

ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	806
Number of 16mers from the input sequence	791
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	RRLAGDDPEVNEEWNC	260	0.95
2	PYLAGTARTPVVRLSP	725	0.93
3	GGRPLADEVARAQVCA	524	0.91
3	PDVITTLIRGGDPK	288	0.91
3	RWAFYATQPDVITTP	279	0.91
4	HIAATGPTQPEAGEAI	692	0.90
4	LRLRKAARRHRVPVYT	411	0.90
4	GALTGTAYRFRARPF	217	0.90
4	SRFTEAKRTFAKPINI	138	0.90
5	LVEVEGQRKPLASCTT	64	0.89
5	VVFPVAPTTKAGAFV	611	0.89
6	PCSVTDMDRVVWLPL	766	0.88
6	AARGRTGVLVGGRVTW	324	0.88
7	AAEIGAADGEAVTVST	743	0.87
7	HSTVTERADVFPVAP	602	0.87
7	LMGIQIPRFCDHPLLE	40	0.87
8	QAGQSDHRVLDALADD	645	0.86
8	PRRAGERGALEAGALP	504	0.86
8	SAAARLADTTGARLAW	487	0.86
8	DCPMCDKGCEPLQNO	114	0.86
9	TVHRQLRVTIGSIVKI	787	0.85
9	SCTTVATDDMVVRTQL	76	0.85
9	PRFCDHPLLEPVGACR	46	0.85
9	TLVIRAAELMGIQIPR	32	0.85
9	PINISAQVLLDRERCI	150	0.85
10	TSEIADKAQHGMELL	92	0.84
10	CASGCAQRTDHRGKV	243	0.84
10	PSVCEHCASGCAQRTD	237	0.84
10	QVGIYADEPFESYFSG	193	0.84
11	TSRGSITLPCSVTDMP	758	0.83
11	RVTWEDAYAYAKFARI	336	0.83
12	LNSAGSTVHRQLRVTI	781	0.82
12	PEAGEAILTGWRMLLD	701	0.82
12	VGGIEPADFADPAVL	571	0.82
12	ARLAWVRRAGERGAL	498	0.82
12	TVPGGEPAALDDLATG	445	0.82
12	APFATGGLHKMSGRLI	428	0.82

12	ITLGTNDIDFRARPHS	351	0.82
12	TLTIDGVEISVPKGTLL	18	0.82
12	GECPLQNQAMSNGRTD	122	0.82
13	AWHIAELPAAAGRADAD	540	0.81
14	AALGIWDGKHAAGPHI	678	0.80
14	AGRHMVSYADLESAP	378	0.80
15	GEAVTVSTSRGSITLP	751	0.79
16	EGRLQDGEPYLAGTAR	717	0.78
16	LTGWRMLLDEGRLQDG	708	0.78
16	GGDPKGALVPTSWSHA	299	0.78
16	MQERGALQVVGIYADE	185	0.78
17	NWEGRYRTFEPALRGS	627	0.77
17	ALVPTSWSHAMAVAAQ	305	0.77
17	DHRRGKVLRRLAGDDP	252	0.77
18	ARTPVVRLSPDTAAEI	731	0.76
18	ARAQVCAAWHIAELPA	533	0.76
18	SGRLIKTVPGGEPAL	439	0.76
19	DIDFRARPHSAEEDAF	357	0.75
20	VGACRQCLVEVEGQRK	57	0.74
20	GALPTLLPGGRPLADE	516	0.74
20	LDDLATGAVGDLLATP	454	0.74
21	PDRVVWLPLNSAGSTV	773	0.73
22	RVLDALADDMGVHLGV	652	0.72
22	FEPALRGSTLQAGQSD	635	0.72
22	AAGRDADGILAAAAD	549	0.72
23	RLSPDTAAEIGAADGE	737	0.71
23	VPTVEAAREELAALGI	667	0.71
23	LATVPGGLSAAARLAD	479	0.71
23	HRVPVYTIAPFATGGL	420	0.71
23	GDPFIDMQERGALQOV	179	0.71
23	SNGRTDSRFTEAKRTF	132	0.71
24	EPFESYFSGNTVQICP	200	0.70
24	ERCILCARCTRFSDQI	162	0.70
25	ADLESAPVLLVGFEP	387	0.69
25	CTRFSDQIAGDPPIDM	170	0.69
26	DDMGVHLGVPTVEAAR	659	0.68
26	DTDIRVGQPEMVTLLTI	6	0.68
26	DPEVNEEWNCDKGRWA	266	0.68
27	LLVGFEPEDESPIVFL	396	0.67
28	QRKPLASCTTVATDDM	70	0.66
28	GAVGDLLATPGAVIIV	460	0.66
28	FRARPFDLVSSPSVCE	226	0.66
29	DMVVRTQLTSEIADKA	84	0.62
30	HAMAVAAQGLAAARGR	313	0.60
31	LATPGAVIIVGERLAT	466	0.58
32	ISVPKGTLVIRAAELM	26	0.57
33	VLAALDATGFVVSLEL	585	0.56
34	DESPIVFLRLRKAARR	404	0.51

OVERLAP DISPLAY

VTQAADTDIRVGQPEMVTLLTIDGVEISVPKGTLVIRAAELMGIQIPRFCDHLPLEPVGACRQCLVEVEGQRKPLASCTTVATDDMVVRTQLTSEIADKAQHGMELLLINHPLDCPMCDKGGECPLQNQAMSNGRDTSRFTEAKRTFAKP:

LVEVEGQRKPLASCTT

SRFTEAKRTFAKP:

