



1 GAGCTTGGCCATTGCATACGTTGTATCCATATCATAATATGTACATTTATATTGGCTCATGTCCAACATTACCGCCATGTTGACATTGATTATTGACTA
101 GTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCGCGTTACATAAATTACGGTAAATGGCCCGCTGGCTGACCGCC
201 CAACGACCCCGCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGATTTACGGTAA
301 ACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCTGGCATTATGCCAGTACA
401 TGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATA
501 GCGGTTTGACTCACGGGGATTCCAAGTCTCCACCCATTGACGTCAATGGGAGTTTGTGGCACCAAATCAACGGGACTTTCCAAAATGTCGTAAC
601 AACTCCGCCCATTTGACGCAAATGGGCGGTAGGCGGTACGGTGGGAGGTCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCTGGAGACGCC
701 ATCCACGCTGTTTGGACCTCCATAGAAGACACCGGGACCGTCCAGCTCCGGTGCACCGATCCTGAGAACTTCAGGgtgagtttggggacccttgattg
801 ttctttcttttgcgtattgtaaaattcatgttatatggagggggcaaagttttcaggggtgtgtttagaatgggaagatgtcccttgatcacctatgga
901 ccctcatgataatgtttgtttctttcactttctactctgttgacaaccattgtctctctttatgtttctttctttctgtactttttcgtaaaccttta
1001 gcttgcaattgtaacgaatgttttaaaattcacttttgtttatgttcagattgtaagtactttctctaatcactttttttcaaggcaatcagggatatt
1101 atattgtacttcagcacagtttttagagaacaattgttataatataatgataaggtagaatattttctgcatataaattctggctggcgtagaaatattctt
1201 attggtagaacaactacaccctggatcatcctgcctttctttatggttacaatgatatacactgtttgagatgaggataaaatactctgagtcca
1301 aaccgggcccctctgctaaccatgttcatgcctttctttctttctacagCTCCTGGCAACGTGCTGGTTGTTGTGCTGTCTCATATTTGGCAAAGA

Agel (1416)

1401 ATTCTCGACGGATCCACCGTCAACATGTTTGTGTTCTTGGTGTGCTTCCACTGGTCAGTTCCTCAATGCGTTAATCTCACACCCGAACCTCAACTCCC
1501 ACCCGCATATACAAATCCTTACCAGAGGAGTGTACTATCCTGACAAAGTGTTCGTTCAAGTGTCTCCACTCTACTCAGGACCTCTTCTGCCTTTC
25▶ P A Y T N S F T R G V Y Y P D K V F R S S V L H S T Q D L F L P F

Δ H69+V70 (1629)

1601 TTTTCTAACGTTACATGGTTTCATGIGATCICTGGGACAAACGGCACAAACGCTTCGACAACCTGTATTGCCATTCAATGATGGGGTGTACTTTGCCT
59▶ F S N V T W F H V I S G T N G T K R F D N P V L P F N D G V Y F A

T95I (1702)

1701 CCATCGAGAAATCCAACATCATTGAGGATGGATTTTCGGGACTACTCTGGACTCAAAGACACAGAGCCTGCTGATCGTTAACAACGCCACAAACGTTGT
92▶ S I E K S N I I R G W I F G T T L D S K T Q S L L I V N N A T N V V

G142D, Δ[V143, Y144, Y145]

1801 CATCAAAGTGTGCGAATTCAGTTTTGCAATGATCCCTTCCTGGACACAAGAATAACAAGTCTGGATGGAGAGCGAATTTCCGGTCTACAGCAGCGCA
125▶ I K V C E F Q F C N D P F L D H K N N K S W M E S E F R V Y S S A
1901 AACAACTGCACCTTCGAGTACGTGAGTCAACCTTTCTGATGGACCTGGAAGGGAAACAGGGAAACTCAAGAACCTGAGAGAGTTTGTCTTAAGAACA
159▶ N N C T F E Y V S Q P F L M D L E G K Q G N F K N L R E F V F K N

ins214EPE (2050)

ΔN211, L212I (2041)

