# 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 ATGGCCACCACCGTACAACTCAGCGACCAATCCCTCCGTCAGCTAGAAACCCTCGCCATC
  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 CACACCGCCCACCTGATTCAGCCCCACGGTTTAGTGGTGGTCCTGCAGGAACCAGACCTC
 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 TGGTAGTCGGTTTAATCGCGGTTGACGTGGCCGTAAAATCCCGCTAGCGGTCTCCTAAAC
 61 L  G  R  T  L  G  E  V  F  D  S  F  Q  I  D  P  I  Q  S  R
181 TTGGGCAGAACCCTAGGGGAAGTGTTTGATAGCTTTCAGATTGATCCCATCCAGAGTCGC
181          190       200       210       220       230
181 AACCCGTCTTGGGATCCCCTTCACAAACTATCGAAAGTCTAACTAGGGTAGGTCTCAGCG
 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 GATTGCCGGCCTGTTTAGTCGTCGGAGTTGGGGTCATTTGAAACCCGCGCCCAGTACCCC
101 D  D  F  V  I  F  D  G  V  F  H  R  N  S  D  G  L  L  V  C
301 GACGACTTTGTCATTTTTGACGGGGTTTTTCATCGCAACAGTGACGGTTTATTGGTATGT
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 CTTGAGCTCGGTCGGATGTGAAGGCTATTAGACGGGAAGGAGCCAAAAATAGTGTACCGG
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 TTGCGACGGGACTTAGCCAACGCGGTTGTTCGATTAGATGCCCTAAAGATGCTACAATAA
161 V  E  E  V  R  R  M  T  G  F  D  R  V  M  L  Y  R  F  D  E
481 GTCGAAGAAGTCCGCCGTATGACTGGCTTTGACCGGGTGATGCTATACCGCTTTGATGAA
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 CTGCACTATCCCGAATCGGATATTCCCCAACCCGCCCGTCGGCTATTTATCCACAACCCC
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 ATTCGAGTAATTCCCGATGTTTATGGTGTGGCGGTGCCCCTGACCCCAGCGGTTAACCCC
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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 TCGTGGTTGGCTCGCCACCTAAATTGTCTTAGGTAAGACGCGTCACGCATGGTAACGGTG
 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 AACTGGATAGACTTTTTATACCCCCATCCTCGCAGAAATTGGTAAAGGGATTAATTCCTG
 281 G  H  L  W  G  L  I  A  C  H  H  Q  T  P  K  V  I  P  F  E
 841 GGCCATCTCTGGGGGCTCATTGCCTGCCACCATCAAACCCCCAAAGTAATTCCCTTTGAA
 841          850       860       870       880       890
 841 CCGGTAGAGACCCCCGAGTAACGGACGGTGGTAGTTTGGGGGTTTCATTAAGGGAAACTT
 301 L  R  K  A  C  E  F  F  G  R  V  V  F  S  N  I  S  A  Q  E
 901 CTGCGTAAAGCCTGCGAATTTTTTGGTCGGGTGGTGTTTAGCAACATTTCCGCCCAGGAA
 901          910       920       930       940       950
 901 GACGCATTTCGGACGCTTAAAAAACCAGCCCACCACAAATCGTTGTAAAGGCGGGTCCTT
 321 D  T  E  T  F  D  Y  R  V  Q  L  A  E  H  E  A  V  L  L  D
 961 GATACGGAAACCTTCGATTACCGGGTGCAGCTGGCGGAGCATGAAGCGGTTTTATTGGAC
 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 AAAATGACCACGGCGGCGGATTTTGTCGAAGGATTAACTAATCATCCCGATCGCCTGTTG
1021          1030      1040      1050      1060      1070
1021 TTTTACTGGTGCCGCCGCCTAAAACAGCTTCCTAATTGATTAGTAGGGCTAGCGGACAAC
 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 GAAACCCCGGACGAGAAAGCAGTGCAATATTTACTGCAATGGTTGGAGAATCGGGAAGTG
1141          1150      1160      1170      1180      1190
1141 CTTTGGGGCCTGCTCTTTCGTCACGTTATAAATGACGTTACCAACCTCTTAGCCCTTCAC
 401 Q  D  V  F  F  T  S  S  L  S  Q  I  Y  P  D  A  V  N  F  K
1201 CAAGACGTTTTCTTCACCTCTTCCCTCTCACAAATTTATCCTGATGCAGTGAATTTTAAA
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 AGGCACCGGTCACCGAATAACCGGTAAGGGTAACGGGCAGTGTTGAAAAACGAGACCAAA
 441 R  P  E  V  L  Q  T  V  N  W  G  G  D  P  N  H  A  Y  E  A
1321 CGCCCTGAAGTGTTGCAAACGGTTAATTGGGGCGGTGACCCAAATCATGCTTACGAAGCT
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 ACCCAGGAAGACGGTAAAATCGAGCTCCATCCCCGCCAATCCTTTGACCTCTGGAAAGAA
1381          1390      1400      1410      1420      1430
1381 TGGGTCCTTCTGCCATTTTAGCTCGAGGTAGGGGCGGTTAGGAAACTGGAGACCTTTCTT
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 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 TTTTTCCGCTAGCAGTTGGAGTAAAACGCGGTCCGTCTTCTTAACGTATACCGCCGACCA
 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 CAATTCGTTGACCGCCTACTGGCGTGCGACGACTACCGCCCCCATTCAGTGCTGAACGCG
 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 GCAGAATCGATCAATAAAGATATCGAAGAGTGCAACGCCATCATTGAGCAGTTTATCGAC
1681          1690      1700      1710      1720      1730
1681 CGTCTTAGCTAGTTATTTCTATAGCTTCTCACGTTGCGGTAGTAACTCGTCAAATAGCTG
 581 Y  L  R  T  G  Q  E  M  P  M  E  M  A  D  L  N  A  V  L  G
1741 TACCTGCGCACCGGGCAGGAGATGCCGATGGAAATGGCGGATCTTAATGCAGTACTCGGT
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 TCGTAACTTCACTTTTACGTGGGCGACAGCTAGTTTGCGCGCCACCGCTTATACCACCAG
 641 N  A  A  R  Y  G  N  G  W  V  K  V  S  S  G  T  E  P  N  R
1921 AACGCCGCCCGTTATGGCAATGGCTGGGTCAAAGTCAGCAGCGGAACGGAGCCGAATCGC
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 CGGACCAAGGTCCACCTTCTACTGCCAGGCCCTTAACGCGGCCTTGTTGCATTCGTGGAC
 681 F  Q  P  F  V  R  G  D  S  A  R  T  I  S  G  T  G  L  G  L
2041 TTCCAGCCGTTTGTCCGCGGCGACAGTGCGCGCACCATTAGCGGCACGGGATTAGGGCTG
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 CGTTAACACGTCGCATAGCACCTATTGGTATTGCCCTACGACCTCGAACCGTGGTCGCTC
 721 R  G  G  L  S  I  R  A  W  L  P  V  P  V  T  R  A  Q  G  M
2161 CGGGGCGGGCTTTCCATTCGCGCCTGGCTGCCAGTGCCGGTAACGCGGGCGCAGGGCATG
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2161      2170      2180      2190      2200      2210
2161 GCCCCGCCCGAAAGGTAAGCGCGGACCGACGGTCACGGCCATTGCGCCCGCGTCCCGTAC
 741 T  K  E  G  *
2221 ACAAAAGAAGGGTAA
2221      2230
2221 TGTTTTCTTCCCATT
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