NO 1 + A942P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIK/CEFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
10 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSM TKTSDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMI AQYTSALLAGTITCGWTFGAGAC LQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
SAI
GKIQDSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNF GAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
DKAHPREGV FVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

25
SEQ ID NO 240: SEQ ID NO 1 + A892P + D614N

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIK/CEFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
30 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
35 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSM TKTSDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
SAI
GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNF GAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
40 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
DKAHPREGV FVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

45
SEQ ID NO 241: SEQ ID NO 1 + A892P + T572I

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLD SKTQSLIVNNATNVVIK/CEFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
50 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
DSTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEV
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMS
5 LGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGNFQSILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
GLTVLPPLLTDEMIQAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIG
KIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICHG
10 KAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

15 SEQ ID NO 242: SEQ ID NO 1 + A892P + N532P

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRLDPLQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
DSTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEV
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMS
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGNFQSILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEMIQAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

35 SEQ ID NO 243: SEQ ID NO 1 + A892P + G880C + F888C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
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ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRLDPLQGFSALEPLVDLP
40 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
DSTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
45 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMS
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGNFQSILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEMIQAQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
50 GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

5 SEQ ID NO 244: SEQ ID NO 1 + A892P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIK/CEFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
10 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVG YLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKL PDDFTGCVI AWNSNNLDSKVG GNYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSM TKTSDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPD PPSKPSKRFIEDLLFNKVT LADAGFIKQYGDCLGDIAARDL ICAQKF
NGLTVLPPLLTD EMI AQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SAI
GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNF GAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGVFVSNGTWHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

25
SEQ ID NO 245: SEQ ID NO 1 + D614N + T572I

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIK/CEFCNDPFLGVYYHKNNKSWM
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVG YLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKL PDDFTGCVI AWNSNNLDSKVG GNYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
35 NGLTGTGVLTESNKKFLPFQFGRIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSM TKTSDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPD PPSKPSKRFIEDLLFNKVT LADAGFIKQYGDCLGDIAARDL ICAQKF
NGLTVLPPLLTD EMI AQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SAI
40 GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNF GAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGVFVSNGTWHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

45
SEQ ID NO 246: SEQ ID NO 1 + D614N + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
50 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIK/CEFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVG YLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFER
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5 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
GKIQDLSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
10 GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLGCCSCGSCCKFDEDDSEPVLGKVLHYT

15 SEQ ID NO 247: SEQ ID NO 1 + D614N + G880C + F888C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIVKCEFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFER
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
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NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
GKIQDLSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLGCCSCGSCCKFDEDDSEPVLGKVLHYT

35
SEQ ID NO 248: SEQ ID NO 1 + D614N + S884C + A893C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
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40 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFER
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
45 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
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NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGACLQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
50 GKIQDLSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
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GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT

SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

5 SEQ ID NO 249: SEQ ID NO 1 + T572I + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
10 INITRFQTLALHRSYLTSGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQGTGKIADYNYKLDDFTGCVIWNNSNLDKVGNGNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
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15 VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKFN
GLTVLPPLLTDEMAIQYTSALLAGTITSGWTFGAGAAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
KIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQ
20 QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHG
KAHFPREGVVFVSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

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SEQ ID NO 250: SEQ ID NO 1 + T572I + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
30 INITRFQTLALHRSYLTSGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQGTGKIADYNYKLDDFTGCVIWNNSNLDKVGNGNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
35 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVP
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LGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKFN
GLTVLPPLLTDEMAIQYTSALLACTITSGWTCGAGAAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
40 KIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHG
KAHFPREGVVFVSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

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SEQ ID NO 251: SEQ ID NO 1 + T572I + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
50 INITRFQTLALHRSYLTSGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNKRISNCVADYSVLNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEV
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMS
5 LGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGNFSQLPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
GLTVLPPLLTDEMIQAQYTSALLAGTITCGWTFGAGACQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNNSAIG
KIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFSPQSAPHGVVFLHVTYVPAQEKNTTAPAICHG
10 KAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

15 SEQ ID NO 252: SEQ ID NO 1 + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPLQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEV
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMS
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGNFSQLPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEMIQAQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNNSAI
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVT
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFSPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

35
SEQ ID NO 253: SEQ ID NO 1 + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
40 ESEFRVYSSANNCTFEYVSQPFLLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPLQGFSALEPLVDLP
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
45 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMS
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGNFSQLPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEMIQAQYTSALLAGTITCGWTFGAGACQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNNSAI
50 GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFSPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT

SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

5 SEQ ID NO 254: SEQ ID NO 1 + A942P + A892P + D614N

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVECFQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDL PQGFSALEPLVDLP
10 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSM TKTSDCTMYICGDSTEC SNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKR SFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGA ISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGV FVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

25
SEQ ID NO 255: SEQ ID NO 1 + A942P + A892P + T572I

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVECFQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDL PQGFSALEPLVDLP
30 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVP
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNIAIPTNFTISVTTEILPVSM TKTSDCTMYICGDSTEC SNLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKR SFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
GLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
40 KIAQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGA ISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
KAHFPREGV FVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

45
SEQ ID NO 256: SEQ ID NO 1 + A942P + A892P + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVECFQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDL PQGFSALEPLVDLP
50 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
5 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGNFSQLPDPSPKSRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
GKIQDLSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
10 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLGCCSCGSCCKFDEDDSEPVLGKVLHYT

15 SEQ ID NO 257: SEQ ID NO 1 + A942P + A892P + G880C + F888C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGNFSQLPDPSPKSRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
GKIQDLSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLGCCSCGSCCKFDEDDSEPVLGKVLHYT

35 SEQ ID NO 258: SEQ ID NO 1 + A942P + A892P + S884C + A893C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
40 INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
45 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGNFSQLPDPSPKSRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
50 GKIQDLSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

5 SEQ ID NO 259: SEQ ID NO 1 + A942P + D614N + T572I

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVECFQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLP
10 INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGNYLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

25
SEQ ID NO 260: SEQ ID NO 1 + A942P + D614N + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVECFQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLP
30 INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGNYLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNF
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
40 GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

45
SEQ ID NO 261: SEQ ID NO 1 + A942P + D614N + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVECFQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLP
50 INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
5 SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDSPKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSSTSPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
10 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLGCCSCGSCCKFDEDDSEPVLGKVLHYT

15 SEQ ID NO 262: SEQ ID NO 1 + A942P + D614N + S884C + A893C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDSPKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGACQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSSTSPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLGCCSCGSCCKFDEDDSEPVLGKVLHYT

35
SEQ ID NO 263: SEQ ID NO 1 + A942P + T572I + N532P

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
40 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
45 NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVP
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDSPKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
GLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIG
50 KIQDLSSTSPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
KAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP

DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

5 SEQ ID NO 264: SEQ ID NO 1 + A942P + T572I + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIK/CEFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
10 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNGYNYLYRFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVP
15 VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKFN
GLTVLPPLLTDEMI AQYTSALLACTITSGWTCGAGAA LQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SAIG
KIQDSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRQLSLQTYVTQ
20 QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHDG
KAHFPREGV FVSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

