



2801 TATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCA
2901 AGAAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAA
3001 GCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACA
114 C D P A Y D S I L E R C M G C P S V V R I S R D V E D S Y P H R V
3101 GCCACAATGGTGTCAAAGCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGT
80 A V I T D F D K Q G N S V A S G I A I A E A C V T V R G I Y A E I H
3201 GGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGTGTTGTCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTC
47 V A S I I E G T K T R I A A G V H H K N D E Y L M T I K E T A V E
3301 CACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTA
14 V L E L D Q Q S I N F T K M
3401 ATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCCTAAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCATT
3501 TCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCCTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGGA
3601 ATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGT
3701 AGGAAAGTCCCATAAGGTCATGTACTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGA
3801 TGTAAGTCCAAGTGGGAGTTTACCCTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACG
3901 TCAATGGGCGGGGTCGTTGGCGGTACAGCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAG
4001 CAAAAGGCCAGGAACCGTAAAAAGGCCGCTTCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAGAAAAATCGACGCTCAAGTCAGAGGT
4101 GCGGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCCTGGAAGTCCCTCGTGGCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTC
4201 CGCCTTTCTCCCTTCGGGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGTTCCGCTCAAGCTGGGCTGTGTGCAC
4301 GAACCCCCGTTACGCCCAGCCGCTGCGCTTATCCGTAACATCGTCTTGAAGTCCACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTG
4401 GTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTG
4501 CGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTATCCGGCAAAACAAACCACCGCTGGTAGCGGTGGTTTTTTGTTTGAAGCAG
4601 CAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAAACTCACGTTAAGGGATTTTGG
4701 TCATGGCTAGTTAATTAACATTTAATCAGCGGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACCTAACA
4801 TACGCTCTCCATCAAAACAAACGAAACAAACAAACTAGCAAAATAGGCTGTCCCAGTGCAAGTGACAGGTGCCAGAACATTTCTCTATCGAA