



1 GGACCTGCAGGGCTGAATAACCTCTGAAAGAGGAAGCTGGTTAGGTACCTTCTGAGGCGGAAAGAACAGCTGTGGAATGTGTGTCAGTTAGGGTGTG  
 101 GAAAGTCCCAGGCTCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGAAAGTCCCAGGCTCCCAGCAGGCAG  
 201 AAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCACTAGTCTCCGGTCCCGTCACTGGCAGAGCGCACATCGCCACAGTCCCCGA  
 301 GAAAGTGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGGTGGCGGGGTAACCTGGGAAAGTGTGCTGTACTGGCTCCGCTTTTTCCC  
 401 GAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGGCTC  
 501 GCATCTCTCTTACGCGCCCGCCGCCCTACCTGAGGCCGCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGC  
 601 GTCCGCGCTTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCCTCACGCTTTGC

**Agel (791)**

701 CTGACCCTGCTTCTCAACTCTACGTCTTTGTTTCTGTTCTGCGCAGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTCAA  
 801 CATGTTTGTGTTCTTGGTGTGCTTCCACTGGTCAAGTCCCAATGCGTTAATCTCACCACCCGAACTCACTCCACCCGCATATACAAATTCCTTACC  
 1 M F V F L V L L P L V S S Q C V N L T T R T Q L P P A Y T N S F T  
 901 AGAGGAGTGTACTATCCTGACAAAGTGTTCGGTCAAGTGTCTCCACTCTACTCAGGACCTCTTTCTGCCTTTCTTTCTAACGTTACATGGTTTCATG  
 34 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 F S N V T W F H  
 T951 (1083)  
 1001 CAATCCATGTGTCTGGGACAAACGGCACCAACGCTTCGACAACCCTGTATTGCCATTCAATGATGGGGTGTACTTTGCCTCCATCGAGAAATCCAACAT  
 67 A I H V S G T N G T K R F D N P V L P F N D G V Y F A S I E K S N I  
 1101 CATTGAGGATGGATTTTCGGGACTACTCTGGACTCAAAGACACAGAGCCTGTGATCGTTAAACAACGCCACAACGTTGTGATCAAAAGTGTGCGGAATTC  
 100 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 I K V C E F

ins145N (1236)  
 Y145S (1233)  
 Y144T (1230)

1201 CAGTTTTGCAATGATCCCTTCTGGGAGTGCACCAAGAATAACAAGTCTGGATGGAGAGCGAATTTCCGGTCTACAGCAGCGCAAACT  
 134 Q F C N D P F L G V T S N H K N N K S W M E S E F R V Y S S A N N  
 1301 GCACCTTCGAGTACGTGAGTCAACCTTTCTGATGGACCTGGAAGGAAACAGGAACTTCAAGAACCTGAGAGAGTTTGTCTTTAAGAATCGACGG  
 167 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 I D G  
 1401 CTATTTAAGATCTATAGTAAGCATACGCCTATCAACCTGGTAAGGGATCTTCCCGAGGGCTTTCCAGCCCTGGAACCTTTGGTTGACTTGCCATTGGT  
 200 Y F K I Y S K H T P I N L V R D L P Q G F S A L E P L V D L P I G  
 1501 ATCAATATCACCAGATTTAGACCTTCTGGCATTGCAICGGTCTTATCTTACTCCAGGTGATTCCTCCTCCGGTGGACTGCCGGCGCCGCTGCCTACT  
 234 I N I T R F Q T L L A L H R S Y L T P G D S S G W T A G A A A Y  
 1601 ATGTCGGTATCTGCAACCAAGAACCTTCTGCTCAAGTACAACGAAACGGCACTATTACGGATGCTGTTGATTGTGCCCTGGACCTCTGTGAGAC  
 267 Y V G Y L Q P R T F L L K Y N E N G T I T D A V D C A L D P L S E T  
 1701 TAAATGCACCCTCAAGAGCTTTACCGTTGAGAAGGGGATTTACCAAACAGTAATTTCCGGGTCACCCACCGAAAGCATTGTGCGGTTCCCAAATATC  
 300 K C T L K S F T V E K G I Y Q T S N F R V Q P T E S I V R F P N I

