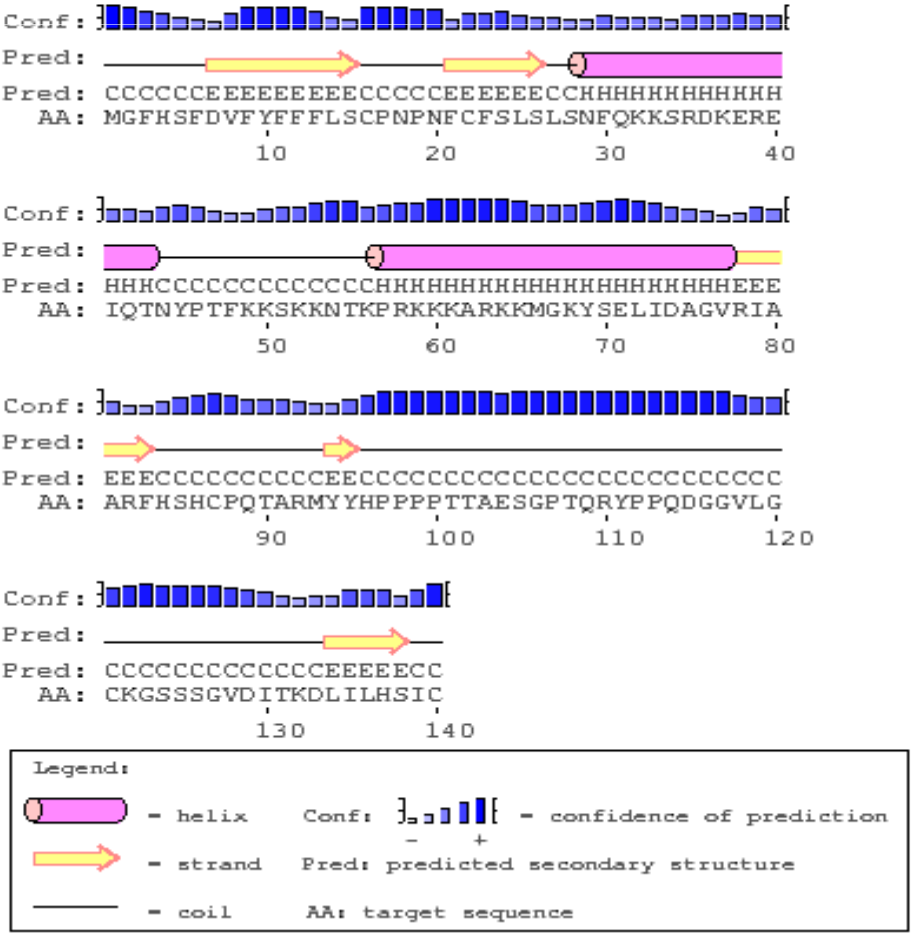
Figure S1

A

```
  1 - GCAAACCACAGCCTTTTTCCCTTTAC                                  - 26
 27 - ATGGGATTTCATTCCTTTGACGTCTTCTACTTTTTCTTTCTTTCTTGCCCTAACCCTAAT - 86
  1 -  M  G  F  H  S  F  D  V  F  Y  F  F  F  L  S  C  P  N  P  N  - 20

 87 - TTCTGTTTTTCTCTCTCTTTATCAAATTTCCAGAAAAAATCTCGAGATAAAGAGAGGGAG - 146
 21 -  F  C  F  S  L  S  L  S  N  F  Q  K  K  S  R  D  K  E  R  E  - 40

147 - ATTCAGACCAATTATCCTACATTCAAAAAATCCAAAAAAAATACAAAACCCAGAAAGAAA - 206
 41 -  I  Q  T  N  Y  P  T  F  K  K  S  K  K  N  T  K  P  R  K  K  - 60

207 - AAGGCAAGAAAAAAAATGGGGAAGTATTCAGAGTTGATAGATGCAGGGGTAAGAATTGCT - 266
 61 -  K  A  R  K  K  M  G  K  Y  S  E  L  I  D  A  G  V  R  I  A  - 80

267 - GCCCGATTTCATTCTCACTGCCCGCAAACTGCCCGGATGTATTATCACCCTCCTCCTCCG - 326
 81 -  A  R  F  H  S  H  C  P  Q  T  A  R  M  Y  Y  H  P  P  P  P  - 100

327 - ACCACCGCGGAGTCGGGCCCCACCCAACGATATCCACCGCAAGACGGCGGCGTTTTGGGT - 386
101 -  T  T  A  E  S  G  P  T  Q  R  Y  P  P  Q  D  G  G  V  L  G  - 120

387 - TGCAAAGGAAGCTCTTCTGGAGTTGATATTACCAAGGATCTGATTCTTCATTCGATTTGT - 446
121 -  C  K  G  S  S  S  G  V  D  I  T  K  D  L  I  L  H  S  I  C  - 140

447 - TGA - 449
141 -  *
450 - TTTTTAAAAAAAAATTCTGATTGGAAGCTAGAGTTATGTTAGAAACATTTAGGT
      TGAATCCTATTAACACAAAAAAAAAAAAAAAAAA                         - 537
```

B