

ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	304
Number of 16mers from the input sequence	289
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	DGLVDRGGAHRAATGP	19	0.96
2	GGRSITAESRDARVQL	163	0.93
3	AGHRQPPPVSHPEGRP	56	0.89
3	RAATGPGRIPDAGDPP	29	0.89
4	LPDLSGPTPRAPQRNP	126	0.88
5	PAAAVRTPQDPDASL	96	0.87
5	GASAPVTGPAAAVRTP	88	0.87
6	GRPTNPPAAADARLNR	69	0.85
6	PAEGGAGSRGDSAAGS	146	0.85
7	ASMQIRRIDPWSTLKV	189	0.83

8	SGTIFGGAFGLVNI	257	0.82
9	GRIPDAGDPPPWQRAA	35	0.81
10	LVLGGMGVWAKLNSNV	225	0.80
10	CGDGSPAEAYASELPD	113	0.80
11	QRAATRQSQAGHRQPP	47	0.77
11	LSKGDGPNADGLVDRG	10	0.77
12	VTAPNEPGALSCKDGP	1	0.76
13	AESRDARVQLSARRSR	169	0.75
14	LATIGAFVYNLITDLI	278	0.74
15	GSRGDSAAGSSGGRSI	152	0.73
16	RVQLSARRSRGPVRAS	175	0.72
17	VWAKLNSNVGDLLNNA	232	0.71
18	PQRNPAPARPAEGGAG	137	0.70
19	IVLMTALATIGAFVYN	272	0.64
20	VYNLITDLIGGIEVTL	285	0.63
20	LIGLVNIVLMTALATI	266	0.63
21	DLLNNASGSSAELVSS	242	0.58
21	FFVWMITVAFLYLVLG	213	0.58
22	AAADARLNRFISGASA	76	0.52

OVERLAP DISPLAY

VTAPNEPGALS KGDGPNADGLVDRGGAHRAATGPGRIPDAGDPPPWQRAATRQSQAG
HRQPPPVSHPEGRPTNPPAAADARLNRFIGSASAPVTGPAAAVRTPQPDPDASLGCGDGS
PAEAYASELPDLSGPTPRAPQRNPAPARPAEGGAGSRGDSAAGSSGGRSITAESRDARV
QLSARRSRGPVRASMQIRRIDPWSTLKVSLLSVALFFVWMITVAFLYLVLGGMGVWA
KLNSNVGDLLNNASGSSAELVSSGTIFGG AFLIGLVNIVLMTALATIGAFVYNLITDLIGG
IEVTLADRD304

-----DGLVDRGGAHRAATGP-----

-----GGRSITAESRDARVQL-----

-----AGHRQPPPVSHPEGRP-----

-----RAATGPGRIPDAGDPP-----

-----LPDLSGPTPRAPQRNP-----

PAAAVRTPQPDPDASL-----

GASAPVTGPAAAVRTP-----

-----GRPTNPPAAADARLNR-----

-----PAEGGAGSRGDSAAGS-----

-----ASMQIRRIDPWSTLKV-----

-----SGTIFGG AFLIGLVNI-----

-----GRIPDAGDPPPWQRAA-----

LVLGGMGVWAKLNSNV-----

CGDGSPAEAYASELPD

QRAATRQSQAGHRQPP

LSKGDGPNADGLVDRG

VTAPNEPGALSKGDGP

AESRDARVQLSARRSR

LATIGAFVYNLITDLI

GSRGDSAAGSSGGRSI

RVQLSARRSRGPVRAS

VWAKLNSNVGDLLNNA

PQRNPAPARPAEGGAG

IVLMTALATIGAFVYN

VYNLITDLIGGIEVTL

LIGLVNIVLMTALATI

DLLNNASGSSAELVSS

FFVWMITVAFLYLVLG

AAADARLNRFISGASA