25

SEQ ID NO 265: SEQ ID NO 1 + A942P + T572I + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIK/CEFCNDPFLGVYYHKNNKSWM
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNGYNYLYRFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
35 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVP
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKFN
GLTVLPPLLTDEMI AQYTSALLAGTITCGWTFGAGAC LQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SAIG
40 KIQDSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRQLSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHDG
KAHFPREGV FVSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

45

SEQ ID NO 266: SEQ ID NO 1 + A942P + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
50 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIK/CEFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
5 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
GKIQDLSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
10 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLGCCSCGSCCKFDEDDSEPVLGKVLHYT

15 SEQ ID NO 267: SEQ ID NO 1 + A942P + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGACQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
GKIQDLSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLGCCSCGSCCKFDEDDSEPVLGKVLHYT

35 SEQ ID NO 268: SEQ ID NO 1 + A892P + D614N + T572I

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
40 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
45 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
50 GKIQDLSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

5 SEQ ID NO 269: SEQ ID NO 1 + A892P + D614N + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
10 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNGNYLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTE
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQ SAPHGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGV FVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

25
SEQ ID NO 270: SEQ ID NO 1 + A892P + D614N + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
30 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNGNYLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTE
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEMI AQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
40 GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQ SAPHGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGV FVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

45
SEQ ID NO 271: SEQ ID NO 1 + A892P + D614N + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
50 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
5 SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLICAQKF
NGLTVLPPLLTDEMIQAQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
10 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCSCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

15 SEQ ID NO 272: SEQ ID NO 1 + A892P + T572I + N532P

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
25 VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLICAQKF
GLTVLPPLLTDEMIQAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAIG
KIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQ
30 QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
KAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

35 SEQ ID NO 273: SEQ ID NO 1 + A892P + T572I + G880C + F888C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
40 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
45 NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLICAQKF
GLTVLPPLLTDEMIQAQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAIG
50 KIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
KAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP

DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

5 SEQ ID NO 274: SEQ ID NO 1 + A892P + T572I + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
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ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
10 INITRFQTLALHRSYLTSGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKLDDFTGCVIWNNSNNLDSKVGNGNYLYRLFRKSNLKPFR
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15 VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLQYGSFCTQLNRALTGIAVEQDKN
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GLTVLPPLLTDEMAIQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
KIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQ
20 QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSPHGVVFLHVTYVPAQEKNTTAPAICHG
KAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

25
SEQ ID NO 275: SEQ ID NO 1 + A892P + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
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ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
30 INITRFQTLALHRSYLTSGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
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35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
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NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
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40 GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSPHGVVFLHVTYVPAQEKNTTAPAICHG
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMTIMLCCMT
SCCCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

45
SEQ ID NO 276: SEQ ID NO 1 + A892P + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
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ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
50 INITRFQTLALHRSYLTSGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
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LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
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NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
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5 SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
10 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLGCCSCGSCCKFDEDDSEPVLGKVLHYT

15 SEQ ID NO 277: SEQ ID NO 1 + D614N + T572I + N532P

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFFHAIHVSGTNGTK
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ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
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25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
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GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLGCCSCGSCCKFDEDDSEPVLGKVLHYT

35 SEQ ID NO 278: SEQ ID NO 1 + D614N + T572I + G880C + F888C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFFHAIHVSGTNGTK
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40 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
45 NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
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SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
50 GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

5 SEQ ID NO 279: SEQ ID NO 1 + D614N + T572I + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
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ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLP
10 INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGNYLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
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15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
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NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGACLQIPFAMQAMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAIVSSVNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

25
SEQ ID NO 280: SEQ ID NO 1 + D614N + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
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30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGNYLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNF
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
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40 GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAIVSSVNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

45
SEQ ID NO 281: SEQ ID NO 1 + D614N + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
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50 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
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5 SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
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GKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTVYVPAQEKNFTTAPAICH
10 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCSCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

15 SEQ ID NO 282: SEQ ID NO 1 + T572I + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGDDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
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25 VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
GLTVLPPLLTDEMIQAQYTSALLACTITSGWTCGAGAAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIG
KIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQ
30 QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTVYVPAQEKNFTTAPAICH
KAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

35 SEQ ID NO 283: SEQ ID NO 1 + T572I + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
40 INITRFQTLALHRSYLTGDDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
45 NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
GLTVLPPLLTDEMIQAQYTSALLAGTITCGWTFGAGACLIQPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIG
50 KIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTVYVPAQEKNFTTAPAICH
KAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP

DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPV LKGVKLHYT

5 SEQ ID NO 284: SEQ ID NO 1 + A942P + A892P + D614N + T572I

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIK/CEFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDL PQGFSALEPLVDLP
10 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKL PDDFTGCVI AWNSNNLDSKVG GNYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
15 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSM TKTSDCTMYICGDSTEC SNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKR SFIEDLLFNKVT LADAGFIKQYGDCLGDIAARDL
NGLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYR FNIGIGVTQNVLYENQKLIANQFN
20 GKIQDSLSTSPSALGKLQDVVNQNAQALNTLVKQLSSNFGA ISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPV LKGVKLHYT

25
SEQ ID NO 285: SEQ ID NO 1 + A942P + A892P + D614N + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIK/CEFCNDPFLGVYYHKNNKSWM
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDL PQGFSALEPLVDLP
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKL PDDFTGCVI AWNSNNLDSKVG GNYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNF
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSM TKTSDCTMYICGDSTEC SNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKR SFIEDLLFNKVT LADAGFIKQYGDCLGDIAARDL
NGLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYR FNIGIGVTQNVLYENQKLIANQFN
40 GKIQDSLSTSPSALGKLQDVVNQNAQALNTLVKQLSSNFGA ISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPV LKGVKLHYT

45
SEQ ID NO 286: SEQ ID NO 1 + A942P + A892P + D614N + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
50 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIK/CEFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDL PQGFSALEPLVDLP
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
 DISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
 5 SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
 NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
 GKIQDLSSTSPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
 10 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
 SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVLHYT

15 SEQ ID NO 287: SEQ ID NO 1 + A942P + A892P + D614N + S884C + A893C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHKNKNSWM
 ESEFRVYSSANNCTFEYVSQPFLLMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
 20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
 LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
 DISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
 25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
 SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
 NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
 GKIQDLSSTSPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
 30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
 SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVLHYT

35
 SEQ ID NO 288: SEQ ID NO 1 + A942P + A892P + T572I + N532P

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHKNKNSWM
 40 ESEFRVYSSANNCTFEYVSQPFLLMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
 LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
 DISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
 45 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
 VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMS
 LGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
 TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
 GLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
 50 KIQDLSSTSPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQ
 QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHTSP

DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

5 SEQ ID NO 289: SEQ ID NO 1 + A942P + A892P + T572I + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
10 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTE
15 VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKFN
GLTVLPPLLTDEMIAQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
SAIGKIQDSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQ
20 QLIRAAEIRASANLAATKMSECVLGQSKRVD FCGKGYHLMSFPQSAPHGVVFLHVTVYVPAQEKNFTTAPAICH
DGHKAHFPREGV FVSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

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SEQ ID NO 290: SEQ ID NO 1 + A942P + A892P + T572I + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
30 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTE
35 VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKFN
GLTVLPPLLTDEMIAQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
SAIGKIQDSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQ
40 QLIRAAEIRASANLAATKMSECVLGQSKRVD FCGKGYHLMSFPQSAPHGVVFLHVTVYVPAQEKNFTTAPAICH
DGHKAHFPREGV FVSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

