



1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCCGCCCTACCTGAGGCC
301 GCCATCCACGCCGGTTGAGTCCGCTTCTGCCGCTCCCGCTGTGGTGCCTCTGAAGCTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCTACCTGAGATCACCGGTAGGAGGGCCATGAAGACACAGTGGCGTCTACCTGGCTC
601 CTGGGCATGACGTTGATTCTCTGCTCAGTTCATATCTACAGTCTTAGGAGATGCTGATTTCTGTGGACATGCGCCTCATAGAAAAGAGTTTCCACGAGA
111▶ L G M T L I L C S V H I Y S L R R C L I S V D M R L I E K S F H E
701 TCAAGAGAGCCATGCAAATAAGGACACCTTAAAAATGTCACCATCTGTCCCTGGAGAACCTCAGGAGCATTAAAGCTGGAGATGTGTGCTGCATGAC
44▶ I K R A M Q T K D T F K N V T I L S L E N L R S I K P G D V C C M T
801 CAACAACCTGCTGACATTCTACAGAGACAGGTTCCAGGACCATCAGGAGAGAAGCCTTAGGTTCTTAAGGAGAATCAGCAGCATTGCCAACTCTTTC
77▶ N N L L T F Y R D R V F Q D H Q E R S L E V L R R I S S I A N S F
901 CTCTGCGTGCAGAAATCTCTGGAGCGATGTCAGGTGCACAGACAATGTAAGTGCAGTCAGGAAGCCACCAATGCAACTAGGATCATCCATGACAACTACA
111▶ L C V Q K S L E R C Q V H R Q C N C S Q E A T N A T R I I H D N Y
1001 ATCAGCTGGAGGTCTCATCTGCTGCCCTTAAAGTCTTAAAGGAGAAGTGAACATACTTTTAGCCTGGATTGACAGGAATCATCTGAAACTCCTGCAGCCTG
144▶ N Q L E V S S A A L K S L G E L N I L L A W I D R N H L E T P A A •

1101 ACACGAAACGCCTCGTCTGATTATCTAAATGCTAGTGGCCAGACATGATAAGATACATTGATGAGTTGGACAAACCACAACCTAGAATGCAGTGAAAAA
177▶

1201 AATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACCTGATTTCATTTTATGTT
1301 TCAGGTTCAAGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTC
1401 CAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTGCAGCCTCACCTTC
1501 TTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGGTTGAACTAGCTCTTCATTTCTTTATGTTTTAAATGCAGTACCTCCCACATTCCCTTTTAG
1601 TAAAATATTCAGAATAATTTAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCA
1701 GTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTAAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGGAT
141▶ • N R T Y K L P I
1801 GAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAG
132▶ L E E I T T K V L K G N M E I L V F C D P A Y D S I L E R C M G C
1901 GGGCTGACCACCTGATGGATCTGTCCACTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACC
98▶ P S V V R I S R D V E D S Y P H R V A V I T D F D K Q G N S V A S G
2001 CAATGGCAATGGCTTCCAGCAGACAGTGCACCTGCCAATGTAGGCCCTCAATGTGGACAGCAGAGATGATCTCCCAAGTCTTGGTCTGATGGCCGCCC
65▶ I A I A E A C V T V R G I Y A E I H V A S I I E G T K T R I A A G
2101 GACATGGTGTGTTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCAGCTCCACAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTG
32▶ V H H K N D E Y L M T I K E T A V E V L E L D Q Q S I N F T K M
2201 GCCCTCTATAGTGAATGCTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTC
2301 ACTAAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTT
2401 GATTTACTAGTCAAAACAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGACTGCCA
2501 AAACCGCATCATCATGTAATAGCGATGACTAATACGTAGATGACTGCAAGTAGGAAAGTCCATAAGGTCATGACTGGGCATAATGCCAGGCGGGC
2601 CATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACTTGTACTGCAAGTGGGCGAGTTTACCGTAAATACTCCACCCATTGAC
2701 GTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTAC
2801 CGTAAGTTATGTAACGCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCTTTTTCC
2901 ATAGGCTCCGCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCTGG
3001 AAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGC
3101 TGTAGGTATCTCAGTTCGGTGTAGTTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCCGTTCCAGCCGACCGCTGCGCTTATCCGGTAACTATC

3201 GTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTT
3301 CTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCT
3401 TGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCT
3501 TTTCTACGGGGTCTGACGCTCAGTGAACGAAAACACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGGGCCGCAATAAAATA
3601 TCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAT
3701 AGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA