

Translation Map results

Results for 2235 residue sequence "Untitled" starting "ATGGCCACCA"

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1 M A T T V Q L S D Q S L R Q L E T L A I
1 ATGGCCACCACCGTACAACCTCAGCGACCAATCCCTCCGTCAGCTAGAAACCCCTCGCCATC
1          10          20          30          40          50
1 TACCGGTGGTGGCATGTTGAGTCGCTGGTTAGGGAGGCAGTCGATCTTTGGGAGCGGTAG
21 H T A H L I Q P H G L V V V L Q E P D L
61 CACACCGCCCACCTGATTCAGCCCCACGGTTTGTAGTGGTGGTCTCTGCAGGAACCAGACCTC
61          70          80          90          100         110
61 GTGTGGCGGGTGGACTAAGTCGGGGTGCCAAATCACCACCAGGACGTCCTTGGTCTGGAG
41 T I S Q I S A N C T G I L G R S P E D L
121 ACCATCAGCCAAATTAGCGCCAACTGCACCGGCATTTTAGGGCGATCGCCAGAGGATTTG
121          130         140         150         160         170
121 TGGTAGTCGGTTTAATCGCGGTTGACGTGGCCGTAATAATCCCGCTAGCGGTCTCCTAAAC
61 L G R T L G E V F D S F Q I D P I Q S R
181 TTGGGCAGAACCCTAGGGGAAGTGTGATAGCTTTCAGATTGATCCCATCCAGAGTTCG
181          190         200         210         220         230
181 AACCCGTCTTGGGATCCCCTTCACAACTATCGAAAGTCTAACTAGGGTAGGTCTCAGCG
81 L T A G Q I S S L N P S K L W A R V M G
241 CTAACGGCCGGACAAATCAGCAGCCTCAACCCCAGTAAACTTTGGGCGCGGGTCATGGGG
241          250         260         270         280         290
241 GATTGCCGGCCTGTTTGTAGTCGTCGGAGTTGGGGTCATTTGAAACCCGCGCCAGTACCCC
101 D D F V I F D G V F H R N S D G L L V C
301 GACGACTTTGTTCATTTTTGACGGGGTTTTTCATCGCAACAGTGACGGTTTATTGGTATGT
301          310         320         330         340         350
301 CTGCTGAAACAGTAAAAACTGCCCCAAAAAGTAGCGTTGTCACTGCCAAATAACCATACA
121 E L E P A Y T S D N L P F L G F Y H M A
361 GAACTCGAGCCAGCCTACACTTCCGATAATCTGCCCTTCCTCGGTTTTTATCACATGGCC
361          370         380         390         400         410
361 CTTGAGCTCGGTTCGGATGTGAAGGCTATTAGACGGGAAGGAGCCAAAAATAGTGTACCGG
141 N A A L N R L R Q Q A N L R D F Y D V I
421 AACGCTGCCCTGAATCGGTTGCGCCAACAAGCTAATCTACGGGATTTCTACGATGTTATT
421          430         440         450         460         470
421 TTGCGACGGGACTTAGCCAACGCGGTTGTTTCGATTAGATGCCCTAAAGATGCTACAATAA
161 V E E V R R M T G F D R V M L Y R F D E
481 GTCGAAGAAGTCCGCCGTATGACTGGCTTTGACCGGGTGATGCTATAACCGCTTTGATGAA
481          490         500         510         520         530
481 CAGCTTCTTCAGGCGGCATACTGACCGAAACTGGCCCACTACGATATGGCGAAACTACTT
181 N N H G D V I A E D K R D D M E P Y L G
541 AATAACCACGGTGATGTCATTGCCGAAGATAAACGGGATGATATGGAACCCTATTTGGGC
541          550         560         570         580         590
541 TTATTGGTGCCACTACAGTAACGGCTTCTATTTGCCCTACTATACCTTGGGATAAACCCG
201 L H Y P E S D I P Q P A R R L F I H N P
601 CTGCACTATCCCGAATCGGATATTCCCAACCCGCGCGCTATTTATCCACAACCCC
601          610         620         630         640         650