45

SEQ ID NO 291: SEQ ID NO 1 + A942P + A892P + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
50 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNKRISNCVADYSVLNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
5 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNLSAI
GKIQDLSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
10 GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVLHYT

15 SEQ ID NO 292: SEQ ID NO 1 + A942P + A892P + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDLPQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNLSAI
GKIQDLSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVLHYT

35
SEQ ID NO 293: SEQ ID NO 1 + A942P + D614N + T572I + N532P

MFVFLVLLPLVSSQCVNLTRTQLPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
40 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
45 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNLSAI
50 GKIQDLSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

5 SEQ ID NO 294: SEQ ID NO 1 + A942P + D614N + T572I + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLP
10 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQPSAPHGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

25

SEQ ID NO 295: SEQ ID NO 1 + A942P + D614N + T572I + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLP
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
35 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGACLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
40 GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQPSAPHGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

45

SEQ ID NO 296: SEQ ID NO 1 + A942P + D614N + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
50 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLP
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFER
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
5 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMIQAQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSSTSPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
10 GKAHFPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

15 SEQ ID NO 297: SEQ ID NO 1 + A942P + D614N + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRLDPLQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFER
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMIQAQYTSALLAGTITCGWTFGAGACQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSSTSPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

35 SEQ ID NO 298: SEQ ID NO 1 + A942P + T572I + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
40 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRLDPLQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFER
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
45 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
GLTVLPPLLTDEMIQAQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIG
50 KIQDLSSTSPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
KAHFPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP

DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPV LKGVLHYT

5 SEQ ID NO 299: SEQ ID NO 1 + A942P + T572I + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
10 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNGNYLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVP
15 VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKFN
GLTVLPPLLTDEMAIQYTSALLAGTITCGWTFGAGACLPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
KIQDSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQ
20 QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNFTTAPAICH
KAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPV LKGVLHYT

25
SEQ ID NO 300: SEQ ID NO 1 + A892P + D614N + T572I + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
30 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNGNYLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNF
35 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTE
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEMAIQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
40 GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMTIMLCCMT
SCCCLKGCCSCGSCCKFDEDDSEPV LKGVLHYT

45
SEQ ID NO 301: SEQ ID NO 1 + A892P + D614N + T572I + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
50 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
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5 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
10 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLGCCSCGSCCKFDEDDSEPVLGKVLHYT

15 SEQ ID NO 302: SEQ ID NO 1 + A892P + D614N + T572I + S884C + A893C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVT
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLGCCSCGSCCKFDEDDSEPVLGKVLHYT

35 SEQ ID NO 303: SEQ ID NO 1 + A892P + D614N + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
40 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
45 NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
50 GKIQDLSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT

SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

5 SEQ ID NO 304: SEQ ID NO 1 + A892P + D614N + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLP
10 INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKLDPDFTGCVIWNNSNLDKVGNGNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVVFVSNGTWFWVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

25

SEQ ID NO 305: SEQ ID NO 1 + A892P + T572I + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLP
30 INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKLDPDFTGCVIWNNSNLDKVGNGNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVP
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
GLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
40 KIAQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
KAHFPREGVVFVSNGTWFWVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHTSP
DVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

45

SEQ ID NO 306: SEQ ID NO 1 + A892P + T572I + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLP
50 INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTMS
5 LGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGNFSQLPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKFN
GLTVLPPLLTDEMIQAQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNLSAIG
KIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICHG
10 KAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

15 SEQ ID NO 307: SEQ ID NO 1 + D614N + T572I + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLLMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTMS
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGNFSQLPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKFN
NGLTVLPPLLTDEMIQAQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNLSAIG
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICHG
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

35 SEQ ID NO 308: SEQ ID NO 1 + D614N + T572I + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLLMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
40 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
45 NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTMS
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGNFSQLPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKFN
NGLTVLPPLLTDEMIQAQYTSALLAGTITCGWTFGAGACLQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNLSAIG
50 GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICHG
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

5 SEQ ID NO 309: SEQ ID NO 1 + A942P + A892P + D614N + T572I + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLP
10 INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVRIAPGQTGKIADYNYKLDPDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQIMAYRFRNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

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SEQ ID NO 310: SEQ ID NO 1 + A942P + A892P + D614N + T572I + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLP
30 INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVRIAPGQTGKIADYNYKLDPDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
35 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGPALQIPFAMQIMAYRFRNGIGVTQNVLYENQKLIANQFNSAI
40 GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

45

SEQ ID NO 311: SEQ ID NO 1 + A942P + A892P + D614N + T572I + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLP
50 INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
5 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSSTSPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPACHD
10 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

15 SEQ ID NO 312: SEQ ID NO 1 + A942P + A892P + D614N + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLNATNVVIKVCDFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSSTSPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPACHD
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

35 SEQ ID NO 313: SEQ ID NO 1 + A942P + A892P + D614N + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLNATNVVIKVCDFQFCNDPFLGVYHYHNNKSWM
40 ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
45 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
50 GKIQDLSSTSPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPACHD
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT

SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

5 SEQ ID NO 314: SEQ ID NO 1 + A942P + A892P + T572I + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTW FHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIK/CEFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLP
10 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVRIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVP
15 VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKFN
GLTVLPPLTDEMIAQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
KIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQ
20 QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPPQSAPHGVVFLHVTVYVPAQEKNFTTAPAICHG
KAHFPREGVVFVSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

25

SEQ ID NO 315: SEQ ID NO 1 + A942P + A892P + T572I + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTW FHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIK/CEFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLP
30 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVRIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
35 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVP
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKFN
GLTVLPPLTDEMIAQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
40 KIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPPQSAPHGVVFLHVTVYVPAQEKNFTTAPAICHG
KAHFPREGVVFVSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

45

SEQ ID NO 316: SEQ ID NO 1 + A942P + D614N + T572I + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTW FHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIK/CEFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLP
50 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
5 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
GKIQDLSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
10 GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLGCCSCGSCCKFEDDDSEPVLGKVLHYT

15 SEQ ID NO 317: SEQ ID NO 1 + A942P + D614N + T572I + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTLLDSKTQSLIVNNATNVVIKVECFQCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGACQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
GKIQDLSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLGCCSCGSCCKFEDDDSEPVLGKVLHYT

35 SEQ ID NO 318: SEQ ID NO 1 + A892P + D614N + T572I + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTLLDSKTQSLIVNNATNVVIKVECFQCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLP
40 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
45 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
50 GKIQDLSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

5 SEQ ID NO 319: SEQ ID NO 1 + A892P + D614N + T572I + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIK/CEFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLP
10 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNGYNYLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEMI AQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQPSAPHGVVFLHVTYVPAQEKNF TTAICH
GKAHFPREGV FVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

25

SEQ ID NO 320: SEQ ID NO 1 + A942P + A892P + D614N + T572I + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIK/CEFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLP
30 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNGYNYLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNF
35 NGLTGTGVLTESNKKFLPFQFGRIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEMI AQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
40 GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQPSAPHGVVFLHVTYVPAQEKNF TTAICH
GKAHFPREGV FVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