2001 TCGACGGCTATTTAAGATCTATAGTAAGCATACGCCATCATTTGTAAGGGAGAGGATCTTCCCAGGGCTTTTTCAGCCTGGAACCTTTGGTTGA
192▶ I D G Y F K I Y S K H T P I I V R E P E D L P Q G F S A L E P L V D
2101 CTTGCCTATTGGTATCAATATCACCAGATTTTCAGACCTTCTGGCATTGCATCGGTCTTACTTACTCCAGGTGATTCCTCTCCGGTGGACTGCCGGC
225▶ L P I G I N I T R F Q T L L A L H R S Y L T P G D S S S G W T A G
2201 GCCGCTGCCTACTATGTCGGCTATCTGCAACCAAGAACGTTCTGCTCAAGTACAACGAAACGGCACTATTACGGATGCTGTTGATTGTGCCCTGGACC
259▶ A A A Y Y V G Y L Q P R T F L L K Y N E N G T I T D A V D C A L D
2301 CTCTGTCTGAGACTAAATGCACCCTCAAGAGCTTTACCCTGAGAAGGGGATTTACCAAACAGTAATTTCCGGGTCCAACCCACCGAAAGCATTGTGGC
292▶ P L S E T K C T L K S F T V E K G I Y Q T S N F R V Q P T E S I V R

G339D (2431)

2401 GTTCCCAAATATCACCAATCTGTGTCCCTTTGATGAAGTGTCAATGCTACAAGTGTGCTTCTGTGTACGCATGGAATAGGAAACGCATCTCCAATTGT
325▶ F P N I T N L C P F D E V F N A T R F A S V Y A W N R K R I S N C

S373P (2533)

S371L (2527) S375F (2539)

2501 GTCGCTGATTACTCCGTGCTGTACAATCTGGCCCAATCTTACCTTCAAGTGTATGGGTTTACCTACCAAACCTAACGACCTGTGCTTCACTAATG
359▶ V A D Y S V L Y N L A P F F T F K C Y G V S P T K L N D L C F T N

K417N (2665)

2601 TGTATGCCGACTCTTTTGTGATACGAGGCGATGAAGTGTGAGACAGATTGCACCAGGGCAGACCGGCACATTGCCGACTACAACCTACAAGCTTCCAGATGA
392▶ V Y A D S F V I R G D E V R Q I A P G Q T G N I A D Y N Y K L P D D

2701 CTTTACCGGATGTGTTATTGCATGGAACCTCAAAC**N440K (2734)** **G446S (2752)** **AGC**CTGGATTCCAAGGT**GAGC**GGCAACTATAACTACCTGTATAGACTGTTCCAGGAAATCCAACCTG
425▶ F T G C V I A W N S N K L D S K V S G N Y N Y L Y R L F R K S N L

2801 AAACCATTGAGCGAGATATAAGCACAGAAATCTACCAGGCTGGAA**S477N, T478K (2845)** **E484A (2866)** **Q493R (2893)** **AACAAA**CCCTGCAACGGCGT**GCT**GGGTTCAACTGCTACTTCCATT**GCCG**AGTT
459▶ K P F E R D I S T E I Y Q A G N K P C N G V A G F N C Y F P L R S

2901 AC**G496S (2902)** **AGAC**CTACAT**N501Y (2917)** **TAC**GGGGTGGGT**Y505H (2929)** **CAC**CAACCTATCGTGTCTAGTCTCTGAGTTTTGAGCTCCTCCATGCCCCAGCCACAGTCTGTGGCCCCAA
492▶ Y S F R P T Y G V G H Q P Y R V V V L S F E L L H A P A T V C G P K

3001 GAAAAGCACCAATCTGGTGAAGAACAATGCGTGAACCTTTAACTTTAACGGACT**T547K (3055)** **AAAG**GGAACCGCGTATTGACGGAGAGTAAACAAGAGTCTCTGCCA
525▶ K S T N L V K N K C V N F N F N G L K G T G V L T E S N K K F L P

3101 TTCCAGCAGTTCGGTCGCGATATTGCCGACACTACCGACGCTGTCCGAGATCCCCAGACATTGGAGATTCTTGATATCACACCCTGTAGTTTCGGCGGAG
559▶ F Q Q F G R D I A D T T D A V R D P Q T L E I L D I T P C S F G G

3201 TGAGCGTGATTACGCCCGGAACCAATACCAGCAATCAGGTTGCCGTCTGTATCAG**D614G (3256)** **GGG**CGTGAATTGCACCGAGGTACCTGTCCGATCCACGCTGACCA
592▶ V S V I T P G T N T S N Q V A V L Y Q G V N C T E V P V A I H A D Q

