

ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	626
Number of 16mers from the input sequence	611
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	RVHNGEPPEAPKVLTD	275	0.95	
2	AGEVTGTNPPAGTTVP	531	0.93	
3	SGPATKDIPDVAGQTV	490	0.91	
4	TGMLDKGADV DAGGSQ	584	0.90	
5	LQKPDSTIPPDHVIGT	387	0.88	
5	SGPRTDPLPRQDLDDT	305	0.88	
5	GEPPFTGDSPPSVAYQ	212	0.88	
5	AVKVMDFGIARAIADS	151	0.88	
6	GFKIRTLQKPDSTIPP	381	0.87	
7	DVDAGGSQHNRVVYQN	592	0.86	
7	PSHLSDRYELGEILGF	4	0.86	

8	PYIVMEYVDGVTLRDI	88	0.85	
8	IVAVYDTGEAETPAGP	71	0.85	
8	ARDPSFYLRFRREAQN	47	0.85	
8	GKVIQTNPPANQTSAI	465	0.85	
8	LLSSAAGNLSGPRTDP	296	0.85	
8	ENRYQTAEMRADLVR	260	0.85	
8	GGMSEVHLARDLRLHR	20	0.85	
8	IGTAQYLSPEQARGDS	177	0.85	
8	FGIARAIADSGNSVTQ	157	0.85	
8	PMTPKRAIEVIADACQ	109	0.85	
9	DHVIQTDPAANTSVSA	397	0.84	
9	TRDVQVPDVRGQSSAD	357	0.84	
9	RQDLDDTDRDRSIGSV	314	0.84	
9	REDPIPPSARHEGLSA	230	0.84	
10	AEMRADLVRVHNGEPP	267	0.83	
10	EQARGDSVDARSDVYS	186	0.83	
11	SVSAGDEITVNVSTGP	409	0.82	
11	DRSIGSVGRWVAVVAV	323	0.82	
11	NGIIHRDVKPANIMIS	132	0.82	
12	TGEAETPAGPLPYIVM	77	0.81	
13	GVTLRDIVHTEGPMTTP	97	0.80	
13	DVAGQTVDVAQKNLNV	499	0.80	
14	MFWVDAEPRLRALGWT	569	0.79	
14	NIMISATNAVKVMDFG	143	0.79	
15	FVMPDLSGMFWVDAEP	561	0.78	
15	SVDSRPAGEVTGTNP	524	0.78	
16	ANSPSTPELVGKVIGT	455	0.77	
16	TVNVSTGPEQREIPDV	417	0.77	
16	DSPVSVAYQHVREDPI	219	0.77	
17	DVSTLTYAEAVKKLTA	431	0.76	
17	DVRGQSSADAIATLQN	364	0.76	
18	TSAITNVVHIVGSGP	477	0.75	
19	DSVIELQVSKGNQFVM	548	0.74	
19	VVTIAINTFGGITRDV	345	0.74	

20	NRVVYQNPPAGTGVNR	601	0.72	
20	KKLTAAGFGRFKQANS	442	0.72	
20	DAERTSLLSSAAGNLS	290	0.72	
21	AVLAVLTVVVVTAINT	337	0.71	
21	VGRWVAVVAVLAVLTV	329	0.71	
22	VVIIIVSGSPATKDIP	483	0.70	
22	HLARDLRLHRDVAVKV	26	0.70	
23	NPPAGTGVNRDGIITL	607	0.69	
23	VLKALAKNPENRYQTA	251	0.69	
24	ADACQALNFHQNGII	120	0.66	
25	NPPAGTTVPVDSVIEL	538	0.65	
25	DAIATLQNRGFKIRTL	372	0.65	
25	ARHEGLSADLDAVVLK	238	0.65	
26	DVAQKNLNVYGFTKFS	506	0.64	
27	RFRREAQNAAALNHPA	55	0.59	
28	RSDVYSLGCVLYEVL	196	0.57	
29	SADLDAVVLKALAKNP	244	0.56	

OVERLAP DISPLAY

MTTPSHLSDRYELGEILGFSGMSEVHLARDLRLHRDVAVKVLRADLARDPSFYLRFRREAQNAAALNHPAIVAVYDTGEAETPAGPLPYIVMEYVDGV
TLRDIVHTEGPMTPKRAIEVIADACQALNFHQNGI IHRDVKPANIMI SATNAVKVMDFGIARAIADSGNSVTQTAAVIGTAQYLSPEQARGDSVDAR
SDVYSLGCVLYEVLTEGPPFTGDSVSVAYQHVREDPI PPSARHEGLSADLDAVVLKALAKNPENRYQTAAEMRADLVRVHNGEPPEAPKVLTDART
SLLSSAAGNLSGPRTDPLPRQDLDDTDRDRSIGSVGRWVAVVAVLAVLTVVVVTAINTFGGITRDVQVPDVRGQSSADAIATLQNRGFKIRTLQKPD
TIPPDHVI GTDPAANTSVSAGDEITVNVSTGPEQREIPDVSTLTAYAEAVKKLTAAGFGRFKQANS PSTPELVGKVI GTNPPANQTSAITNVV I I VGS
GPATKDI PDVAGQTV DVAQKNLNVYGFTKFSQASVDS PRPAGEVTGTNPPAGTTVPVDSVIELQVSKGNQFVMPDLSGMFWVDAEPRLRALGWTGMLD
KGADV DAGGSQHNRVVYQNPPAGTGVNRDGIITLRFQG⁶²⁶

RVHNGEPPEAPKVLTD

AGEVTGTNPPAGTTVP

SGPATKDIPDVAGQTV

TGMLDKGADV DAGGSQ

LQKPDSTIPPDHVIGT

SGPRTDPLPRQDLDDT

GEPPFTGDSPVSVAYQ

AVKVMDFGIARAIADS

GFKIRTLQKPDSTIPP

---DVDAGGSQHNRRVYQN-----

---PSHLSDRYELGEILGF-----

---PYIVMEYVDGVTLRDI-----

---IVAVYDTGEAETPAGP-----

---ARDPSFYLRFRREAQN-----

---GKVIQTNPPANQTSAI-----

---LLSSAAGNLSGPRTDP-----

---ENRYQTAAEMRADLVR-----

---GGMSEVHLARDLRLHR-----

IGTAQYLSPEQARGDS

FGIARAIADSGNSVTQ

PMTPKRAIEVIADACQ

DHVIQTDPAANTSVSA

TRDVQVPDVRGQSSAD

RQDLDDTDRDRSIGSV

REDPIPPSARHEGLSA

AEMRADLVRVHNGEPP

EQARGDSVDARSDVYS

SVSAGDEITVNVSTGP

DRSIGSVGRWVAVVAV

NGIIHRDVKPANIMIS

TGEAETPAGPLPYIVM

GVTLRDIVHTEGPMTF

DVAGQTVQKLNLV

MFWVDAEPRLRALGWT

NIMISATNAVKVMDFG

FVMPDLSGMFWVDAEP

SVDSPRPAGEVTGTNP

ANSPSTPELVGKVIGT

TVNVSTGPEQREIPDV

DSPVSVAYQHVREDPI

DVSTLTAYAEAVKKLTA

DVRGQSSADAIATLQN

TSAITNVVIIIVGSGP

DSVIELQVSKGNQFVM

VVTIAINTFGGITRDV

NRVVYQNPPAGTGVNR

KKLTAAGFGRFKQANS

DAERTSLLSSAAGNLS

AVLAVLTVVVTIAINT

VGRWVAVVAVLAVLTV

VVIIIVGSGPATKDIP

HLARDLRLHRDVAVKV

NPPAGTGVNRDGIITL

VLKALAKNPENRYQTA

ADACQALNFHQNGII

NPPAGTTVPVDSVIEL

DAIATLQNRGFKIRTL

ARHEGLSADLDAVVLK

DVAQKNLNVYGFTKFS

RFRREAQNAAALNHPA

RSDVYSLGCVLYEVL

SADLDAVVLKALAKNP