45

SEQ ID NO 321: SEQ ID NO 1 + A942P + A892P + D614N + T572I + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIK/CEFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLP
50 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
5 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
GKIQDLSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
10 GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVLHYT

15 SEQ ID NO 322: SEQ ID NO 195 + A942P

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPLQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEV
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
GKIQDLSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRLQSLQTYVT
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVLHYT

35
SEQ ID NO 323: SEQ ID NO 195 + A892P

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPLQGFSALEPLVDLP
40 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
45 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
50 GKIQDLSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT

SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

5 SEQ ID NO 324: SEQ ID NO 195 + D614N

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIK/CEFCNDPFLGVYHKNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
10 INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVRIAPGQTGKIADYNYKLDDFTGCVIWNNSNLDKVGNGNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEMIQAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
SAIGKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSMFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
DKAHPREGVVFVSNHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

25
SEQ ID NO 325: SEQ ID NO 195 + T572I

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIK/CEFCNDPFLGVYHKNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
30 INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVRIAPGQTGKIADYNYKLDDFTGCVIWNNSNLDKVGNGNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVP
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
GLTVLPPLLTDEMIQAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
40 SAIGKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSMFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
DKAHPREGVVFVSNHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHTSP
DVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
45 CSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

SEQ ID NO 326: SEQ ID NO 195 + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
50 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIK/CEFCNDPFLGVYHKNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
5 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
10 GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVLHYT

15 SEQ ID NO 327: SEQ ID NO 195 + G880C + F888C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVLHYT

35 SEQ ID NO 328: SEQ ID NO 195 + S884C + A893C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLP
40 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
45 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGACLQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
50 GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

5 SEQ ID NO 329: SEQ ID NO 195 + A942P + A892P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIK/CEFQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
10 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFRNGIGVTQNVLYENQKLIANQFNLSAI
GKIQDLSSTSPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

25
SEQ ID NO 330: SEQ ID NO 195 + A942P + D614N

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIK/CEFQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
30 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFRNGIGVTQNVLYENQKLIANQFNLSAI
40 GKIQDLSSTSPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

45
SEQ ID NO 331: SEQ ID NO 195 + A942P + T572I

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
50 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIK/CEFQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND

LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEV
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMS
5 LGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGNFQSILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
GLTVLPPLLTDEMIQAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAIG
KIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFSPQSAPHGVVFLHVTYVPAQEKNTTAPAICHG
10 KAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

15 SEQ ID NO 332: SEQ ID NO 195 + A942P + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEV
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMS
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGNFQSILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEMIQAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFN
GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRLQSLQTYVT
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFSPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

35 SEQ ID NO 333: SEQ ID NO 195 + A942P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
40 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
45 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMS
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGNFQSILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEMIQAQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFN
50 GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFSPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

5 SEQ ID NO 334: SEQ ID NO 195 + A942P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
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ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
10 INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKLDDFTGCVIWNNSNLDKVGNGNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
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15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEMIQAQYTSALLAGTITCGWTFGAGACLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

25
SEQ ID NO 335: SEQ ID NO 195 + A892P + D614N

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
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30 INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
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40 GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQSAPHGVVFLHVTYVPAQEKNTTAPAICH
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SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

45
SEQ ID NO 336: SEQ ID NO 195 + A892P + T572I

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
50 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIK/CEFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
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NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEV
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5 LGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGNFQSILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
GLTVLPPLLTDEMIQAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIG
KIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVTQ
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10 KAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
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15 SEQ ID NO 337: SEQ ID NO 195 + A892P + N532P

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFFHAIHVSNGTNGTK
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20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
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LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
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25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMS
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NTQEVFAQVKQIYKTPPIKDFGGNFQSILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEMIQAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFSPQSAPHGVVFLHVTYVPAQEKNTTAPAICHG
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

35
SEQ ID NO 338: SEQ ID NO 195 + A892P + G880C + F888C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFFHAIHVSNGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCFQCNDFLGVYHYHNNKSWM
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40 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
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45 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSIVITPGTNTSNQVAVLYQDVNCTEV
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NTQEVFAQVKQIYKTPPIKDFGGNFQSILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
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50 GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
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GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

5 SEQ ID NO 339: SEQ ID NO 195 + A892P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIK/CEFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLP
10 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNGNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGFRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKR SFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEMI AQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SAI
GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGV FVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

25
SEQ ID NO 340: SEQ ID NO 195 + D614N + T572I

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIK/CEFCNDPFLGVYYHKNNKSWM
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLP
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNGNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
35 NGLTGTGVLTESNKKFLPFQFGFRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
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SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKR SFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SAI
40 GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGV FVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

45
SEQ ID NO 341: SEQ ID NO 195 + D614N + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
50 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIK/CEFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLP
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
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5 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
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10 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLGCCSCGSCCKFDEDDSEPVLGKVLHYT

15 SEQ ID NO 342: SEQ ID NO 195 + D614N + G880C + F888C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
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ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDLPQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
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25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
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30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLGCCSCGSCCKFDEDDSEPVLGKVLHYT

35 SEQ ID NO 343: SEQ ID NO 195 + D614N + S884C + A893C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
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40 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
45 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGACLQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
50 GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT

SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

5 SEQ ID NO 344: SEQ ID NO 195 + T572I + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
10 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGITDAVDCALDPLSETKCTLSFTVEKG
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15 VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKFN
GLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGAA LQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
SAIGKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGR
LQSLQTYVTQ
20 QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSF PQSAPHGVVFLHVTVYVPAQEKNFTTAPAICH
DGAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

25
SEQ ID NO 345: SEQ ID NO 195 + T572I + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
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30 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVRIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNGNYLYRLFRKSNLKP
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35 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTE
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40 QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSF PQSAPHGVVFLHVTVYVPAQEKNFTTAPAICH
DGAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
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CSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

45
SEQ ID NO 346: SEQ ID NO 195 + T572I + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
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50 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGITDAVDCALDPLSETKCTLSFTVEKG
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5 LGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
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KIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVTQ
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10 KAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

15 SEQ ID NO 347: SEQ ID NO 195 + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFFHAIHVSGTNGTK
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20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
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30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
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SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

35 SEQ ID NO 348: SEQ ID NO 195 + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFFHAIHVSGTNGTK
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40 ESEFRVYSSANNCTFEYVSQPFLLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPLQGFSALEPLVDLP
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
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50 GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
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SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

5 SEQ ID NO 349: SEQ ID NO 195 + A942P + A892P + D614N

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
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10 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
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LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKP
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20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQ SAPHGVVFLHVTYVPAQEKNFTTAPAICH
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SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

25
SEQ ID NO 350: SEQ ID NO 195 + A942P + A892P + T572I

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
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ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
30 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
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35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVP
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40 KIQDSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGA ISSVLNDILSRLDPPEAEVQIDRLITGRQLSLQTYVTQ
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DKAHPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

45
SEQ ID NO 351: SEQ ID NO 195 + A942P + A892P + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
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ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
50 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
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5 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
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GKIQDLSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
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10 GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
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15 SEQ ID NO 352: SEQ ID NO 195 + A942P + A892P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
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ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
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25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
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NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
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30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
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SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLGCCSCGSCCKFDEDDSEPVLGKVLHYT

35 SEQ ID NO 353: SEQ ID NO 195 + A942P + A892P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
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40 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
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45 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
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50 GKIQDLSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
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SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