**R246K (1839)**

1801 ACCAATCTGTGTCCTTTGGCGAAGTGTCAATGCTACAAGTTTGTCTGTGTACGCATGGAATAGGAAACGCATCTCCAATTGTGTCGCTGATTACT  
 334 T N L C P F G E V F N A T K F A S V Y A W N R K R I S N C V A D Y  
 1901 CCGTGTGTACAATTCCGCTCTTTCTCAACCTTCAAGTGTATGGCGTTTACCTACCAAACCTAACGACCTGTGCTTCACTAATGTGTATGCCGACTC  
 367 S V L Y N S A S F S T F K C Y G V S P T K L N D L C F T N V Y A D S  
 2001 TTTTGTGATACGAGGCGATGAAGTGAAGTGTGACAGATTTGACCCAGGGCAGACCGGCAAAATGCCGACTACAACCTACAAGCTTCCAGATGACTTTACCGGATGT  
 400 F V I R G D E V R Q I A P G Q T G K I A D Y N Y K L P D D F T G C  
 2101 GTTATTGCATGGAACCTCAACAACTCTGGATTCCAAGTGGGTGGCAACTATAACTACCTGTATAGACTGTTCAAGAAATCCAACCTGAAACCATTCGAGC  
 434 V I A W N S N N L D S K V G G N Y N Y L Y R L F R K S N L K P F E

**E484K (2253)**

2201 GAGATATAAGCACAGAAATCTACCAGGCTGGAAGTACGCCCTGCAACGGCGTGAGGGGTTCAACTGCTACTTCCCATTGCAGAGTTACGGATTCCAGCC  
 467 R D I S T E I Y Q A G S T P C N G V K G F N C Y F P L Q S Y G F Q P

**N501Y (2304)**

2301 TACAATGGGGTGGGATACCAACCTATCGTGTGCTAGTCTGAGTTTGTGCTCCTCCATGCCCCAGCCACAGTCTGTGCCCAAGAAAAGCACCAAT  
 500 T Y G V G Y Q P Y R V V L S F E L L H A P A T V C G P K K S T N  
 2401 CTGGTGAAGAACAATGCGTGAACCTTAACTTTAACGACTCACAGGAACCGCGTATTGACGGAGAGTAACAAGAAGTTCTGCCATTCCAGCAGTTCCG  
 534 L V K N K C V N F N F N G L T G T G V L T E S N K K F L P F Q Q F  
 2501 GTCGCGATATTGCCGACACTACCGACGCTGTCGAGATCCCCAGACATTGGAGATTCTTGATATCACACCCTGTAGTTTCCGGCGAGTGAGCGTGATTAC  
 567 G R D I A D T T D A V R D P Q T L E I L D I T P C S F G G V S V I T

**D614G (2643)**

2601 GCCCGAACCAATACCAGCAATCAGGTTGCCGTCCTGTATCAGGGCTGGAATTGCACCGAGGTACCTGTGCCATCCACGCTGACCAACTTACACCCACA  
600▶ 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 L T P T  
2701 TGGCGAGTATATCCACCGGCTCCAACGCTTTTCAGACACGTGCTGGATGTCTGATCGGTGCAGAACCGTTAATAATAGCTACGAGTGTGATATCCCCA  
634▶ W R V Y S T G S N V F Q T R A G C L I G A E H V N N S Y E C D I P

**P681H (2844) Furin cleavage site (2856)**

2801 TCGGTGCTGGAATATGCGCCTCTTATCAAACCTCAAACCAACTCTCACAGGCGGGCAGTAGTGTAGCATCCCCAAGTATCATTGCCTACACAATGAGCCT  
667▶ I G A G I C A S Y Q T Q T N S H R R A R S V A S Q S I I A Y T M S L  
2901 CGGTGCTGAGAATTCTGTGCGCTACAGCAAACTCCATTGCTATCCCTACTAACTTCAAACTCAGTGTGACAACTGAAATTTCTGCCGTATCTATGACC  
700▶ G A E N S V A Y S N N S I A I P T N F T I S V T T E I L P V S M T  
3001 AAAACAAGCGTTGACTGCACCATGTACATCTGTGGCATTCTACCGAATGTAGCAATCTCCTCCTGCAATACGGATCATTCTGCACATCAGTGAATCGTG  
734▶ K T S V D C T M Y I C G D S T E C S N L L L Q Y G S F C T Q L N R  
3101 CCCTCACAGGTATTGCAGTTGAGCAGGACAAGAATACGCGAAGTGTGGCCAGGTGAAGCAAATCTACAAAACCTCACCCATAAAAGACTTTGGCGG  
767▶ A L T G I A V E Q D K N T Q E V F A Q V K Q I Y K T P P I K D F G G  
3201 ATTC AATTTCTCAGACATCCTGCCGATCCCTCAAACCTCAAGCGTAGCTTTATCGAGGATCTGCTCTTCAACAAGGTAAACCCTCGCAGATGCCGGT  
800▶ F N F S Q I L P D P S K P S K R S F I E D L L F N K V T L A D A G  
3301 TTCATCAAGCAGTATGGCGATTGCTGGGAGACATCGCCGCTCGGGACCTGATCTGTGCACAGAAGTCAATGGACTGACCGTGTGCCTCCCTTGTGTA  
834▶ F I K A Q Y G D C L G D I A A R D L I C A Q K F N G L T V L P P L L  
3401 CCGACGAGATGATAGCCCAACTACACTAGCGCCTGTGGCCGGCACCATCCTTCTGGTGGACATTGGAGCTGGCGCTTGCCTTCCAGATTTCTTTTGC  
867▶ T D E M I A Q Y T S A L L A G T I T S G W T F G A G A A L Q I P F A  
3501 TATGCAGATGGCCTACCGCTTTAACGGCATCGGTGTGACACAAAACGTTCTGTATGAAAACAGAACTCATCGCAACCAGTTCAACAGTGTATCGGT  
900▶ M Q M A Y R F N G I G V T Q N V L Y E N Q K L I A N Q F N S A I G

**D950N (3651)**

3601 AAGATACAGGATAGCCTGTCATCCACTGCCAGCGCATTGGGAAAGTTGCAGAACCTAGTGAACCAGAATGCCAGGCCTTAACACCCTGGTGAACAGC  
934▶ K I Q D S L S S T A S A L G K L Q N V N Q N A Q A L N T L V K Q  
3701 TCTCTCAAATTTTGGTGCCATTTCTAGCGTGTGAATGACATACTGAGCCGTTGGACAAGGTGGAGGCTGAAGTGCAGATTGATAGGCTGATAACTGG  
967▶ L S S N F G A I S S V L N D I L S R L D K V E A E V Q I D R L I T G  
3801 GCGCCTTCAGTCTCTTACAGACCTATGTGACCCAGCAGCTCATCCGCGTGTGAAATTCGCGCATCCGCTAACCTGGCAGCAACCAAAATGTCGGAGTGT  
1000▶ R L Q S L Q T Y V T Q Q L I R A A E I R A S A N L A A T K M S E C  
3901 GTGCTGGGTGAGTCTAAGAGAGTGGACTTTTGGCGGAAGGGGTATCACCTGATGCTTTTTCTCAGTCTGCACCCCATGGTGTGGTCTTTCTGCACGTGA  
1034▶ 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 F L H V  
4001 CTTATGTCAGTCTCAGGAAAAGAACTTCACTACAGCCCGCCATCTGCCACGATGGGAAAAGCCACTTTCCAGGGAAGCGTATTCTGTGTCCTTGG  
1067▶ T Y V P A Q E K N F T T A P A I C H D G K A H F P R E G V F V S N G  
4101 TACTCATTGGTTGCTCACTCAGAGAAAATTTCTACGAGCCCGAGATTATAACCACTGACAATACATTTGTATCCGGCAATTGTGATGTGGTTATCGGGATT  
1100▶ 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 V I G I  
4201 GTGAATAACTGTTTACGATCCTTTCAGCCAGAGCTGGACTCCTTCAAGGAGGAGCTTGACAAATATTTAAGAATCACACATCACCTGACGTGACCC  
1134▶ V N N T V Y D P L Q P E L D S F K E E L D K Y F K N H T S P D V D  
4301 TCGGAGATATTTAGGAATCAATGCTTCCGTGGTCAATATTGAGAAGGAGATAGACAGGCTGAATGAGGTTGCCAAGAACCTCAACGAGTCTCTGATCGA  
1167▶ L G D I S G I N A S V V N I Q K E I D R L N E V A K N L N E S L I D  
4401 TCTGCAGGAGTTGGGCAAGTACGAACAGTATATCAAATGGCCCTTGGTACATTTGGCTTGGGTTTATTGCTGGGCTGATAGCTATCGTCATGGTGACAATT  
1200▶ 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 M V T I

**NheI (4570)**

4501 ATGTTGTGTTGCATGACATCCTGCTGTAGTTGTCTGAAGGGCTGCTGCTCATGCGGCAGCTGTTGCTAAAGCTAGTGGCCAGACATGATAAGATACATT  
1234▶ M L C C M T S C C S C L K G C C S C G S C C •  
4601 GATGAGTTTGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCA  

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4701 ATAAACAAGTTAAACAACAATTGCATTATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGG  

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4801 TATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGCATAGGCATCAGGGG  
▶ ◀  
4901 CTGTTGCCAATGTGATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCAAGGTTTGAAGTACTGCTTTCATTCTT  

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5001 TATGTTTTAAATGCACTGACCTCCCACATTCCTTTTTAGTAAAATATTCAGAAAATATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAG  

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5101 GCAGAATCCAGATGCTCAAGGCCCTTATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAG  

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5201 CGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTC  
141▶ • N R T Y K L P I L E E I T T K V L K G N M E I L V F C D  
5301 AGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACA  
112▶ P A Y D S I L E R C M G C P S V V R I S R D V E D S Y P H R V A V  
5401 ATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAAATGGCAATGGCTTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAG  
78▶ I T D F D K Q G N S V A S G I A I A E A C V T V R G I Y A E I H V A  
5501 CAGAGATGATCTCCAGTCTTGGTCTGATGGCCCGCCGACATGGTCTTGTGCTCATAGAGCATGGTGTATCTCTCAGTGGCGACCTCCACCAG  
45▶ S I I E G T K T R I A A G V H H K N D E Y L M T I K E T A V E V L  
5601 CTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCTGATGGCCCTCTATAGTGGTCTGATTATACTATGCGGATATACTATGCCGATGATTAATTGTC  
12▶ E L D Q Q S I N F T K M ◀  
5701 AAACAGCGTGGATGGCTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTCGCTC  
▶ ◀

5801 AATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCC GTT GATTTACTAGTCAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCC  
5901 GTGAGTCAAACCGCTATCCACGCCCATTTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAA  
6001 GTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACT  
6101 GCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATG  
6201 GGC GGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAACGCCTGCAGGTTAATTAAAGAACATGTGAGCAAAGGCCAGCAAAG  
6301 GCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAA  
6401 ACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCCTT  
6501 TCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCC  
6601 CCCGTT CAGCCCACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACA  
6701 GGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCT  
6801 GCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGGCAAGCAGCAGATT  
6901 ACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGG  
7001 CTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTAATCGTAACTAACATACGCT  
7101 CTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA