```
     GCTAGGAGACATTGCGGCGGCGGTGGCGGCGTTGGCAGCAGCTGCAGACATGCTGCTGCT
  1  ---------+---------+---------+---------+---------+---------+   60
     CGATCCTCTGTAACGCCGCCGCCACCGCCGCAACCGTCGTCGACGTCTGTACGACGACGA
                                                   M  L  L  L

     CAAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAGCTGGGCTCGGG
 61  ---------+---------+---------+---------+---------+---------+  120
     GTTCTTTGTCTGCCTCCTGTAGTCGTCACAGATACTCTAGGCCCTCTTCGACCCGAGCCC
      K  K  Q  T  E  D  I  S  S  V  Y  E  I  R  E  K  L  G  S  G

     TGCCTTCTCTGAGGTGATGCTGGCCCAGGAAAGGGGCTCTGCTCATCTTGTGGCCCTCAA
121  ---------+---------+---------+---------+---------+---------+  180
     ACGGAAGAGACTCCACTACGACCGGGTCCTTTCCCCGAGACGAGTAGAACACCGGGAGTT
      A  F  S  E  V  M  L  A  Q  E  R  G  S  A  H  L  V  A  L  K

     GTGCATTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGGTGGAGAATGAGATCGCAGT
181  ---------+---------+---------+---------+---------+---------+  240
     CACGTAAGGGTTCTTTCGTGAAGCCCCGTTCCTCCGGGACCACCTCTTACTCTAGCGTCA
      C  I  P  K  K  A  L  R  G  K  E  A  L  V  E  N  E  I  A  V

     ACTCCGCAGGATTAGCCACCCCAACATTGTGGCTCTGGAGGACGTCCACGAGAGCCCTTC
241  ---------+---------+---------+---------+---------+---------+  300
     TGAGGCGTCCTAATCGGTGGGGTTGTAACACCGAGACCTCCTGCAGGTGCTCTCGGGAAG
      L  R  R  I  S  H  P  N  I  V  A  L  E  D  V  H  E  S  P  S

     CCATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACTGTTTGACCGAATCATGGA
301  ---------+---------+---------+---------+---------+---------+  360
     GGTAGAGATGAACCGGTACCTCGACCATTGTCCACCACTTGACAAACTGGCTTAGTACCT
      H  L  Y  L  A  M  E  L  V  T  G  G  E  L  F  D  R  I  M  E

     GCGGGGCTCCTACACAGAGAAGGATGCGAGCCACCTTGTAGGGCAGGTCCTTGGTGCTGT
361  ---------+---------+---------+---------+---------+---------+  420
     CGCCCCGAGGATGTGTCTCTTCCTACGCTCGGTGGAACATCCCGTCCAGGAACCACGACA
      R  G  S  Y  T  E  K  D  A  S  H  L  V  G  Q  V  L  G  A  V

     CTCCTACCTTCATAGCCTGGGCATCGTGCACCGGGACCTCAAGCCTGAAAACCTCCTCTA
421  ---------+---------+---------+---------+---------+---------+  480
     GAGGATGGAAGTATCGGACCCGTAGCACGTGGCCCTGGAGTTCGGACTTTTGGAGGAGAT
      S  Y  L  H  S  L  G  I  V  H  R  D  L  K  P  E  N  L  L  Y

     TGCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTGTCCAAAATTCA
481  ---------+---------+---------+---------+---------+---------+  540
     ACGGTGTGGAAAACTCCTGAGGTTCTAGTACCAGAGACTGAAACCGGACAGGTTTTAAGT
      A  T  P  F  E  D  S  K  I  M  V  S  D  F  G  L  S  K  I  Q
```

FIG. 6A