601 GACGTGATAGGGCTTAGCCTATAAGGGGTTGGGCGGGCAGCCGATAAATAGGTGTTGGGG
221 I R V I P D V Y G V A V P L T P A V N P
661 ATTCGAGTAATCCCGATGTTTATGGTGTGGCGGTGCCCTGACCCAGCGGTTAACCCC
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661 670 680 690 700 710
661 TAAGCTCATTAAGGGCTACAAATACCACACCGCCACGGGGACTGGGGTCGCCAATTGGGG
241 S T N R A V D L T E S I L R S A Y H C H
721 AGCACCAACCGAGCGGTGGATTTAACAGAATCCATTCTGCGCAGTGCGTACCATTGCCAC
721 730 740 750 760 770
721 TCGTGGTTGGCTCGCCACCTAAATTTGTCTTAGGTAAGACGCGTCACGCATGGTAACGGTG
261 L T Y L K N M G V G A S L T I S L I K D
781 TTGACCTATCTGAAAAATATGGGGGTAGGAGCGTCTTTAACCATTTCCCTAATTAAGGAC
781 790 800 810 820 830
781 AACTGGATAGACTTTTTATACCCCCATCCTCGCAGAAATGGTAAAGGGATTAATTCCTG
281 G H L W G L I A C H H Q T P K V I P F E
841 GGCCATCTCTGGGGGCTCATTGCCTGCCACCATCAAACCCCCAAAGTAATTCCTTTGAA
841 850 860 870 880 890
841 CCGGTAGAGACCCCCGAGTAACGGACGGTGGTAGTTTGGGGGTTTCATTAAGGGAACTT
301 L R K A C E F F G R V V F S N I S A Q E
901 CTGCGTAAAGCCTGCGAATTTTTTGGTTCGGGTGGTGTTTAGCAACATTTCCGCCCAGGAA
901 910 920 930 940 950
901 GACGCATTTTCGGACGCTTAAAAAACAGCCCACCACAAATCGTTGTAAAGGCGGGTCCTT
321 D T E T F D Y R V Q L A E H E A V L L D
961 GATACGAAACCTTCGATTACCGGGTGCAGCTGGCGGAGCATGAAGCGGTTTTATTGGAC
961 970 980 990 1000 1010
961 CTATGCCTTTGGAAGCTAATGGCCCACGTCGACCGCCTCGTACTTCGCCAAAATAACCTG
341 K M T T A A D F V E G L T N H P D R L L
1021 AAAATGACCACGGCGGCGGATTTTGTCTGAAGGATTAATAATCATCCCGATCGCCTGTTG
1021 1030 1040 1050 1060 1070
1021 TTTTACTGGTGGCCCGCCCTAAAACAGCTTCCTAATTGATTAGTAGGGCTAGCGGACAAC
361 G L T G S Q G A A I C F G E K L I L V G
1081 GGATTAACGGGCTCCCAGGGGGCGGCCATTTGCTTTGGGGAAAAATTGATTTTAGTAGGG
1081 1090 1100 1110 1120 1130
1081 CCTAATTGCCCGAGGGTCCCCCGCCGGTAAACGAAACCCCTTTTTAACTAAAATCATCCC
381 E T P D E K A V Q Y L L Q W L E N R E V
1141 GAAACCCCGGACGAGAAAGCAGTGCAATATTTACTGCAATGGTTGGAGAATCGGGAAAGTG
1141 1150 1160 1170 1180 1190
1141 CTTTGGGGCCTGCTCTTTTCGTACGTTATAAATGACGTTACCAACCTCTTAGCCCTTCAC
401 Q D V F F T S S L S Q I Y P D A V N F K
1201 CAAGACGTTTTCTTCACCTTTCCTCTCACAAATTTATCCTGATGCAGTGAATTTTAAA
1201 1210 1220 1230 1240 1250
1201 GTTCTGCAAAAGAAGTGGAGAAGGGAGAGTGTTTAAATAGGACTACGTCACTTAAAATTT
421 S V A S G L L A I P I A R H N F L L W F
1261 TCCGTGGCCAGTGGCTTATTGGCCATTCCCATTGCCCGTCACAACTTTTTGCTCTGGTTT
1261 1270 1280 1290 1300 1310
1261 AGGCACCGGTCACCGAATAACCGGTAAGGGTAACGGGCAGTGTGAAAAACGAGACCAAA
441 R P E V L Q T V N W G G D P N H A Y E A
1321 CGCCCTGAAGTGTGCAAACGGTTAATTGGGGCGGTGACCCAAATCATGCTTACGAAGCT
1321 1330 1340 1350 1360 1370
1321 GCGGGACTTCACAACGTTTGCCAATTAACCCCGCCACTGGGTTTAGTACGAATGCTTCGA
461 T Q E D G K I E L H P R Q S F D L W K E
1381 ACCCAGGAAGACGGTAAAATCGAGCTCCATCCCCGCAATCCTTTGACCTCTGGAAAGAA
1381 1390 1400 1410 1420 1430
1381 TGGGTCCTTCTGCCATTTTAGCTCGAGGTAGGGCGGTTAGGAAACTGGAGACCTTTCTT

481 I V R L Q S L P W Q S V E I Q S A L A L
1441 ATTGTCCGACTCCAATCTTTGCCCTGGCAATCGGTGGAAATCCAAAGTGCCCTGGCCCTG
1441 1450 1460 1470 1480 1490
1441 TAACAGGCTGAGGTTAGAAACGGGACCGTTAGCCACCTTTAGGTTTCACGGGACCGGGAC
501 K K A I V N L I L R Q A E E L H M A A G
1501 AAAAAGGCGATCGTCAACCTCATTTTGCGCCAGGCAGAAGAATTGCATATGGCGGCTGGT
1501 1510 1520 1530 1540 1550
1501 TTTTTCCGCTAGCAGTTGGAGTAAAACGCGGTCCGTCTTCTTAACGTATAACGCCGACCA
521 V K Q L A D D R T L L M A G V S H D L R
1561 GTTAAGCAACTGGCGGATGACCGCACGCTGCTGATGGCGGGGGTAAGTCACGACTTGCGC
1561 1570 1580 1590 1600 1610
1561 CAATTCGTTGACCGCCTACTGGCGTGCAGACTACCGCCCCATTTCAGTGCTGAACGCG
541 T P L T R I R L A T E M M S E Q D G Y L
1621 ACGCCGCTGACGCGTATTCGCCTGGCGACTGAGATGATGAGCGAGCAGGATGGCTATCTG
1621 1630 1640 1650 1660 1670
1621 TGCGGCGACTGCGCATAAGCGGACCGCTGACTCTACTACTCGCTCGTCCTACCGATAGAC
561 A E S I N K D I E E C N A I I E Q F I D
1681 GCAGAATCGATCAATAAAGATATCGAAGAGTGCAACGCCATCATTTGAGCAGTTTATCGAC
1681 1690 1700 1710 1720 1730
1681 CGTCTTAGCTAGTTATTTCTATAGCTTCTCACGTTGCGGTAGTAACCTCGTCAAATAGCTG
581 Y L R T G Q E M P M E M A D L N A V L G
1741 TACCTGCGCACC GGCAGGAGATGCCGATGGAAATGGCGGATCTTAATGCAGTACTCGGT
1741 1750 1760 1770 1780 1790
1741 ATGGACGCGTGGCCCGTCCTCTACGGCTACCTTTACCGCCTAGAATTACGTCATGAGCCA
601 E V I A A E S G Y E R E I E T A L Y P G
1801 GAGGTGATTGCTGCCGAAAGTGGCTATGAGCGGGAAATTGAAACCGCGCTTTACCCCGGC
1801 1810 1820 1830 1840 1850
1801 CTCCACTAACGACGGCTTTCACCGATACTCGCCCTTTAACTTTGGCGCGAAATGGGGCCG
621 S I E V K M H P L S I K R A V A N M V V
1861 AGCATTGAAGTGAAAATGCACCCGCTGTCGATCAAACGCGCGGTGGCGAATATGGTGGTC
1861 1870 1880 1890 1900 1910
1861 TCGTAACTTCACTTTTACGTGGGCGACAGCTAGTTTGC GCGCCACCGCTTATAACCACAG
641 N A A R Y G N G W V K V S S G T E P N R
1921 AACGCCGCCGTTATGGCAATGGCTGGGTCAAAGTCAGCAGCGGAACGGAGCCGAATCGC
1921 1930 1940 1950 1960 1970
1921 TTGCGGCGGGCAATACCGTTACCGACCCAGTTTCAGTCGTCGCCTTGCCTCGGCTTAGCG
661 A W F Q V E D D G P G I A P E Q R K H L
1981 GCCTGGTTCCAGGTGGAAGATGACGGTCCGGGAATTGCGCCGGAACAACGTAAGCACCTG
1981 1990 2000 2010 2020 2030
1981 CGGACCAAGGTCCACCTTCTACTGCCAGGCCCTTAACGCGGCCTTGTTGCATTTCGTGGAC
681 F Q P F V R G D S A R T I S G T G L G L
2041 TTCCAGCCGTTTGTCCGCGGCACAGTGC GCGCACCATTAGCGGCACGGGATTAGGGCTG
2041 2050 2060 2070 2080 2090
2041 AAGGTCGGCAAACAGGCGCCGCTGTCACGCGCGTGGTAATCGCCGTGCCCTAATCCCGAC
701 A I V Q R I V D N H N G M L E L G T S E
2101 GCAATTGTGCAGCGTATCGTGGATAACCATAACGGGATGCTGGAGCTTGGCACCAGCGAG
2101 2110 2120 2130 2140 2150
2101 CGTTAACACGTCGCATAGCACCTATTGGTATTGCCCTACGACCTCGAACCGTGGTTCGCTC
721 R G G L S I R A W L P V P V T R A Q G M
2161 CGGGGCGGGCTTTCATTTCGCGCCTGGCTGCCAGTGCCGGTAACGCGGGCGCAGGGCATG

2161 2170 2180 2190 2200 2210
2161 G C C C C G C C C G A A A G G T A A G C G C G G A C C G A C G G T C A C G G C C A T T G C G C C C G C G T C C C G T A C
741 T K E G *
2221 A C A A A A G A A G G G T A A
2221 2230
2221 T G T T T T C T T C C C A T T

