

1 ATGCCGTGGACATGTGCAACAGGACTCTGTATGGTGTGAGACACGCCCTTTGCCAGATCTTCTGAACTAGACVGAACAGCACTGGATACAGACAGCTTTCTG 150  
1 M A W D M C A C N Q D S V W S D I E C A A L V G E D Q P L L C P D L P E A L D L S E I D V N D L D T D S F L 50  
151 GGTGGACTCAAGTGGTGCAGTGACCAATCAGAAATAATATCTAATCAGTACAACAACGAGCCTTCAAACATATTTGAGAAGATAGATGAAGAGAATGAGGCAAACCTTGCTAGCGGTCCTCACAGAGACTGGACAGTCTCCCTGTGGAT 300  
51 G G L K W C S D Q S E I I S N Q Y N N E P S N I F E K I D E E N E A N L L A V L T E T L D S L P V D 100  
301 GAAGACGGATTGCCCTCATTGATGACTGACAGATGGAGATGTGACCACCGAGAATGAGGCTAGTCCTTCTCCATGCCTGACGGCACCCCTCCGCCTCAGGAGGCAGAAGAGCCGCTCTACTTAAGAAGCTTACTGGCACCAGCC 450  
101 E D G L P S F D A L T D G D V T T E N E A S P S S M P D G T P P P Q E A E E P S L L K K L L L A P A 150  
451 AACACTCAGCTAAGTTATAATGAATGCAGTGGCCTCAGTACCCAGAACCATGCAAACCATAATCACAGGATCAGAACAACCCCTGCAGTTGTTAAGACCGAGAATTCATGGAGCAATAAAGCGAAGAGCATTGTGCAACAGCAAAAGCCA 600  
151 N T Q L S Y N E C S G L S T Q N H A N H N H R I R T N P A V V K T E N S W S N K A K S I C Q Q Q K P 200  
601 CAAAGACGTCCGTGCTCAGAGCTTCTCAAGTATCTGACCACAAATGATGACCCTCTCACACAAAACCCACAGAGAACCAGCAACAGCAGAGACAAATGCACCTCCAAAAAGAAGGCCACACACAATCGCAGACACAACATCTACAA 750  
201 Q R R P C S E L L K Y L T T N D D P P H T K P T E N R N S S R D K C T S K K K A H T Q S Q T Q H L Q 250  
751 GCCAAACCAACAACCTTTATCTTCTCTGACCCAGAGTCACCAATGACCCCAAGGGTTCCTCCATTTGAGAACAAGACTATTGAACGAACCTTAAGTGTGGAACCTCTGGAACCTGACGGCCTAACTCCACCACAACCTCTCTCAT 900  
251 A K P T T L S L P L T P E S P N D P K G S P F E N K T I E R T L S V E L S G T A G L T P P T T P P H 300  
901 AAAGCCAACCAAGATAACCCCTTTCAGGGCTTCTCAAAGCTGAAGCCCTCTTGAAGACTGTGGTACCTCCACCATCCAAGAAGGCCCGGTACAGTGAGTCTTCTGTACCAAGGCAGTAATCCACCAAGAAGGGGCTGAGCAGTCT 1050  
301 K A N Q D N P F R A S P K L K P S C K T V V P P P S K K A R Y S E S S C T Q G S N S T K K G P E Q S 350  
1051 GAGTTGTACGCACAGCTCAGCAAGACCTCTGTGCTCACCAGTGGACAGGAAAGGAAGGCCAAACGGCCAGTCTCCGGCTGTTTGGTGACCATGACTATTGTGAGTGCATTAATCCAAAATGAAATACTCGTTAGTACATCACAG 1200  
351 E L Y A Q L S K T S V L T S G H E E R K A K R P S L R L F G D H D Y C Q S I N S K M E I L V S T S Q 400  