5 SEQ ID NO 354: SEQ ID NO 195 + A942P + D614N + T572I

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
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10 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
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LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNGYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGFRDIADITDAVRDPQTLEILDITPCSFGGVS VITPGTNTSNQVAVLYQNVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSM TKTSDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKR SFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SAI
GKIQDLSSTSPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQ SAPHGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

25
SEQ ID NO 355: SEQ ID NO 195 + A942P + D614N + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
30 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNGYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
35 NGLTGTGVLTESNKKFLPFQFGFRDIADTTDAVRDPQTLEILDITPCSFGGVS VITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSM TKTSDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKR SFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SAI
40 GKIQDLSSTSPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQ SAPHGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

45
SEQ ID NO 356: SEQ ID NO 195 + A942P + D614N + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
50 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
5 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
10 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLGCCSCGSCCKFDEDDSEPVLGKVLHYT

15 SEQ ID NO 357: SEQ ID NO 195 + A942P + D614N + S884C + A893C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRLDPQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGACQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLGCCSCGSCCKFDEDDSEPVLGKVLHYT

35 SEQ ID NO 358: SEQ ID NO 195 + A942P + T572I + N532P

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
40 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRLDPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
45 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
GLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
50 KIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
KAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHTSP

DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

5 SEQ ID NO 359: SEQ ID NO 195 + A942P + T572I + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIK/CEFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
10 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNGYNYLYRFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTE
15 VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLQYGSFCTQLNRALTGIAVEQDN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKFN
GLTVLPPLLTDEMAIQYTSALLACTITSGWTCGAGAA LQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
KIQDSLSTSPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRQLSLQTYVTQ
20 QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
KAHFPREGVVFVSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

25
SEQ ID NO 360: SEQ ID NO 195 + A942P + T572I + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIK/CEFCNDPFLGVYYHKNNKSWM
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNGYNYLYRFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
35 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTE
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLQYGSFCTQLNRALTGIAVEQDN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKFN
GLTVLPPLLTDEMAIQYTSALLAGTITCGWTFGAGAC LQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
40 KIQDSLSTSPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRQLSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
KAHFPREGVVFVSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

45
SEQ ID NO 361: SEQ ID NO 195 + A942P + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
50 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIK/CEFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
5 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
GKIQDLSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
10 GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVLHYT

15 SEQ ID NO 362: SEQ ID NO 195 + A942P + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPLQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
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NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGACQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
GKIQDLSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVLHYT

35
SEQ ID NO 363: SEQ ID NO 195 + A892P + D614N + T572I

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPLQGFSALEPLVDLP
40 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
45 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
50 GKIQDLSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

5 SEQ ID NO 364: SEQ ID NO 195 + A892P + D614N + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
10 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVRIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNGNYLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTE
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGV FVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

25

SEQ ID NO 365: SEQ ID NO 195 + A892P + D614N + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVRIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNGNYLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTE
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEMI AQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
40 GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGV FVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

45

SEQ ID NO 366: SEQ ID NO 195 + A892P + D614N + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
50 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DSTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
5 SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMIQAQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNLSAI
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTVYVPAQEKNFTTAPAICH
10 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCSCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

15 SEQ ID NO 367: SEQ ID NO 195 + A892P + T572I + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTLLDSKTQSLIVNNATNVVIKVEFCFQCNDFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRLDLPQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGDDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DSTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
25 VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
GLTVLPPLLTDEMIQAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNLSAIG
KIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVTQ
30 QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTVYVPAQEKNFTTAPAICH
KAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

35 SEQ ID NO 368: SEQ ID NO 195 + A892P + T572I + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTLLDSKTQSLIVNNATNVVIKVEFCFQCNDFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRLDLPQGFSALEPLVDLP
40 INITRFQTLALHRSYLTGDDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DSTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
45 VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
GLTVLPPLLTDEMIQAQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNLSAIG
KIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVTQ
50 QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTVYVPAQEKNFTTAPAICH
KAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP

DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

5 SEQ ID NO 369: SEQ ID NO 195 + A892P + T572I + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVYHKNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
10 INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQGTGKIADYNYKLDDFTGCVIWNNSNLDKVGNGNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEIDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVP
15 VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKFN
GLTVLPPLLTDEMAIQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
KIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRLQSLQTYVTQ
20 QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICHG
KAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

25
SEQ ID NO 370: SEQ ID NO 195 + A892P + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVYHKNKSWM
30 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQGTGKIADYNYKLDDFTGCVIWNNSNLDKVGNGNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEIDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEMAIQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
40 GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICHG
GKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMTIMLCCMT
SCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

45
SEQ ID NO 371: SEQ ID NO 195 + A892P + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
50 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVYHKNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DSTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
5 SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
10 GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLGCCSCGSCCKFDEDDSEPVLGKVLHYT

15 SEQ ID NO 372: SEQ ID NO 195 + D614N + T572I + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DSTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLGCCSCGSCCKFDEDDSEPVLGKVLHYT

35 SEQ ID NO 373: SEQ ID NO 195 + D614N + T572I + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
40 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DSTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
45 NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNSAI
50 GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

5 SEQ ID NO 374: SEQ ID NO 195 + D614N + T572I + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLNATNVVIKVCFCNDPFLGVYHKNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
10 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKLDDFTGCVIWNNSNLDKVGNGYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMI AQYTSALLAGTITCGWTFGAGACLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

25

SEQ ID NO 375: SEQ ID NO 195 + D614N + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLNATNVVIKVCFCNDPFLGVYHKNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
30 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKLDDFTGCVIWNNSNLDKVGNGYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEMI AQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
40 GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

45

SEQ ID NO 376: SEQ ID NO 195 + D614N + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLNATNVVIKVCFCNDPFLGVYHKNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
50 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTM
5 SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLICAQKF
NGLTVLPPLLTDEMIQAQYTSALLAGTITCGWTFGAGACLIQPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPAEVQIDRLITGRQLSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
10 GKAHFPREGVFVSNQTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCSCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

15 SEQ ID NO 377: SEQ ID NO 195 + T572I + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGDDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
25 VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLICAQKF
GLTVLPPLLTDEMIQAQYTSALLACTITSGWTCGAGAAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIG
KIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPAEVQIDRLITGRQLSLQTYVTQ
30 QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
KAHFPREGVFVSNQTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

35 SEQ ID NO 378: SEQ ID NO 195 + T572I + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
40 INITRFQTLALHRSYLTGDDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
45 VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLICAQKF
GLTVLPPLLTDEMIQAQYTSALLAGTITCGWTFGAGACLIQPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIG
KIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPAEVQIDRLITGRQLSLQTYVTQ
50 QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
KAHFPREGVFVSNQTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP

DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

5 SEQ ID NO 379: SEQ ID NO 195 + A942P + A892P + D614N + T572I

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLPIG
10 INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGYNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQPMAYRFNGIGVTQNVLYENQKLIANQFNLSAI
GKIQDLSSTSPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQPSAPHGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

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SEQ ID NO 380: SEQ ID NO 195 + A942P + A892P + D614N + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLPIG
30 INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGNGYNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQPMAYRFNGIGVTQNVLYENQKLIANQFNLSAI
40 GKIQDLSSTSPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQPSAPHGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGVFSVNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

