

A

1 ATGTTTATCATGATACGCTTCGAACGTGCGTGTTCCCGATTCATTGGAAAGTGGTTATTT 60

61 TCACAAGATTCTTTGTCCCCGGATCTACTGTTTCTTATTCTTCTGATTTTGGTTTTTCGTA 120

121 TCACGGATGTTGGTTCGCGCTTTATGGCCCCGTCTGCAGTATTGACGTCTCGCATTTTC 180

181 ACTACTTTTGTTGTTCTTTCTTCAGCGGTTTTGAGTGGATCGGTGGCACACGCCGCTGAT 240

241 AACGAACCTATTAATAATGGGGCAGCTCCCGCTGCTTACGGATCCGGGGCAGAAGGACCC 300

301 TCAAATTCCGCCTTATTCACCTATACTTCCGATTTGGCGGAAGATTCGGTCAGTTCCGGG 360

361 CGTAGTAGAAGTACCGCCTCGTCCTCCTTTTTTCCAAGGACTTTCGGGGCCAGATTCCCACG 420

421 GCACCAAATTCCCCCGGGGAAGAAGTACAGCAGAACCTTCCAAACTTTTTATCCCTGCCA 480

481 GAGGAGGATACGGTGGAGCACTTATTAGGGGCAGGAAGAGCAGCCGGAGGAGCCGGGGGC 540

541 GCAGGTGGGGCCGCTGGAAGTGCCCCTGCAGCTGAGCAAATCCAGGGAGAAGATCATGCC 600

601 GGGTTCGTGCCAGATCTCCACCAAATTCAGCATGATGTTATAAGAAACAGACTTGCTACT 660

661 TCAACTCCCACAAGTGAAGTAAGCGACGATGAGATAGACGCACGCATTTTTTCTTAAGAAA 720

721 GATATTATCGATCGCATGGCCCAATTAGACCCGGACCGGGATGGATTCTGGAATGAGCAA 780

781 AAGGACCACTTAGTCGCTCATGGAATCCTCAATAAGGGTAAAGAGTATACCTTCCAGGGA 840

841 CTGATAAACCTCTGTAAAAATTTAAATAAATGCGATGCAAACAGTCCTCTTTTCAATAAA 900

901 ATAAAGAAAATAAATAAGTACTAA

B

1 MFIMIRFERACSRFIGKWLFSQDSLSPDLLFLILLILVFVSRMLVRALWPRSAVLTSRIF 60

61 TTFVVLSSAVLSGSVAHAADNEPINNGAAPAAYGSGAEGPSNSALFTYTSDLAEDSVSSG 120

121 RSRSTASSSFFQGLSGQIPTAPNSPGEEVQQNLPNFLSLPEEDTVEHLLGAGRAAGGAGG 180

181 AGGAAGTAPAAEQIQGEDHAGFVPDLHQIQHDVIRNRLATSTPTSEVSDDEIDARIFLKK 240

241 DIIDRMAQLDPDRDGFWNEQKDHLVAHGILNKGKEYTFQGLINLCKNLNKCDANSPLFNK 300

301 IKKINKY*