

ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	314
Number of 16mers from the input sequence	299
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	CSHIAPANVYGPQRQDP	168	0.97	
2	VGGPDDPEFHPPRLGD	259	0.93	
3	VRRSVADPQFDAAVNV	83	0.92	
4	GTPPEYPTPETAPTDP	127	0.91	
5	LLSGKPTRVFGDGTNT	197	0.89	
5	SSGGSIYGTPPEYPTP	120	0.89	
6	DGTNTRDYVFVDDVV	208	0.88	
7	GWRPQIELADGVRRTV	290	0.86	
7	RHLYGLDCSHIAPANV	161	0.86	
8	SADVGGGLRFNIGTGK	229	0.85	
9	AGFIGSTLVDRLLADG	9	0.84	

9	TAPTDPASPYAAGKVA	137	0.84
10	DGVRRTVEYFRHKHTD	299	0.80
11	RKIVHTSSGGSIYGTP	114	0.79
11	VRLAEAARQTGVRKIV	102	0.79
12	AILEQHRPEVVFHLLAA	64	0.78
12	AGEIYLNTFRHLYGLD	152	0.78
13	FATGRATNLEHLADNS	33	0.75
13	FHPPRLGDLKRSCLDI	267	0.75
14	YGPRQDPHGEAGVVAI	177	0.74
15	SPYAAGKVAGEIYLNT	144	0.73
16	FNIGTGKETSDRQLHS	238	0.72
17	HSVVG LDNFATGRATN	25	0.71
18	YVFVDDVVDAFVRVSA	215	0.70
19	SCLDIGLAERVLGWRP	278	0.69
19	VDRLLADGHHSVVG LDN	17	0.69
20	FHLAAQIDVRRSVA D P	75	0.68
20	ALVTGAAGFIGSTLVD	3	0.68
21	KETSDRQLHSAVAAA V	244	0.59
22	VFVEADIVTADLHAIL	51	0.58
23	LEHLADNSAHVFVEAD	41	0.57
24	LAERVLGWRPQIELAD	284	0.53

OVERLAP DISPLAY

VRALVTGAAGFIGSTLVDRLLADGHSVVG LDNFATGRATNLEHLADNSAHVFVEADIVTADLHAILEQHRPEVVFH LAAQIDV
 RRSVADPQFDAAVNVIGTVRLAEAARQTGVRKIVHTSSGGSIYGPPEYPTPETAPTDASP YAGKVAGEIYLNTFRHLYGL
 DCSHIA PANVY GPRQDPHGEAGVVAIFAQALLSGKP TRVFGDGTNTRDYVFVDDVVDAFVRVSADVGGGLRFNIGT GKTSDR
 QLHSAVAAAVGGPDDPEFHPPR LGDLKRSCL DIGLAERVLGWR PQIELADGV RRTVEYFRHKHTD³¹⁴

CSHIAPANVYGPRODP.

VGGPDDPEFHPPRLGD

VRRSVADPQFDAAVNV

GTPPEYPTPETAPTDP

LLSGKPTRVFGDGTNT

SSGGSIYGTPPEYPTP

DGTNTRDYVFVDDVVD

GWRPQIELADGVRRTV

RHLYGLDCSHIAPANV

SADVGGLRFNIGTGK

AGFIGSTLVDRILLADG

TAPTDPASPYAAGKVA

DGVRRTVEYFRHKHTD

RKIVHTSSGGSIYGTP

VRLAEAARQQTGVRKIV

AILEQHRPEVVFHAA

AGEIYLNTFRHLYGLD

FATGRATNLEHLADNS

FHPPRLGDLKRSCLDI

YGPRQDPHGEAGVVAI

SPYAAGKVAGEIYLNT

FNIGTGKETSDRQLHS

HSVVGLDNFATGRATN

YVFVDDVVDAFVRVSA

SCLDIGLAERVLGWRP

VDRLLADGHHSVGLDN

FHLAAQIDVRRSVADP

ALVTGAAGFIGSTLVD-----

KETSDRQLHSAVAAAV-----

VFVEADIVTADLHAIL-----

LEHLADNSAHVFVEAD-----

LAERVLGWRPQIELAD-----