45

SEQ ID NO 381: SEQ ID NO 195 + A942P + A892P + D614N + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLPIG
50 INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
5 SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSSTSPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
10 GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVLHYT

15 SEQ ID NO 382: SEQ ID NO 195 + A942P + A892P + D614N + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSSTSPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVLHYT

35

SEQ ID NO 383: SEQ ID NO 195 + A942P + A892P + T572I + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
40 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
45 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
GLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIG
50 KIQDLSSTSPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
KAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP

DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

5 SEQ ID NO 384: SEQ ID NO 195 + A942P + A892P + T572I + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLP
10 INITRFQTLALHRSYLTSGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVP
15 VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKFN
GLTVLPPLLTDEMIAQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
KIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRLQSLQTYVTQ
20 QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPPQSAPHGVVFLHVTVYPAQEKNFTTAPAICHG
KAHFPREGVVFVSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

25

SEQ ID NO 385: SEQ ID NO 195 + A942P + A892P + T572I + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLP
30 INITRFQTLALHRSYLTSGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKLDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
35 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVP
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKFN
GLTVLPPLLTDEMIAQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
40 KIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPPQSAPHGVVFLHVTVYPAQEKNFTTAPAICHG
KAHFPREGVVFVSNGTHWVFTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

45

SEQ ID NO 386: SEQ ID NO 195 + A942P + A892P + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLP
50 INITRFQTLALHRSYLTSGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
5 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
10 GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLGCCSCGSCCKFDEDDSEPVLGKVKLHYT

15 SEQ ID NO 387: SEQ ID NO 195 + A942P + A892P + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLGCCSCGSCCKFDEDDSEPVLGKVKLHYT

35 SEQ ID NO 388: SEQ ID NO 195 + A942P + D614N + T572I + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
40 INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
45 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
50 GKIQDLSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

5 SEQ ID NO 389: SEQ ID NO 195 + A942P + D614N + T572I + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLP
10 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNGNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSM TKTSDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKR SFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMI AQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SAI
GKIQDSLSTSPSALGKLQDVVNQNAQALNTLVKQLSSNF GAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQ SAPHGVVFLHVTYVPAQEKNFTTAPAICH D
GKAHFPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

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SEQ ID NO 390: SEQ ID NO 195 + A942P + D614N + T572I + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLP
30 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNGNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFN
35 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSM TKTSDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKR SFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMI AQYTSALLAGTITCGWTFGAGACLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SAI
40 GKIQDSLSTSPSALGKLQDVVNQNAQALNTLVKQLSSNF GAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQ SAPHGVVFLHVTYVPAQEKNFTTAPAICH D
GKAHFPREGVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

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SEQ ID NO 391: SEQ ID NO 195 + A942P + D614N + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLP
50 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
5 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
10 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVLHYT

15 SEQ ID NO 392: SEQ ID NO 195 + A942P + D614N + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGACQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVLHYT

35 SEQ ID NO 393: SEQ ID NO 195 + A942P + T572I + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
40 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
45 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLICAQKF
GLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIG
50 KIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
KAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP

DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

5 SEQ ID NO 394: SEQ ID NO 195 + A942P + T572I + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLP
10 INITRFQTLALHRSYLTSGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKLDDFTGCVIWNNSNLDKVGNGNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVP
15 VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKFN
GLTVLPPLLTDEMAIQYTSALLAGTITCGWTFGAGACLPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
KIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRLQSLQTYVTQ
20 QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH
KAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

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SEQ ID NO 395: SEQ ID NO 195 + A892P + D614N + T572I + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLP
30 INITRFQTLALHRSYLTSGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKLDDFTGCVIWNNSNLDKVGNGNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
35 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEMAIQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
40 GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVVFVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

45

SEQ ID NO 396: SEQ ID NO 195 + A892P + D614N + T572I + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGFSALEPLVDLP
50 INITRFQTLALHRSYLTSGDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
5 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
10 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLGCCSCGSCCKFEDDDSEPVLGKVLHYT

15 SEQ ID NO 397: SEQ ID NO 195 + A892P + D614N + T572I + S884C + A893C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPGGSALEPLVDLP
20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNGTITDAVDCALDPLSETKCTLSFTVEK
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSP
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLGCCSCGSCCKFEDDDSEPVLGKVLHYT

35 SEQ ID NO 398: SEQ ID NO 195 + A892P + D614N + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRDLPGGSALEPLVDLP
40 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNGTITDAVDCALDPLSETKCTLSFTVEK
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSP
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
45 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
50 GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT

SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

5 SEQ ID NO 399: SEQ ID NO 195 + A892P + D614N + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGSALEPLVDLP
10 INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYGYLQPRFTLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKLDDFTGCVIWNNSNLDKVGNGNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEMIQAQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
GKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVVFVSNHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

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SEQ ID NO 400: SEQ ID NO 195 + A892P + T572I + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGSALEPLVDLP
30 INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYGYLQPRFTLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVQRAPGQTGKIADYNYKLDDFTGCVIWNNSNLDKVGNGNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFN
35 NGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVP
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
GLTVLPPLLTDEMIQAQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
40 KIAQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSPHGVVFLHVTYVPAQEKNTTAPAICH
KAHFPREGVVFVSNHWFVTQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDPLQPELDSFKEELDKYFNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
CCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

45

SEQ ID NO 401: SEQ ID NO 195 + A892P + T572I + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPPQGSALEPLVDLP
50 INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYGYLQPRFTLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMS
5 LGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKN
TQEVFAQVKQIYKTPPIKDFGGNFSQLPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
GLTVLPPLLTDEMIQAQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIG
KIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPAEVQIDRLITGRLQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICHG
10 KAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

15 SEQ ID NO 402: SEQ ID NO 195 + D614N + T572I + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLLMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGNFSQLPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMIQAQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPAEVQIDRLITGRLQSLQTYVT
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVKLHYT

35 SEQ ID NO 403: SEQ ID NO 195 + D614N + T572I + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLLMDLEGKQGNFKNLREFVFKNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
40 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
45 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGNFSQLPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMIQAQYTSALLAGTITCGWTFGAGACLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
GKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPAEVQIDRLITGRLQSLQTYVT
50 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFQPSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

5 SEQ ID NO 404: SEQ ID NO 195 + A942P + A892P + D614N + T572I + N532P

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIK/CEFCNDPFLGVYHKNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLP
10 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVRIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNGNYLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSM TKTSDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

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SEQ ID NO 405: SEQ ID NO 195 + A942P + A892P + D614N + T572I + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIK/CEFCNDPFLGVYHKNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLP
30 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVRIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGNGNYLYRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
35 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSM TKTSDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
40 GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPFQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

45

SEQ ID NO 406: SEQ ID NO 195 + A942P + A892P + D614N + T572I + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIK/CEFCNDPFLGVYHKNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLP
50 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYGYLQPRTFLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
5 SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
10 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLGCCSCGSCCKFDEDDSEPVLGKVLHYT

15 SEQ ID NO 407: SEQ ID NO 195 + A942P + A892P + D614N + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFQFCNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLGCCSCGSCCKFDEDDSEPVLGKVLHYT

35 SEQ ID NO 408: SEQ ID NO 195 + A942P + A892P + D614N + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKCEFQFCNDPFLGVYHYHNNKSWM
40 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYKHTPINLVRLDPLQGFSALEPLVDLP
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPKLN
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
45 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
50 GKIQDLSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT

SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

5 SEQ ID NO 409: SEQ ID NO 195 + A942P + A892P + T572I + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTW FHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
10 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSEKTKLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVRIAPGQTGKIADYNYKL PDDFTGCVI AWNSNNLDSKVG GNYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNF
NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVP
15 VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLQYGSFCTQLNRALTGIAVEQDN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVT LADAGFIKQYGDCLGDIAARDLCAQKFN
GLTVLPPLLTDEMI AQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SAIG
KIQDSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGA ISSVLNDILSRDLPPEAEVQIDRLITGR LQSLQTYVTQ
20 QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSF PQSAPHGVVFLHVTYVPAQEKNFTTAPAICH DG
KAHFPREGV FVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

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SEQ ID NO 410: SEQ ID NO 195 + A942P + A892P + T572I + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTW FHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
30 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSEKTKLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN
LCFTNVYADSFVIRGDEVRIAPGQTGKIADYNYKL PDDFTGCVI AWNSNNLDSKVG GNYNYLRLFRKSNLKP
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNF
35 NGLTGTGVLTESNKKFLPFQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVP
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSECDIPGAGICASYQTQTNSPRRARSVASQSIIAYTMS
LGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLQYGSFCTQLNRALTGIAVEQDN
TQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVT LADAGFIKQYGDCLGDIAARDLCAQKFN
GLTVLPPLLTDEMI AQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SAIG
40 KIQDSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGA ISSVLNDILSRDLPPEAEVQIDRLITGR LQSLQTYVTQ
QLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSF PQSAPHGVVFLHVTYVPAQEKNFTTAPAICH DG
KAHFPREGV FVSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSP
DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSC
CSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT

45

SEQ ID NO 411: SEQ ID NO 195 + A942P + D614N + T572I + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTW FHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLP
50 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSEKTKLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLN

LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
5 SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
10 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVLHYT

15 SEQ ID NO 412: SEQ ID NO 195 + A942P + D614N + T572I + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIK/CEFCQNDPFLGVYHYHNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPLQGFSALEPLVDLP
20 INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
25 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGACQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
30 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVLHYT

35 SEQ ID NO 413: SEQ ID NO 195 + A892P + D614N + T572I + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIK/CEFCQNDPFLGVYHYHNNKSWM
40 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPLQGFSALEPLVDLP
INITRFQTLALHRSYLTGPDSSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQGTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
45 NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLCAQKF
NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTCGAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
50 GKIQDLSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFNHT

SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

5 SEQ ID NO 414: SEQ ID NO 195 + A892P + D614N + T572I + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLP
10 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQFGFRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
15 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSM TKTSDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPD PPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDL ICAQKF
NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTF GAGPCLQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SAI
GKIQDSLSTASALGKLQDVVNQNAQALNTLVK QLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
20 QQLIRAAEIRASANLAATKMSECVLGQSKRVDF CGKGYHLMSPFQPSAPHGVVFLHVTYVPAQEKNFTTAPAICH D
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIIT DNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNL NESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIM LCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

25

SEQ ID NO 415: SEQ ID NO 195 + A942P + A892P + D614N + T572I + N532P + G880C + F888C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLP
30 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
35 NGLTGTGVLTESNKKFLPFQFGFRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSM TKTSDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPD PPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDL ICAQKF
NGLTVLPPLLTDEIMIAQYTSALLACTITSGWTC GAGPALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN SAI
40 GKIQDSLSTPSALGKLQDVVNQNAQALNTLVK QLSSNFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDF CGKGYHLMSPFQPSAPHGVVFLHVTYVPAQEKNFTTAPAICH D
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIIT DNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNL NESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIM LCCMT
SCCSCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

45

SEQ ID NO 416: SEQ ID NO 195 + A942P + A892P + D614N + T572I + N532P + S884C + A893C

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS GTNGTK
RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFLGVYYHKNNKSWM
ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRLDPQGFSALEPLVDLP
50 INITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND

LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFER
 DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
 NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTM
 5 SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
 NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
 NGLTVLPPLLTDEIMIAQYTSALLAGTITCGWTFGAGPCLQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNLSAI
 GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRQLSLQTYVT
 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH
 10 GKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGVNNNTVYDPLQPELDSFKEELDKYFKNHT
 SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCMT
 SCCSCLKGCCSCGSCCKFDEDDSEPVLGKVLHYT

SEQ ID NO: 417 (COR201225) - S protein - R682S R685G N532P T572I D614G G880C F888C A944P
 15 V987P no foldon

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRLDPLQGFSALEPLVDLPIG
 20 INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFER
 DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTPLVKNKCVNFNF
 NGLTGTGVLTESNKKFLPFQQFGRDIADITDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQgVNCTEV
 25 VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNSYECDIPIGAGICASYQTQTNSPRAgSVASQSIIAYTM
 SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKNT
 QEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKFNG
 LTVLPPLLTDEIMIAQYTSALLAcTITSGWTcGAGAALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNLSAIGKI
 QDLSSTASpLGLKQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDkPEAEVQIDRLITGRQLSLQTYVTQQL
 30 IRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKA
 HFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGVNNNTVYDPLQPELDSFKEELDKYFKNHTSPDV
 DLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

Signal peptide

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SEQ ID NO: 418 (COR200619) - S protein - R682S R685G A892P A942P D614N V987P no foldon

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFWHAIHVSGTNGTK
 RFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVECFQFCNDPFLGVYHYHNNKSWM
 ESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRLDPLQGFSALEPLVDLPIG
 40 INITRFQTLALHRSYLTGDSGSSGWTAGAAAYYVGYLQPRFTLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
 IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASFSTFKCYGVSPTKLND
 LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLRLFRKSNLKPFER
 DISTEIQAGSTPCNGVEGFNCFYPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQNVNCTEV
 PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNSYECDIPIGAGICASYQTQTNSPRAgSVASQSIIAYTM
 SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDK
 50 NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
 NGLTVLPPLLTDEIMIAQYTSALLAGTITSGWTFGAGPALQIPFAMQMAYRFNGIGVGTQNVLYENQKLIANQFNLSAI
 GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDkPEAEVQIDRLITGRQLSLQTYVT
 QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICH

GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGVNNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

Signal peptide

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SEQ ID NO: 419 (COR200627) - Soluble stabilized SARS-CoV-S S protein (furinKO+PP+Foldon) with
sortaseA-Ctag and A942P mutation

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
10 RFDNPVLPFNDGVYFASTEKSNIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
15 LCFTNVYADSFVIRGDEVRIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGNGYNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQFGRIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPSRAGSVASQSIAYTM
SLGAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKF
20 NGLTVLPPLTDEMI AQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
GKIQDLSSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLPPEAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTYVPAQEKNTTAPAICH
GKAHFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGVNNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQSGSYIPEAPRDGQAYVRKDGWVLLSTFLL
25 PATGGSEPEA

Signal peptide

SEQ ID NO: 420 (COR201291)

