

3 CCCAGCGCGGCCGCTCTATGGGGACGCTGTGGCTGTGGGGCGCCGTCCTCCTCCTCCTCCTCCTCGCCTGCCTGGCTGCGCTG 92  
 1 P S A A P S M G T L W L W G A V P L L L L L L L A C L A A L 30

Transmembrane domain

Intron 4

93 GGGCACAGATGGACACGGGCTCAGATGGGTGGACCCACAGAGACGCCGGGAGCTCAGAGCCCCCAAAGCCCCCAGCCCAGACCTC 182  
 31 G H R W T R A Q M G R T P Q R R R E L R A P P K P P S P D L 60

Intron 5

183 CCTGCACTGCGCTTCCTGCAGGTGCTGCAGACCGGCCGTTTCTCTGCGGTGTGGCGGGCACCTGCAGCAGCGCCGGTGCCTATCAAG 272  
 61 P A L R F L Q V L Q T G R F S A V W R G T L Q Q R P V A I K 90

Protein kinase domain

273 GCTTTCGCTGCCGGTTCATCCCGCGCTGGCGGCAGAGCGGGCGGTGCATGAACTGCCACTAATGGAGCACGAGAACGTGGCCAACTG 362  
 91 A F A A G S S R R W A A E R A V H E L P L M E H E N V A K L 120

Intron 6

363 CTGGGAACGAGGGGGCCGGACCGTGCGCCAGGGGGGGCTCCTGGTGTGCAGCTGTACCCGGCTGGTCCCTGCAGCACTTCCTACGC 452  
 121 L G T R G A G P C A R G G L L V L Q L Y P A G S L Q H F L R 150

453 CATCATGTCTCCATGGGCCGTTACCGTGCAGCTGGCGCTGTCCCTGGCGGGGTCTGGCCTTCCTGCACCAGGAGCTGTGGCGAGAC 542  
 151 H H V S P W A G T V R L A L S L A R G L A F L H Q E L W R D 180

Intron 7

543 GGTCTGTACAAACCCCGTGGTTCACCGCATCTCAGCAGCAGAACGTGCTGGTTCGGCAGGACGGGACCTGCGCCATCGGGGACTTC 632  
 181 G L Y K P R V V H R D L S S Q N V L V R Q D G T C A I G D F 210

Intron 8

633 GGGCTGGCCATGGCGCTACCGGCCGAGCGACCGGAACCGGGCAGAGAACGGAGCAACTGCGGAGGGCCGGCACCCAGCGCTATTTGGCC 722  
 211 G L A M A L P A R A T G T G Q R T E Q L R R A G T Q R Y L A 240

723 CCCGAGATCCTGGACGAGAGCCTGGACCTTCGCTGCTGGGGCGTGCATTGCTGCAGGCTGATGTGTACGCGCTGGCGCTGCTGCTGTGG 812  
 241 P E I L D E S L D L R C W G R A L L Q A D V Y A L A L L L W 270

Intron 9

813 GAGATCCTGAGCCGCTGCCAGAGCCTGAGCCCCGGTGTCCCGGTGCCGGAGTTCCTGCTGGCCTATGAGGCTGAGTTGGGGGGCAGCCCC 902  
 271 E I L S R C Q S L S P G V P V P E F R L A Y E A E L G G S P 300

Intron 10

903 ACGGCGGCGCAGCTCCGGCGGTTGGCGGTGGAGGAGAGAAGGAGACCATTGATCCCCACAACGTGGCACCGCACAGCGCAGCCGTCGGGG 992  
 301 T A A Q L R R L A V E E R R R P L I P T T W H R T A Q P S G 330

993 GCTCTGCAGGAGCTGCTGGAGGATTGTTGGGACCCGACCCGAGGCTCGTCTGTCGGCTGAGCGGCCCTGCAGCGCCTGCAGCGCCTG 1082  
 331 A L Q E L L E D C W D P D P E A R L S A E R A L Q R L Q R L 360

1083 GCGGCCCCCCGGAACCAACACGGAGCTGA 1115

361 A A P P E P P T R S \* 370

1116 ACGGGTCCCAGAGCAGTTTTACCATGTGGGACCCCAATGCAGCAGCGACTCTGACTGATGTTAATGCCCCCATGTCCTGGGGCCACC 1205  
 1206 CGTGTCTCCTGTGGGACCCACCCAGGACCTCCAGGACCCAGCACTGCCGGGACCACCTGGAGCACATGAGCACCTGGGACC 1295  
 1296 ATCCGTGGCCACCCATGTCCATGGAGACCCCCCATGTCCCTATAGACCACCCCATATCCATATAGACTACCCCATATCCATATAGACC 1385  
 1386 ACTCCATATCCATGCAGACCATCCCATATCCATGCAGACCACCTATATCCATGCAGACCACCTATATCCATGTAGACCACCCCATATC 1475  
 1476 CATGCAGACCGCCTATATCCATGTAGACCATCCCATATCCATGTAGACCACCTATATCCATGCAGACCACCTATATCCATGTAGACC 1565  
 1566 ACCCTATATCCATATAGACCACCTATATCCATGGAGACCCCCCATGTCCATGCAGACCACCTATATCCATGTAGACCACCCCATAT 1655  
 1656 CCATGCAGACCACCTATATCCATGTAGACCACCTATATCCATGTAGACCACCCCATGTCCATGTAGATCACTCTATATCCATGTAGAC 1745  
 1746 CACCCTGTATCTGGGTCCCATCCATGACCCTCAGGACACCTGGAACCAACCCAGCACCACCTGATGATCCACGACCACCCAGGAGCT 1835  
 1836 GCCTGGGCCACCCGTGACCACCCCATATCCATAGGACCCCTGTGACCCCCCATATCCACCTGTCCATTTGGAAGCATCATGGCCG 1925  
 1926 CCACATCCCATCCCGACCGTGCCTATGCCCCATGTTCTTACCCCATGGGGCCTGCGCCTTGTGTGGGTGCTGGGGGGTGTATTG 2015  
 2016 GGGGTGTGAGCATATTATGGGGTGTCACTGTGGGTTTCCAGTCCCATTGTGGGGCTGCTGGGGCTCTGTGTTGCCAGCTGCCGATGT 2105  
 2106 TGCTGCTGCTGCTCCCAATAAAGCCAGAGAAGCCTCAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2177