3301 ACTTACACCCACATGGCGAGTATATTCCACCGGCTCCAACGCTTTTCAGACACGTGCTGGATGTCTGATCGGTGCAGAA**H655Y (3379)** **TAI**GTTAAATAAGCTACGAG
625▶ L T P T W R V Y S T G S N V F Q T R A G C L I G A E Y V N N S Y E

3401 TGTGATATCCCATCGGTGCTGGAATATGCGCCTTTATCAAACCTCAAACC**N764K (3706)** **AAA**TCT**CAC**AGCGGGCA**Furin cleavage site (3469)** **CGTAGT**GTAGCATCCCAAAGTATCATTGCCT
659▶ C D I P I G A G I C A S Y Q T Q T K S H R R A R S V A S Q S I I A
3501 ACACAATGAGCCTCGGTGCTGAGAATTCTGTGCGCTACAGCAACAACCTCATTGCTATCCCTACTAACTTCAACATCAGTGTGACAACTGAAATTCTGCC
692▶ Y T M S L G A E N S V A Y S N N S I A I P T N F T I S V T T E I L P
3601 CGTATCTATGACCAAAACAAGCGTTGACTGCACCATGTACATCTGTGGCGATTCTACCGAATGTAGCAATCTCCTCCTGCAATACGGATCATTCTGCACT
725▶ V S M T K T S V D C T M Y I C G D S T E C S N L L L Q Y G S F C T

3701 CAGCTG**N764K (3706)** **AAAG**CGTGCCCTCACAGTATTGCGATTGAGCAGGACAAGAATACGCGAGGAAGTGTGGCCAGGTGAAGCAAATCTACAAAACCTCCACCCATAA
759▶ Q L K R A L T G I A V E Q D K N T Q E V F A Q V K Q I Y K T P P I

3801 AA**D796Y (3802)** **TAC**TTTTGGCGATTCAATTTCTCACAGATCTGCCCGATCCCTCAAACCTCCAAGCGTAGCTTTATCGAGGATCTGCTCTTCAACAAGTAACCT
792▶ K Y F G G F N F S Q I L P D P S K P S K R S F I E D L L F N K V T L

3901 CGCAGATGCCGGTTTCATCAAGCAGTATGGCGATTGTCTGGGAGACATCGCCGCTCGGGACCTGATCTGTGCACAGAAGTTC**N856K (3982)** **AAA**GGACTGACCGTCTG
825▶ A D A G F I K Q Y G D C L G D I A A R D L I C A Q K F K G L T V L
4001 CCTCCCTTGCTGACCGCAGATGATAGCCCAATACACTAGCGCCCTGCTGGCCGGCACCATCCTTCTGGGTGGACATTCCGAGCTGGCGCTGCCCTTC
859▶ P P L L T D E M I A Q Y T S A L L A G T P T I T S G W T F G A G A A L
4101 AGATTCCTTTTGTATGCAGATGGCCTACCGCTTTAACGGCATCGGTGTGACACAAAACGTTCTGTATGAAAACCAGAAAACCTCATGCCCAACCAAGTCAA
892▶ Q I P F A M Q M A Y R F N G I G V T Q N V L Y E N Q K L I A N Q F N

4201 CAGTGCTATCGGTAAGATACAGGATAGCCTGTCTCCACTGCCAGCGCATTGGGAAAGTTGCAGGATGTAGTGAAC**Q954H (4276)** **CAC**AATGCCCAGGCACCTAACACC
925▶ S A I G K I Q D S L S S T A S A L G K L Q D V V N H N A Q A L N T

4301 CTGGTGAACAGCTCTCTTCA**N969K (4321)** **AAAG**TTTTGGTGCATTCTTAGCGTGTGAATGACATA**L981F (4357)** **TTT**AGCCGGTTGGACAAGGTGGAGGCTGAAGTGCAGATTGATA
959▶ L V K Q L S S K F G A I S S V L N D I F S R L D K V E A E V Q I D
4401 GGCTGATAACTGGGCGCTTTCAGTCTCTTTCAGACCTATGTGACCCAGCAGCTCATCCGCGCTGCTGAAATTCGCGCATCCGCTAACCTGGCAGCAACCAA
992▶ R L I T G R L Q S L Q T Y V T Q Q L I R A A E I R A S A N L A A T K
4501 AATGTCCGAGTGTGTGCTGGGTGAGTAAAGAGTGGACTTTTGGCGGAAGGGGTATCACCTGATGTCTTTTCTCAGTCTGCACCCCATGGTGTGGTC
1025▶ M S E C V L G Q S K R V D F C G K G Y H L M S F P Q S A P H G V V
4601 TTTCTGCAGCTGACTTATGTCCAGCTCAGGAAAAGAATCTACTACAGCCAGCCAGCCATCTGCCAGATGGGAAAGCCCACTTTCCAGGGAAGGCGTAT
1059▶ F L H V T Y V P A Q E K N F T T A P A I C H D G K A H F P R E G V
4701 TCGTGTCCAATGGTACTCATTGGTTCGTCAGTACTCAGAGAAAATTTCTACGAGCCAGATTATAACCACTGACAATACATTTGTATCCGGCAATTGTGATGT
1092▶ F V S N G T H W F V T Q R N F Y E P Q I I T T D N T F V S G N C D V
4801 GGTATCGGGATTGTGAATAACTGTTTACGATCCTTTGACGCCAGAGCTGGACTCCTTCAAGGAGGAGCTTGACAAATATTTAAGAATCACACATCA
1125▶ V I G I V N N T V Y D P L Q P E L D S F K E E L D K Y F K N H T S
4901 CCTGACGTGACCTCGGAGATATTTCAGGAATCAATGCTTCCGTGGTCAATATTGAGAAGGAGATAGACAGGCTGAATGAGGTTGCCAAGAACCTCAACG
1159▶ P D V D L G D I S G I N A S V V N I Q K E I D R L N E V A K N L N
5001 AGTCTCTGATCGATCTGCAGGAGTTGGCAAGTACGAAACAGTATATCAAATGGCCTTGKATACATTTGGCTTGGGTTTATTGCTGGGCTGATAGCTATCGT
1192▶ E S L I D L Q E L G K Y E Q Y I K W P W Y I W L G F I A G L I A I V

5101 CATGGTGACAATTATGTTGTGTTGCATGACATCCTGCTGTAGTTGTCTGAAGGCTGCTGCTCATGGCGCAGCTGTTGCTAAAGCTAGCCTCGAGGGATC
1225▶ M V T I M L C C M T S C C S C L K G C C S C G S C C •