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
30 RFDNPVLPFNDGVYFASTEKSNIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
INITRFQTLALHRSYLTGDSGSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSEKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN
35 LCFTNVYADSFVIRGDEVRIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGNGYNYLYRLFRKSNLKPFR
DISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTpLVKNKCVNFNF
NGLTGTGVLTESNKKFLPFQFGRIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQgVNCTEVP
VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPpRagSVASQSIAYTM
GAENSVAYSNNISAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLQYGSFCTQLNRALTGIAVEQDKNT
40 QEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLCAQKFNG
LTVLPPLTDEMI AQYTSALLAcTITSGWTcGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKI
QDLSSTASpLGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVTQQL
IRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQSAHPGVVFLHVTYVPAQEKNTTAPAICHGKA
HFPREGVFVSNNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGVNNNTVYDPLQPELDSFKEELDKYFKNHTSPDV
45 DLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ

SEQ ID NO: 421 (COR200017)

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MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTK
RFDNPVLPFNDGVYFASTEKSNIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCFCNDPFLGVYHKNKNSWM
ESEFRVYSSANNCTFEYVSPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG

INITRFQTLALHRSYLTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLSFTVEKG
IYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKISNCVADYSVLYNSASFSTFKCYGVSPTKLND
LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLYRFRKSNLKPFR
DSTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNF
5 NGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEV
PVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSECDIPIGAGICASYQTQTNSP_sRAgSVASQSIIAYTM
SLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLNRALTGIAVEQDK
NTQEVEFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIAARDLICAQKF
NGLTVLPPLLTDEMI AQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAI
10 GKIQDLSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLD_{pp}EAEVQIDRLITGRLQSLQTYVT
QQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQ_sAPHGVVFLHVTYVPAQEKNF_{TT}APAICH
DKAHPREGV_{FVS}NGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPD_{VD}LDGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQGS_{GY}PEAPRDGQAYVRKDG_{EW}VLLSTFLG
RSLEVL_{FQ}GPGLPETGGSDYKDDDDKGGGSGGGGSGGGGSGGGGSGGGGSHHHHHH
15

Claims

1. Recombinant pre-fusion SARS-CoV-2 S protein, or a fragment thereof, comprising an
5 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 P, a mutation of the amino acid at position 892, a
mutation of the amino acid at position 614, a mutation at position 572, a mutation at
position 532, a disulfide bridge between residues 880 and 888, and a disulfide bridge
10 between residues 884 and 893, wherein the numbering of the amino acid positions is
according to the numbering of the amino acid positions in SEQ ID NO: 1.
2. The protein, or fragment thereof, according to claim 1, comprising an amino acid
sequence wherein the amino acid at position 892 is not alanine (A), the amino acid at
15 position 614 is not aspartic acid (D), the amino acid at position 532 is not Asparagine
(N) and/or amino acid at position 572 is not threonine (T).
- 20 3. The protein, or fragment thereof, according to claim 1, or 2, comprising a mutation of
at least one amino acid in the loop region corresponding to amino acid residues 941 –
945 into P, and a mutation selected from the group consisting of a mutation of the
amino acid at position 892, a mutation of the amino acid at position 614, a mutation at
position 572, a mutation at position 532, a disulfide bridge between residues 880 and
25 888 and a disulfide bridge between residues 884 and 893.
4. The protein, or fragment thereof, according to claim 3, comprising a mutation of at
least one amino acid in the loop region corresponding to amino acid residues 941 – 945

into P, and a mutation selected from the group consisting of a mutation of the amino acid at position 892, a mutation of the amino acid at position 614, a mutation at position 572, a mutation at position 532, a disulfide bridge between residues 880 and 888 and a disulfide bridge between residues 884 and 893, provided that the proteins do not comprise both the disulfide bridge between residues 880 and 888 and the disulfide bridge between residues 884 and 893.

5. The protein, or fragment thereof, according to any one of the preceding claims, wherein the disulfide bridge is a disulfide bridge between residues 880 and 888.
6. The protein, or fragment thereof, according to any one of the preceding claims, wherein 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.
7. The protein, or fragment thereof, according to any one of the preceding claims, wherein 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.
8. The protein, or fragment thereof, according to any one of the preceding claims, wherein 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 P.
9. The protein, or fragment thereof, according to any one of the preceding claims, wherein the mutation at position 892 is a mutation into P.

10. The protein, or fragment thereof, according to any one of the preceding claims,
wherein the mutation at position 614 is a mutation into N or G.
11. The protein, or fragment thereof, according to any one of the preceding claims,
5 wherein the mutation at position 532 is a mutation into P.
12. The protein, or fragment thereof, according to any one of the preceding claims,
wherein the mutation at position 572 is a mutation into I.
- 10 13. The protein, or fragment thereof, according to any one of the preceding claims,
comprising an amino acid sequence wherein the amino acid at position 892 is proline
(P), the amino acid at position 614 is glycine (G), the amino acid at position 942 is
proline (P) and/or the amino acid at position 944 is proline (P).
- 15 14. The protein, or fragment thereof, according to any one of the preceding claims, further
comprising a deletion of the furin cleavage site.
15. The protein, or fragment thereof, according to claim 14, wherein the deletion of the
20 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.
16. The protein, or fragment thereof, according to any one of the preceding claims, further
comprising a mutation of the amino acids at position 986 and/or 987 into P.

17. The protein according to any of the preceding claims, comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 5-194 and SEQ ID NO: 197-418, SEQ ID NO: 420 and SEQ ID NO: 421, or a fragment thereof.
- 5 18. The protein, or fragment thereof, according to anyone of the preceding claims, wherein the protein, or fragment thereof, does not comprise a signal peptide or a tag sequence.
- 10 19. The protein, or fragment thereof, according to any one of the preceding claims, comprising a truncated S2 domain.
20. The protein, or fragment thereof, according to claim 18 wherein the transmembrane and cytoplasmic domain have been removed.
- 15 21. The protein, or fragment thereof, according to claim 18 or 19, wherein a heterologous trimerization domain has been linked to the truncated S2 domain.
- 20 22. The protein, or fragment thereof, according to claim 21, wherein the heterologous trimerization domain is a foldon domain comprising the amino acid sequence of SEQ ID NO:4.
- 25 23. Nucleic acid molecule encoding a protein, or fragment thereof, according to any one of the preceding claims 1-22.

24. Nucleic acid according to claim 23, wherein the nucleic acid molecule is DNA or RNA.
25. Vector comprising a nucleic acid according to claim 23 or 24.
- 5 26. Vector according to claim 25, wherein the vector is a human recombinant adenoviral vector.
- 10 27. A composition comprising a protein according to any one of the claims 1-22, a nucleic acid according to claim 23 or 24 and/or vector according to claim 25 or 26.
- 15 28. A vaccine against COVID-19 comprising a protein, or fragment thereof, according to any one of the claims 1-22, a nucleic acid according to claim 23 or 24 and/or vector according to claim 25 or 26.
- 20 29. A method for vaccinating a subject against COVID-19, the method comprising administering to the subject a vaccine according to claim 28.
30. A method for reducing infection and/or replication of SARS-CoV-2 in a subject, comprising administering to the subject a composition according to claim 27 or a vaccine according to claim 28.
- 25 31. An isolated host cell comprising a nucleic acid according to claim 23.

32. An isolated host cell comprising a recombinant human adenovirus of serotype 26 comprising a nucleic acid according to claim 23.