

1 tgttccttacagtggaaaggccaactgaacctactgccaagcaagagctgacggtcacaaggaaaggtaca 71
72 ATGATGAAGAGTTTTTCCTAGTTGTGACTATCCTGGCATTAAACCCTGCCATTTTTGGGTGCCCAGGAGCAAAACCAAGAACAACCAATA 161
1 M M K S F F L V V T I L A L T L P F L G A Q E Q N Q E Q P I 30
162 CGCTGTGAGAAAGAGGAAAGATTCTTCAATGACAAAATAGCCAAATATATCCCAATTCAGTATGTGCTGAGTAGGTATCCTAGTTATGGA 251
31 R C E K E E R F F N D K I A K Y I P I Q Y V L S R Y P S Y G 60
252 CTCAATTACTACCAACAGAAACCAGTTGCACTAATTAATAATCAATTTCTGCCATACCCATATTATGCAAAGCCAGCTGCAGTTAGGTCA 341
61 L N Y Y Q Q K P V A L I N N Q F L P Y P Y Y A K P A A V R S 90
342 CCTGCCCAAATTCTTCAATGGCAAGTTTTGCCAAATACTGTGCCTGCCAAGTCCTGCCAAGCCCAGCCAACCTACCATGACACGTCACCCA 431
91 P A Q I L Q W Q V L P N T V P A K S C Q A Q P T T M T R H P 120
432 CACCCACATTTATCATTTATGGCCATTCCACCAAAGAAAAATCAGGATAAAACAGAAATCCCTACCATCAATACCATTGTTAGTGTTGAG 521
121 H P H L S F M A I P P K K N Q D K T E I P T I N T I V S V E 150
522 CCTACAAGTACACCTACCACCGAAGCAATAGAGAACACTGTAGCTACTCTAGAAGCTTCCTCAGAAGTTATTGAGAGTGTACCTGAGACC 611
151 P T S T P T T E A I E N T V A T L E A S S E V I E S V P E T 180
612 AACACAGCCCAAGTTACTTCAACCGTCGTCTAAaaactctaaggagacatcaaagaagacaacacaggtctagctgaaacaaatgacta 701
181 N T A Q V T S T V V * 190
702 cttcaaactttccttttgccagttgtctgccttcagtgaacagagaatatgattttcacagattcggtcctttctegtctctcttaca 791
792 ttttgcatttatgccacatttagttttttgattcctgcatAATAAAgctaatacaaatgc 850