1201 GAGCTCCAGACTCCAGACAAGTAAAGATGCCCCCTCTCAACGGGTGGGGCAAATACACTCTTCCACAGATTCCGACCCGTGCTACCTGAGAGAGACTGCAGAGGTGAGCAGGCAGGTCTCTCCGGCAGCACCAGAAAA 1350  
401 E L H D S R Q L E N K D A P S S N G S G Q I H S S T D S D P C Y L R E T A E V S R Q V S P G S T R K 450  
1351 CAGCTCAAGACCAGAAATCCGAGCCGAGCTGAACAAGCACTTCGGTCATCCAGTCAAGCTGTTTTGACGACAAAGCAGACAAGACCAGTGAACCTGAGGACAGTGATTCAGTAATGAACAATTCTCCAAACTACCTATGTTTATA 1500  
451 Q L Q D Q E I R A E L N K H F G H P S Q A V F D D K A D K T S E L R D S D F S N E Q F S K L P M F I 500  
1501 AATTCAGGACTAGCCATGGATGGCCTGTTTGTGATGACAGCGAAGATGAAAGTGATAAACTGAACTCCCCTTGGGATGGCAGCAGTCTATTTCATTGTTCCATGTGTCGCCTTCTTGTCTTCTTTAACTCTCCATGTAGAGATTCTGTG 1650  
501 N S G L A M D G L F D D S E D E S D K L N S P W D G T Q S Y S L F H V S P S C S S F N S P C R D S V 550  
1651 TCACCACCAAATCTTTATTTCTCAAAGACCCAAAGGATGCGCTCTCGTTCAAGGTCCTTTCTCGACACAGGTATGTTCTCGATCACCATATTCCAGGTCAAGATCAAGTCCCAGGCAGTAGATCTTCTTCAAGATCTTGCTAC 1800  
551 S P P K S L F S Q R P Q R M R S R S R S F S R H R S C S R S P Y S R S R S R S P G S R S S S R S C Y 600  
1801 TACTATGAGTCAGGCCACTGCAGACACCGCACACCGAAATTCGCCCTGTGCGCGAGGTACGTTCAAGATCGCCCCATAGCCGGCGGCCAGGTATGACAGCTACGAGGAATACCAGCACGAAAGGCTCAAGAGGGAAGAATACCGC 1950  
601 Y Y E S G H C R H R T H R N S P L C A R S R S R S P H S R R P R Y D S Y E E Y Q H E R L K R E E Y R 650  
1951 AGAGAGTATGAGAAGCGGAATCTGAAAGGGCAAGCAGAGGGAGAGGCAGAGGCAGAAGGCAATTGAAGAGCGCCGTGTGATTTATGTTGGTAAAATCAGACCTGACACAACACGGACAGAACTGAGGGACCGTTTTGAAGTTTTTGGT 2100  
651 R E Y E K R E S E R A K Q R E R Q R Q K A I E E R R V I Y V G K I R P D T T R T E L R D R F E V F G 700  
2101 GAAATTGAGGAGTGACAGTAAATCTGCGGGATGATGGAGACAGCTATGGTTTCATTACCTACCGTTATACCTGTGATGCTTTTGTGCTCTTGAATAATGGATACACTTTGCGCAGGTGCAATGAAACTGACTTCGAGCTGTACTTTGT 2250  
701 E I E E C T V N L R D D G D S Y G F I T Y R Y T C D A F A A L E N G Y T L R R S N E T D F E L Y F C 750  
2251 GGACGCAAGCAATTTTCAAGTCTAACTATGCAGACCTAGATTCAAATTCAGATGACTTTGACCCTGCTTCCATCAAGAGCAAGTATGACTCTCTGGATTTCGATAGTTTACTGAAAGAAGCCCAGAGAAGCTTACGCAGGTAA 2394  
751 G R K Q F F K S N Y A D L D S N S D D F D P A S I K S K Y D S L D F D S L L K E A Q R S L R R \* 797