

# ABCpred Prediction Server

## INPUT INFORMATION

|  |      |
|--|------|
| Sequence name                            |      |
| Length of the sequence                   | 250  |
| Number of 16mers from the input sequence | 235  |
| Threshold setting (Default value is 0.5) | 0.51 |

## TABULAR RESULT

### Predicted B-cell epitope

The predicted B cell epitopes are ranked according to their score obtained by trained recurrent neural network. Higher score of the peptide means the higher probability to be as epitope. All the peptides shown here are above the threshold value chosen.

| Rank | Sequence          | Start position | Score |
|------|-------------------|----------------|-------|
| 1    | PPYIMWAPNAIWKAFD  | 205            | 0.91  |
| 2    | AGLIVIALAFYLRAKV  | 36             | 0.90  |
| 3    | GEHHTATWLGMTVNTD  | 13             | 0.87  |
| 4    | TWLGMTVNTDITVLSTA | 19             | 0.86  |
| 5    | AGIWRRGIVGHPIKLL  | 146            | 0.84  |
| 6    | RAKVTSTDVPGGVQLF  | 48             | 0.82  |
| 6    | GHPIKLLKGHVTL LAP | 155            | 0.82  |
| 7    | TETILAAQIEVGEHHT  | 2              | 0.77  |
| 8    | FVFCYHTAGIWRRI    | 138            | 0.74  |
| 9    | AVTIFVFILISNWLAV  | 91             | 0.72  |
| 9    | LFFEAITIQMRNQVES  | 62             | 0.72  |
| 10   | IGMRIAPFVLPLAVTI  | 79             | 0.71  |
| 11   | YVLALALFVFCYHTA   | 131            | 0.69  |
| 12   | DVPGGVQLFFEAITIQ  | 55             | 0.68  |
| 12   | HGHTTELLKSAADIN   | 115            | 0.68  |
| 13   | NAIWKAFDLFVGAIQA  | 213            | 0.66  |
| 13   | PVQYTDKKGHTTELLK  | 108            | 0.66  |
| 14   | FILISNWLAVLPVQYT  | 97             | 0.62  |
| 15   | HVTLLAPINLVEEVAK  | 164            | 0.60  |
| 16   | IFAGGILVALIALFPP  | 191            | 0.56  |
| 16   | KPISLSLRLFGNIFAG  | 179            | 0.56  |
| 17   | KSAAADIN YVLALALF | 123            | 0.53  |

## OVERLAP DISPLAY

```

MTETILAAQIEVGEHHTATWLGMTVNTDITVLSTAIAGLIVIALAFYLRAKVTSTDVPGGVQLFFEAITIQMRNQVESAIMGMRIAPFVLPLAVTIFVVFILISNWLAVLPVQYTDKKGHTTELLKSAADIN YVLALALFVFCYHTAGIWRRI
-----
          AGLIVIALAFYLRAKV
-----
-GEHHTATWLGMTVNTD-
-----
      TWLGMTVNTDITVLSTA
-----
          RAKVTSTDVPGGVQLF
-----
          AGIWRRI
-----
TETILAAQIEVGEHHT
-----
          FVFCYHTAGIWRRI
-----
          AVTIFVFILISNWLAV
-----
          LFFEAITIQMRNQVES
-----
          IGMRIAPFVLPLAVTI
-----
          YVLALALFVFCYHTA
-----

```

-----DVPGGVQLFFEAITIQ-----  
-----HGHTTELLKSAADIN-----  
-----PVQYTDKKGHTTELLK-----  
-----FILISNWLAVLPVQYT-----  
-----KSAADINYVLALALF-----