

ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	510
Number of 16mers from the input sequence	495
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	AALTAAPPVSRHRMQV	333	0.93	
2	QAEVRLGVCGDHQVTN	298	0.91	
3	TVAQIAEIVGGAVADI	5	0.89	
3	WGSGEATADHGADRTA	444	0.89	
3	DAYNANPDSMRAGLQA	360	0.89	
3	RGDGVTVIDDAYNANP	351	0.89	
3	VVRVSRDNTGDVWAGP	264	0.89	
3	AELPQAVPHSGAVVLN	232	0.89	
4	HRRVTGTVEFDSRAIG	27	0.88	
5	SGKTSTKDLMAAVLAP	138	0.87	
5	GGLTIIGITGSSGKTS	127	0.87	

6	TGRSISAMHHGAVLEG	427	0.86	
6	LILEMAARHHGNIAAL	184	0.86	
7	AKLTAARVVRVSRDNT	257	0.85	
7	DISPQDAAHRRVTGTV	19	0.85	
8	TGDVWAGPVSLDELAR	272	0.84	
8	ALAEIAPPSIGVVLVN	198	0.84	
9	AMHHGAVLEGAWGSGE	433	0.83	
9	GEMAELEGDAIAEHDR	394	0.83	
9	GEVVAPPGSFNNELGH	155	0.83	
10	CGASVEQVAAALTAAP	324	0.82	
11	TRRSWAVLGEMAEELGE	386	0.81	
12	LGAVADALVADDTCS	492	0.80	
12	ALAWIAHQPEATRRSW	375	0.80	
12	RMQVTTRGDGVTVIDD	345	0.80	
13	AHLGEFGSREVIAQTK	216	0.79	
14	VPAIVVPPVAAPNVLA	80	0.78	
15	SRAIGPGGLFLALPGA	38	0.77	
15	GVCGDHQVTNALCAAA	304	0.77	
16	GVLEHDNDGSGAAVLA	96	0.76	
17	VVLAARPVGVPAIVVP	71	0.75	
17	VVLVKASNAAGLGAVA	481	0.75	
17	SLDELARPRFTLHAHD	281	0.75	
18	ELGHPWTVLRATRRTD	167	0.73	
18	DGSGAAVLAALAKLAT	103	0.73	
19	DRTAVNVADGDAALAL	456	0.72	
20	HDHAASAVAAGAAVVL	58	0.71	
21	GARADGHDHAASAVAA	52	0.70	
21	TADHGADRTAVNVADG	450	0.70	
22	REVIAQTKAELPQAVP	224	0.69	
23	AVVLNADDPAVAAMAK	243	0.68	
24	EDAIAEHDRIGRLAVR	401	0.67	
24	LCAAVALECGASVEQ	315	0.67	
24	LMAAVLAPLGEVVAPP	146	0.67	
25	LHAHDAQAEVRLGVC	292	0.65	

26	ALLRAELRPGDVVLVK	470	0.64	
26	PSIGVVLNVGTAHLGE	205	0.64	
26	HHGNIAALAEIAPPSI	192	0.64	
27	LATAVAAQLVAGGLTI	116	0.63	
28	TVLRATRRTDYLILEM	173	0.62	
29	DRIGRLAVRLDVSRLV	408	0.61	
30	PGSFNNELGHPWTVLR	161	0.59	
31	AVAAGAAVLAARPVG	64	0.58	
32	ADGDAALALLRAELRP	463	0.55	
33	PVAAPNVLAVLEHDN	87	0.54	

OVERLAP DISPLAY

MIELTVAQIAEIVGGAVADISPQDAAHRRVTGTVEFDSRAIGPGGLFLALPGARADGHDHAASAVAAGAAVLAARPVGPVPAI
 VVPPVAAPNVLAVLEHDNDGSGAAVLAALAKLATAVAAQLVAGGLTIIGITGSSGKTSTKDLMAAVLAPLGEVVAPPGSFNN
 ELGHPWTVLRATRRTDYLILEMAARHHGNIAALAEIAPPSIGVVLNVGTAHLGEFGSREVIAQTKAELPQAVPHSGAVVLNAD
 DPAVAAMAKLTAARVVRVSRDNTGDVWAGPVSLELARPRFTLHAHDAQAEVRLGVCGDHQVTNALCAAVALECGASVEQVA
 AALTAAPPVSRHRMQVTTRGDGVTVIDDAYNANPDSMRAGLQALAWIAHQPEATRRSWAVLGEMAELEGDAIAEHDRIGRLAV
 RLDVSRLVVVGTGRSISAMHHGAVLEGAWGSGEATADHGADR TAVNVADGDAALALLRAELRPGDVVLVKASNAAGLGAVADA
 LVADDTCGSVRP⁵¹⁰

AALTAAPPVSRHRMQV-----

QAEVRLGVCGDHQVTN-----

TVAQIAEIVGGAVADI-----

WGSGEATADHGADRTA

DAYNANPDSMRAGLQA

RGDGVTVIDDAYNANP

VVRVSRDNTGDVWAGP

AELPQAVPHSGAVVLN

HRRVTGTVEFDSRAIG

SGKTSTKDLMAAVLAP

GGLTIIGITGSSGKTS

TGRSISAMHHGAVLEG

LILEMAARHHGNIAAL

AKLTAARVVRVSRDNT

DISPQDAAHRRVTGTV

TGDVWAGPVSLELAR

ALAEIAPPSIGVVLNV

AMHHGAVLEGAWGSGE

GEMAELEGDAIAEHDR

GEVVAPPGSFNNELGH

CGASVEQVAAALTAAP

TRRSWAVLGEMAEELGE

LGAVADALVADDTCGS---

ALAWIAHQPEATRRSW

RMQVTTRGDGVTVIDD

AHLGEFGSREVIAQTK

VPAlVPPVAAPNVLA

SRAIGPGLFLALPGA

GVCGDHQVTNALCAAA

GVLEHDNDGSGAAVLA

VVLAARPVGVPAIVVP

VVLVKASNAAGLGAVA

SLDELARPRFTLHAHD

ELGHPWTVLRATRRTD

DGSGAAVLAALAKLAT

DRTAVNVADGDAALAL

HDHAASAVAAGAAVVL

ALLRAELRPGDVVLVK

PSIGVVLNVGTAHLGE

HHGNIAALAEIAPPSI

LATAVAAQLVAGGLTI

TVLRATRRTDYLILEM

DRIGRLAVRLDVSRLV

PGSFNNELGHPWTVLR

AVAAGAAVLAARPVG

ADGDAALALLRAELRP-----

PVAAPNVLAGVLEHDN-----
