

9.3 Antigenic Site Prediction by EMBOSS ANTIGENIC

EMBOSS Antigenic [11] is used for the prediction of probable antigenic sites present in the above protein. The tool would predict the antigenic sites for the user entered protein sequence. The prediction is based on the Kolaskar and Tongaonkar's method. This method of antigenic site prediction is based on the physiochemical properties of the amino acids. The output gives the information about antigenic region along with the indication of site within the region with high potential for being an antigenic site. All the data obtained was tabulated.

9.4 Identification of Peptide with Highest Antigenic Propensity Using EMBOSS Antigenic Tool

See Fig. 9.3.

The above EMBOSS results show that the peptide with highest score or antigenic propensity is the region 5337–5416. This shows the highest score of 1.284 confirming

```
#####
# Program: antigenic
# Rundate: Tue 23 Jun 2020 11:54:42
# Commandline: antigenic
# -auto
# -sequence /var/lib/emboss-explorer/output/199895/.sequence
# -minlen 6
# -outfile outfile
# -rformat2 motif
# Report_format: motif
# Report_file: outfile
#####

#=====
#
# Sequence: YP_009724389.1      from: 1   to: 7096
# HitCount: 323
#=====

Max_score_pos at ""

(1) Score 1.284 length 80 at residues 5337->5416
      *
Sequence: SLRCGACIRRPFLLCCKCCYDHSVISTSHKLVLSVNPYVCNAPGCDVTDVTQLYLGGMSYCKSHKPPISFPLCANGQVFGL
      |
      5337
Max_score_pos: 5352
      |
      5416

(2) Score 1.276 length 14 at residues 4323->4336
      *
Sequence: GASCCLYCRCHIDH
      |
      4323
Max_score_pos: 4329
      |
      4336

(3) Score 1.273 length 21 at residues 3864->3884
      *
Sequence: DVKCTSVVLLSVLQQLRVES
      |
      |
```

Fig. 9.3 Partial output of EMBOSS antigenic tool