5201 CGTCGAGGAATCACT**CCTCAGGTGCAGGCTGCCTATCAGAAGGTGGTGGTGGTGGCCAAATGCCCTGGCTCACAATACCACTGAGATCTTTTCCC**

5301 TCTGCCAAAAATTATGGGGACATCATGAAGCCCTTGAGCATCTGACTTCTGGCTAATAAAGGAAATTTATTTTCATTGCAATAGTGTGTTGGAATTTT
5401 TGTGTCTCTCACTCGGAAGGACATATGGGAGGGCAAATCATTAAAAACATCAGAATGAGTATTTGGTTTAGAGTTTGGCAACATATGCCCATATGCTGGC
5501 TGCCATGAACAAAGGTTGGCTATAAAGAGGTCATCAGTATATGAAACAGCCCTGTGTCCATTCTTATCCATAGAAAAGCCTTGACTTGAGGTTAG
5601 ATTTTTTTTATATTTTGTGTTATTTTTTTCTTAAACATCCCTAAAATTTCTTACATGTTTTACTAGCCAGATTTTTCTCTCTCTCTGACTAC
5701 TCCAGTCATAGCTGTCCCTCTTCTTATGGAGATCCCTCGACGGATCGGCCGAATTCGAATCATGTCATAGCTGTTTCTGTGTGAAATTGTTATC
5801 CGCTCACAATTCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAAGTAACTCACATTAATTGCGTTGCGCTCACT
5901 GCCCGCTTCCAGTCGGGAAACCTGTCTGTCAGCTGCATTAATGAATCGGCCAACGCGGGGAGAGGCGGTTTGCATTTGGGCGCTCTCCGCTTCC
6001 TCGTCACTGACTCGTGCCTCGGTCGGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGCGGTAATACGGTTATCCACAGAATCAGGGGATAACG
6101 CAGGAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTTCTCATTAGGCTCCGCCCCCTGACGAGCA
6201 TCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTGTGCGCTCTCTGTT
6301 CCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTCGGAAGCGTGGCGCTTTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGG
6401 TCGTTCGCTCCAAGCTGGGCTGTGTGCAGAACCCCGTTAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAAGTCCAACCCGGTAAGACA
6501 CGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCTAACTACGGC
6601 TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAACCACCGCTG
6701 GTAGCGGTGGTTTTTTTGTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTG
6801 GAACGAAAACCTCAGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTACCTAGATCCTTTAAATTAATAAATGAAGTTTTAAATCAATCTAA
6901 AGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCATCTGTCTATTTTCGTTTATCCATAGTTGCCTGAC
7001 TCCCGCTGTGTAGATAACTACGATACGGGAGGGCTTACCCTGCCCCAGTGTGCAATGATACCGCGAGACCCACGCTCACGGGCTCCAGATTTATC
263 G T T Y I V V I R S P K G D P G L A A I I G R S G R E G A G S K D
7101 AGCAATAAACCCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCTGCACTTTATCCGCTCCATCCAGTCTATTAATTGTTGCCGGAAGCTAGAGTA
230 A I F W G A P L A S R L L P G A V K D A E M W D I L Q Q R S A L T
7201 AGTAGTTCGCCAGTTAATAGTTTGGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTACGCTCGTCTTGGTATGGCTTTCAGTCCGCTT
196 L L E G T L L K R L T T A M A V P M T T D R E D N P I A E N L E P E
7301 CCCAACGATCAAGGCGAGTTACATGATCCCCATGTTGTGCAAAAAAGCGTTAGCTCCTCGGTCTCCGATCGTTGTCAGAAGTAAAGTTGGCCGAGT
163 W R D L R T V H D G M N H L F A T L E K P G G I T T L L L N A A T
7401 GTTATCACTCATGGTTATGGCAGCACTGCATAATTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAAGTCAACCAAGTCAATC
130 N D S M T I A A S C L E R V T M G D T L H K E T V P S Y E V L D N
7501 TGAGAATAGTGTATGGCGACCGAGTTGCTTTCGCCGCGTCAATACGGGATAATACCGCGCCACATAGCAGAAGTTAAAAAGTCTCATCATTGGA
96 Q S Y H I R R G L Q E Q G A D I R S L V A G C L L V K F T S M M P F
7601 AACGTTCTTCGGGGCGAAAACCTCAAGGATCTTACCCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCAACTGATCTTCAAGTCTTTTAC
63 R E E P R F S E L I K G S N L D L E I Y G V R A G L Q D E A D K V
7701 TTTACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAATGTTGAATACTCATACTTCTCT
30 K V L T E P H A F V P L C F A A F F P I L A V R F H Q I S M
7801 TTTCAATATTATTGAAGCATTATCAGGGTATTGTCTCATGAGCGGATACATATTTGAATGATTTAGAAAAATAACAATAGGGGTTCCGCGCACAT
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8001 ATCGGCAAAATCCCTTATAAATCAAAAAGAAATAGACCGAGATAGGGTGTGAGTGTGTTCCAGTTTGGAAACAAGAGTCCACTATTAAGAACGTGGACTCCA
8101 ACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCACTACGTGAACCATCACCCCTAATCAAGTTTTTGGGGTTCGAGGTGCCGTAAAGCACTAAA
8201 TCGGAACCTAAAGGGAGCCCCGATTTAGAGCTTACGGGGAAAGCCGGCGAACGTTGGCGAGAAAGGAAGGAAGAAAGCGAAAGGAGCGGGCGTAGG
8301 GCGCTGGCAAGTGTAGCGGTACGCTGCGGTAACCACCACACCCGCGGCTTAAATGCGCGCTACAGGGCGCGTCCATTCCGCTTACAGGCTGCGCA
8401 ACTGTTGGGAAGGGGATCGGTGCGGCCTCTTCGCTATTACGCCAGCTGGCGAAAAGGGGATGTGCTGCAAGGCGATTAAGTTGGTAACGCCAGGGTT
8501 TTCCAGTCACGACGTTGTAACACGACGGCCAGTGAGCGCGTAATACGACTCACTATAGGGCGAATTGGAGCTCCACCGCGGTGGCGGCCGCTCTAGA