```
     AGCTGGCAACATGCTAGGCACAGCCTGTGGGACCCCAGGATATGTGGCCCCAGAGCTCCT
541  ---------+---------+---------+---------+---------+---------+  600
     TCGACCGTTGTACGATCCGTGTCGGACACCCTGGGGTCCTATACACCGGGGTCTCGAGGA
      A  G  N  M  L  G  T  A  C  G  T  P  G  Y  V  A  P  E  L  L

     GGAGCAGAAACCCTACGGGAAGGCCGTAGATGTGTGGGCCCTGGGTGTCATCTCCTACAT
601  ---------+---------+---------+---------+---------+---------+  660
     CCTCGTCTTTGGGATGCCCTTCCGGCATCTACACACCCGGGACCCACAGTAGAGGATGTA
      E  Q  K  P  Y  G  K  A  V  D  V  W  A  L  G  V  I  S  Y  I

     CCTGCTGTGTGGGTACCCCCCCTTCTATGATGAGAGCGATCCTGAACTCTTCAGCCAGAT
661  ---------+---------+---------+---------+---------+---------+  720
     GGACGACACACCCATGGGGGGGAAGATACTACTCTCGCTAGGACTTGAGAAGTCGGTCTA
      L  L  C  G  Y  P  P  F  Y  D  E  S  D  P  E  L  F  S  Q  I

     TCTGAGGGCCAGCTACGAGTTTGACTCTCCCTTTTGGGATGACATCTCAGAATCAGCCAA
721  ---------+---------+---------+---------+---------+---------+  780
     AGACTCCCGGTCGATGCTCAAACTGAGAGGGAAAACCCTACTGTAGAGTCTTAGTCGGTT
      L  R  A  S  Y  E  F  D  S  P  F  W  D  D  I  S  E  S  A  K

     AGACTTCATTCGGCACCTTCTGGAACGTGATCCCCAGAAGAGGTTCACCTGCCAACAGGC
781  ---------+---------+---------+---------+---------+---------+  840
     TCTGAAGTAAGCCGTGGAAGACCTTGCACTAGGGGTCTTCTCCAAGTGGACGGTTGTCCG
      D  F  I  R  H  L  L  E  R  D  P  Q  K  R  F  T  C  Q  Q  A

     CTTACAGCATCTCTGGATCTCTGGGGATGCAGCCTTGGACAGGGACATCCTAGGTTCTGT
841  ---------+---------+---------+---------+---------+---------+  900
     GAATGTCGTAGAGACCTAGAGACCCCTACGTCGGAACCTGTCCCTGTAGGATCCAAGACA
      L  Q  H  L  W  I  S  G  D  A  A  L  D  R  D  I  L  G  S  V

     CAGTGAGCAGATCCAGAAGAATTTTGCCAGGACCCACTGGAAGCGTGCATTCAATGCCAC
901  ---------+---------+---------+---------+---------+---------+  960
     GTCACTCGTCTAGGTCTTCTTAAAACGGTCCTGGGTGACCTTCGCACGTAAGTTACGGTG
      S  E  Q  I  Q  K  N  F  A  R  T  H  W  K  R  A  F  N  A  T

     ATCATTCCTACGTCACATCCGTAAGCTGGGACAGAGCCCAGAGGGTGAGGAGGCCTCCAG
961  ---------+---------+---------+---------+---------+---------+  1020
     TAGTAAGGATGCAGTGTAGGCATTCGACCCTGTCTCGGGTCTCCCACTCCTCCGGAGGTC
      S  F  L  R  H  I  R  K  L  G  Q  S  P  E  G  E  E  A  S  R

     GCAGGGTATGACCCGTCACAGCCACCCAGGCCTTGGGACTAGCCAGTCTCCCAAGTGGTG
1021 ---------+---------+---------+---------+---------+---------+  1080
     CGTCCCATACTGGGCAGTGTCGGTGGGTCCGGAACCCTGATCGGTCAGAGGGTTCACCAC
      Q  G  M  T  R  H  S  H  P  G  L  G  T  S  Q  S  P  K  W  V
```

FIG. 6B