

ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	490
Number of 16mers from the input sequence	475
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	NDLVRGPVTF AAGSVP	168	0.95	
2	TPEEVEARHVAAGRNP	113	0.92	
3	GLDWDEGP EVGGPYGP	69	0.91	
4	ARLLAAGEAYHAFSTP	99	0.90	
5	TETVRVRF C PSPTGTP	4	0.89	
6	DEMVAAFDVADVNSSP	301	0.87	
7	DQYVIDPKAAAKELGP	389	0.86	
7	ARHTGGTFVFRIEDTD	34	0.86	
7	ADVNSSPARFDQKKAD	310	0.86	
7	LGWSIADDHDLFGLDE	287	0.86	
7	LAEGRQPVVRLRMPDD	148	0.86	

8	RFCPSPTGTPHVGLVR	10	0.85	
9	SVTDWTAPLIEAALKD	419	0.84	
9	TGTPHVGLVRTALFNW	16	0.84	
10	PVTF AAGSVPDFALTR	174	0.83	
11	EVGGPYGPYRQSQR AE	77	0.82	
11	GSVPDFALTRASGDPL	180	0.82	
12	ALIEGLALKPRKAFSP	435	0.81	
12	AAAKELGPDGAAVLDA	397	0.81	
12	ALMKITHVLRGEDLLP	205	0.81	
13	RQSQR AEIYRDV LARL	86	0.80	
13	VVRLRMPDDDLAWNDL	155	0.80	
13	ARHVAAGRNP KLYDN	119	0.80	
14	AELVQTRIVVLGDAWE	366	0.79	
14	LGEGTKKLSKRDPQSN	251	0.79	
14	RNP KLYDNFDRHLTD	126	0.79	
15	PRKAFSPIRVAATGTT	444	0.78	
15	VRLRDHLDT HGHIAL	342	0.78	
15	AHIRMLDVGDFTVRL	329	0.78	
16	TRASGDPLYTLVNPCD	188	0.74	
17	TGTTVSPPLFESLELL	456	0.73	
18	GDAWELLKFFNDDQYV	377	0.71	
19	APLIEAALKDALIEGL	425	0.70	
19	HVLRGEDLLPSTPRQL	211	0.70	
20	IGVAERIPKFAHLPTV	235	0.69	
21	LDVGDFTVRLRDHLDT	335	0.68	
22	VFRIEDTDAQRDSEES	42	0.67	
22	LTDAQRAAYLAEGRQP	139	0.67	
23	GRDRSMQRLRAARQLV	472	0.66	
23	LDAALAALTSVTDWTA	410	0.66	
24	HGHIALDEAAFAAAA	351	0.65	
24	RFDQKKADALNAEHIR	318	0.65	
25	TDAQRDSEESYLALLD	48	0.64	
26	FAHRDRGFIEPGLLY	268	0.63	
26	DPQSNLFAHRDRGFIP	262	0.63	

27	TALFNWAYARHTGGTF	26	0.57	
27	LYTLVNPCDDALMKIT	195	0.57	
28	RQLALHQALIRIGVAE	224	0.55	

OVERLAP DISPLAY

VTATETVRVRFPCPSPTGTPHVGLVVRTALFNWAYARHTGGTFVFRIEDTDAQRDSEESYLALLDALRWLGLDWDEGPVGGPYG
 PYRQSQRAEIYRDVLRLLAAGEAYHAFSTPEEVEARHVAAGRNPCLGYDNFDRHLTDAQRAAYLAEGRQPVVRLRMPDDDLA
 WNDLVRGPVTF AAGSVPDFALTRASGDPLYTLVNPCDDALMKITHVLRGEDLLPSTPRQLALHQALIRIGVAERIPKFAHLPT
 VLGEGTKKLSKRDPQSNLFAHRDRGFIPEGLLNLYLALLGWSIADDHDLFGLDEMVAADFVADVNSSPARFDQKKADALNAEHI
 RMLDVGDFTVRLRDHLDTHGHHIALDEAAFAAAAEVLVQTRIVVLGDAWELLKFFNDDQYVIDPKAAAKELGPDGAAVLDAAALA
 ALTSVTDWTAPLIEAALKDALIEGLALKPRKAFSPIRVAATGTTVSPPLFESLELLGRDRSMQRLRAARQLVGHA⁴⁹⁰

NDLVRGPVTF AAGSVP

TPEEVEARHVAAGRNP

GLDWDEGPVGGPYG

ARLLAAGEAYHAFSTP

TETVRVRFPCPSPTGTP

DEMVAAFDVADVNSSP

DQYVIDPKAAAKELGPE

ARHTGGTFVFRIEDTD

ADVNSSPARFDQKKAD

LGWSIADDHDLFGLDE

LAEGRQPVVRLRMPDD

RFCPSPTGTPHVGLVR

SVTDWTAPLIEAALKD

TGTPHVGLVRTALEFNW

PVTFAAGSVPDFALTR

EVGGPYGPYRQSQRAE

GSVPDFALTRASGDPL

ALIEGLALKPRKAFSP

AAAKELGPDGAAVLDA

ALMKITHVLRGEDLLP

RQSQRAEIYRDVLARL

VVRLRMPDDDLAWNDL

ARHVAAGRNPCLGYDN

AELVQTRIVVLGDAWE

LGEGTKKLSKRDPQSN

RNPKLGYDNFDRHLLTD

PRKAFSPIRVAATGTT

VRLRDHLDTHGHHIAL

AEHIRMLDVGDFTVRL

TRASGDPLYTLVNP

TGTTVSPPLFESLELL

GDAWELLKFFNDDQYV

APLIEAALKDALIEGL

HVLRGEDLLPSTPRQL

IGVAERIPKFAHLPTV

LDVGDFTVRLRDHLD

VFRIEDTDAQRDSEES

LTDAQRAAYLAEGRP

GRDRSMQRLRAARQLV

LDAALAAALTSVTDWTA

HGHHIALDEAAFAAAA

RFDQKKADALNAEHIR

TDAQRDSEESYLALLD

FAHRDRGF IPEGLLY

DPQSNLFAHRDRGFIP

TALFNWAYARHTGGTF

LYTLVNPCDDALMKIT

RQLALHQALIRIGVAE