

1 - CAGCAACTTCTGCAGTTTTTCATCGTGGATTCACGTGCGCGCATTCTCATCTGCCGGCT - 60
61 - TTTGATATACCTGAGAGCTGACGCTCCAGAAAAGGTAACCTGGTGTTCGCAACGCAAGGAC - 120
121 - TTAGTCTAATTAAGCGCAGTCAGTCTGTAGTTGCTCTTAGTTAGGTTGAGGTTGACCAGTTAGGGA - 180
181 - AGTTGTGGACAGGTGTTGGGACTGAGTGAGATTGTA AACCTGTGCAGTTGCAGGATTA - 240
241 - GCAGGACCAGGAGAAATAAAGGAATAGGAGCGTTAGGTTATGGTTTGTGGACAAAAGCGG - 300
301 - CAAGTATCCAGATTTCCATTGCGCTTTTTGCAAGAAGCTGGTATTCTGCCGTGCCAGTT - 360
361 - GACATCTGGCTTTGATGTTTCAGATACACTCGCTCACAGTCATCGCTTAGAATTTTGCCT - 420
421 - GCTATCTACGACAGCCGTTCTGTGAGTCTTAGGCAACCTTCTCTGAGTACTGTAAAGC - 480
481 - GTGCAACGCTCTATCCAGCACGAAAACAGCAGCAGAGGAGGCAGCTATATAACAGTGTCT - 540
541 - ACTGTACGAGGGCGCATCAACAAC TAGACCAGCAATTGTAAGGGATACATACATCAACAG - 600
601 - ACGACAAAATGGCGCCAGTAGCGGCAGCTAATGCCATGACGAAGATTACGCTTTCTTTCT - 660
1 - M A P V A A A N A M T K I T L S F L - 18
661 - TGGTGTCTTTGCTTGGTGATAAAAACTTCCAAGGGCCGAGGCTCCAGTCAATAGCAAAAT - 720
19 - L S L L G D K N F Q G P E A P V N S K Y - 38
721 - ATCACTGGGCATATAAGGGACCAGAAGGTCCAGACTCTTGGCATGTGCACACAAAATACT - 780
39 - H W A Y K G P E G P D S W H V H Y K Y C - 58
781 - GTGCTGGCGAGCGTCAGTCTCCTATCAACATCAAGACCTCCAGTTGTGAGTACGATCCAA - 840
59 - A G E R O S P I N I K T S S S C E Y D P F - 78
841 - GGTTAGAGCCTATCATTCTAGAAAATTTTGACGCCACGAGTGGATCAGCAGGCCCTTGTA - 900
79 - L E P I I L E N F D A T S G S A G P C I - 98
901 - TTCTTAATGTCACTAACAACGGTCAATGCTGCCAGTGTCCGAGTGTCAACCAGGACATGC - 960
99 - L N V T N N H A A S V R V L N O D M H - 118
961 - ACGTGAGAGGTGGAGGGTTGGGCCAGGATTATAAACGGTCGAGTTTCACTTCCACTGGG - 1020
119 - V R G G G L G Q D Y K T V E H H H W C - 138
1021 - GCAGCACTGATGATTGGCAGTGAGCATGCAATGGCAAGAAATATCCTTTAGAGA - 1080
139 - S T D D V G S E H A V N G K K Y P L E M - 158
1081 - TGCATGTAGTAACTATGCAGAGAAATATGGCAACGTGAAAGCAGCGATGCACAGCCCG - 1140
159 - H V V N Y A E K Y G N V K A A M T Q P D - 178
1141 - ACGGACTGGCAGTTCTCGGTCTTTTTGAGATTACGGAGAAGATAATCCTTACTTTCG - 1200
179 - G L A V L G V F F E I T E K D N P Y F A - 198
1201 - CGGCTGTAGACGAATCTCTGCGACATATTCACAAAGCAGGGACCACGCGACCATCAACC - 1260
199 - A V D E S L R H I H K A G D H A T I N Q - 218
1261 - AACTACGCTGATGTCGCTCTACCTGATGACCTCTCAAGTCTCGAGGTACAACGGCT - 1320
219 - L R L M S L L P D D L S K F W R Y N G S - 238
1321 - CGCTGACCACACCTTCTGCTTCGAATCCGTTATATGGACTGTATTTACGGAACCGCAGA - 1380
239 - L T T P P F C F E S V I W T V F T E P Q K - 258
1381 - AGATTTCGAAATCCAGCTGGAATACTACGAACACTCCTACACGAAGAAGGTACAGATA - 1440
259 - I S K S O L E I L R T L L H E E G H D I - 278
1441 - TAAGCGATCGAGGGGAGCACCCTCTTACACCATCCAGGCTTGTGATAACTGGCGCC - 1500
279 - S D R G E H H S F T P S R L V D N W R F - 298
1501 - CACTCCAACCACTAACGGCGGGTGTCAAGCAGAGTTTTTCGCGGGGATTTTATACACA - 1560
299 - L O P L N G R V I K O S R G D F I H N - 318
1561 - ACAAGCCTCCCTGGACACAAAGATCGCCTCATTTGAAGCGTCCGCGCCGACCTTGGCAA - 1620
319 - K P P L D T K I A S F E A S A P T L A I - 338
1621 - TAGCCAATAAACCCGATAGTTTAGGAGGAATGTAATGTACAACATAAACCTACGTTTC - 1680
339 - A N K P D S L G G T V M Y N I N P T F Q - 358
1681 - AACCAATGGCACCACAAGAGATGACAAAAGATAAAGCAATGCCACAGGCAAGCAGTAAAA - 1740
359 - P M A P Q E M T K D K A M P Q A S S K I - 378
1741 - TACAGGCTCGAATCACGAAATTAATAATCTTAAATCACAGGAAAGTTTGGAAAGGGTC - 1800
379 - Q A R I T E I N N L K S Q E S F G R G P - 398
1801 - CGGTGGAAGAGAAGCTGTTGATATACAACAGGGTCCCTCTGTAGAAATGGGAGTGAATT - 1860
399 - V E E K L L I Y N Q G P S V E M G V N S - 418
1861 - CTTACCTATCACATTAAGCTCGGAGAAGTCTCAGCAAGTTGAGGTGAACAGAGGCATAG - 1920
419 - S P I T L S S E K S Q Q V E V N R G I G - 438
1921 - GCCTGGCGGATCCCCCGGACAACCTGTTTGGACAGATCCAGCAATCGAACCAAGCTC - 1980
439 - L A D A P A T T L F G Q I Q O S N Q A L - 458
1981 - TGACCCTAACAAATGGACCTGAGTCCAGCTACATCACCCAGGGGAGGCAAGTGCTCAGA - 2040
459 - T A N N G P E S S V H H P G E A S A Q M - 478
2041 - TGTCTCGAGTCCGCATTAAGCTGATCTAAAAAGGATGTGGGTAGACTAGAGCAAA - 2100
479 - S S S S A L K A D L K K D V G R L E Q N - 498
2101 - ACAACCAATAACGTCTCCAGTTGTTAATATCGTTTCAAGACCAAGACATGTGTCTTCTT - 2160
499 - N P I T S P V V N I V S R P R H V S S S - 518
2161 - CTGGAGCTAACGGCGTTTTAAGAAATGTTCAAAGCCAGCAAAGTTCAAATCTGGAAAAG - 2220
519 - G A N G V L R N V Q S Q Q S S N S G K V - 538
2221 - TGACAATGGTGATAAATACTAGTACTACAACCTCCGCTTCTCGTGTTCATGTTTCATTAC - 2280
539 - T M V I N T S T T T P S S R V H V S L R - 558
2281 - GTCCTAATCTCTACAAGTTCTGAGATGACCCATCGGTTCAAGTGTACCAATTCGCC - 2340
559 - P N R L Q S S E M Q P S V Q V L P I A Q - 578
2341 - AACAGCAAAAAGCTCAAAGCTCAGAAGCAGCTGGGCGTTCTCAACCTCTACCACCGAAAC - 2400
579 - Q O K A Q S S E A A A G R S Q P L P P K Q - 598
2401 - AACAACTCAAATGCAGCCAAACACAAACCAGCAGCAACAATCAGLCTGCTGTGT - 2460
599 - Q T Q M Q P N T N R Q Q Q Q S A S A V S - 618
2461 - CCCAGTCAAATCTCCGTTCTGGCCAAATAGATAGTGCATAGCCGCTCTAGCTAACAAACA - 2520
619 - Q S N L R S G Q I D S R I A A L A N N I - 638
2521 - TCAGTCTCATCGCCACCTAGCAATAACACAAATCCAACCAACACACAGCCAGCAAAACA - 2580
639 - R S H R H L A I T Q I Q P N T Q P A N N - 658
2581 - ACAATCCCCAAATGCCTCCAGTATCGACACAATAAACAGATTCCCCAGCGATGCAGA - 2640
659 - N P Q M P P V I R H N K Q I P P A M Q N - 678
2641 - ACCAACACGTGACTTGATATCGCAAAGACACAGCAATATTTGTACAGCAACCTCCAC - 2700

679 - Q Q R D L I S Q R Q Q Q Y L L Q Q P P Q - 698
2701 - AACAAATTCAACGCATGAGCAGACCCGCAACTCCGCAACAGCTACGAGCAATATTCGAGA - 2760
699 - Q I Q R M S R P P T P Q Q L R A I F E K - 718
2761 - AGTTGGCTGCATT CAGGCGCGCAAACGCACGGTCTAGAATAATGACATCAGGAGCAGCGA - 2820
719 - L A A F R R A N A R S R I M T S G A A I - 738
2821 - TAATCCCCGACTCAAAC TACAACAAGTGAATTCAGTAAGTGGTACGCGATTCCCTTAGCA - 2880
739 - I P R L K L Q Q V N S V S G T R F L S N - 758
2881 - ATCCTGCTTCTTCTAGGCATCACACAGGTGCGTCAAATGGAAACCAGCAATTTAACATTC - 2940
759 - P A S S R H H T G A S N G N Q Q F N I P - 778
2941 - CTCGAGACAATCCCAGTTCCTTCTCCTGAACCGTCCTCATCCTTG CAGTCATCGTGGA - 3000
779 - R D N S Q F L S P E P S S S L Q S S W T - 798
3001 - CAAACATAAACACAACCTGGACTACAACGGTCAGGCTGGCTCCTCGTATCAACCACCTC - 3060
799 - N I N T N L D Y N G Q A G S S Y Q P P Q - 818
3061 - AATCATATTGGTCACAGCCCTCTCAGCAACAACATACTACAGCGGACTGGATACCAAC - 3120
819 - S Y W S Q P S Q Q Q T Y S Q R T G Y Q Q - 838
3121 - AGAGCATGCCACTACAACAAAACACACAGCAACAGCAGGTGTACCCCAACAACAGCAGG - 3180
839 - S M P L Q Q N T Q Q Q Q V Y P Q Q Q Q V - 858
3181 - TATACCCACAGCAACAGCAGGCATACCCACAGCAACAGCAGGCATACCCCAACAACAAC - 3240
859 - Y P Q Q Q Q A Y P Q Q Q Q A Y P Q Q Q Q - 878
3241 - AACCGCAACAGCAGGCATACCCACAACAACAGCAGCAGCAACAGCAGGCATACCCACAAC - 3300
879 - P Q Q Q A Y P Q Q Q Q Q Q Q A Y P Q Q Q - 898
3301 - AACAGCAGCAGCAACAGCAGGCATACCCCAACAACAACAGCAGGATTACCCGCAACTAC - 3360
899 - Q Q Q Q Q Q A Y P Q Q Q Q Q D Y P Q L Q - 918
3361 - AGCAGGCATACCCCAACAACAGCAGGCATACCCAGCAACAGCCAACCCCAACTCTCC - 3420
919 - Q A Y P Q Q Q Q A Y T Q Q Q P T P T L H - 938
3421 - ATTACCCCCAGCATCCCCACTGCCATGTACTCCTCCCCATGGCCAGATCAGACAACA - 3480
939 - Y T P A S P T A M Y S S P M A R S D N T - 958
3481 - CAAACCTCTACTACACAGCAGGCCCTGGCGTGTCTGGGCGCCAGTTCAAACGCTATGTCTC - 3540
959 - N L Y Y T A G P G V S G A S S N A M S L - 978
3541 - TACCTCAAGTGTCTGGCCATGGACGCGAATGCTCACCAAGTCTATCTGAACAACCAAAAAC - 3600
979 - P Q V S A M D A N A H Q V Y L N N Q K Q - 998
3601 - AGCCAGTGGCGGATATTACGTCCAGTTTATGAGCAAGTCAACAGCAGGCAACAAGCACAGT - 3660
999 - P V R I L R P V Y E Q V N S R Q Q A Q Y - 1018
3661 - ACCAGAACCAGCAGTACCCGTTCTTCGTTTACTGAGTGCGCAACATCTGTCTTATGTCTA - 3720
1019 - Q N Q Q Y P F F V Y * - 1038
3721 - CTGCTGATCTGTTTTATCATCACCATCATAACCACCGATCTGTCTTACCTTGATTTGTCT - 3780
3781 - TGTCATCACTGTCTGTCTTATCATCATCACCAGATCTGTCTTATTATCACTGATATGTCT - 3840
3841 - TATCATTACTGGACTGTCT - 3859