ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	577
Number of 16mers from the input sequence	562
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	LRTWQTAHVMKARRGA	379	0.94	
1	TTTIIGGGTGPAEGTK	158	0.94	
1	NPDIMTGVHRDLVVGP	106	0.94	
2	GGAIAWAAMGDANASI	460	0.92	
2	TGFVEDTIGAIAGRSI	260	0.92	
2	GGASGFKLHEDWGSTP	218	0.92	
3	PSIEVDPDTFTVRIDG	542	0.91	
4	GGTGPAEGTKATTVTP	164	0.90	
5	ISMIGSDSQAMGRVGE	361	0.88	
5	GRSIHAYHTEGAGGGH	272	0.88	
6	PQSIDARLADRLAVNR	504	0.87	

6	SVHFVAPQSIDARLAD	498	0.87	
7	PSGSQAADNNRVRRYI	399	0.86	
7	LVEVTEDRCGGPGLAG	29	0.86	
8	KVLRESMGQGRASRAD	53	0.85	
8	GALEGDPSGSQAADNN	393	0.85	
8	AGGGHAPDIITVAAQP	283	0.85	
8	IVTAGTVDCHVHLICP	132	0.85	
9	MGQGRASRADGAPDTV	59	0.84	
9	TVRIDGQVWQPQPAAE	552	0.84	
9	AAAATAAATSVHFVAP	489	0.84	
9	EGTKATTVTPGEWHLA	170	0.84	
10	TGAVIIDYWGIIKADI	76	0.83	
10	RGLAPVADVRAVGKTD	519	0.83	
10	KLHEDWGSTPAAIDTC	224	0.83	
11	AESRIRPSTIAAEDVL	340	0.82	
11	STEIISGNRRIVTAGT	122	0.82	
12	IVGIGKAGNPDIMTGV	98	0.80	
12	PGLAGDEAVFGGGKVL	40	0.80	
13	AVGKTDLPLNDALPSI	529	0.79	
13	VLPSSTNPTRPHTVNT	300	0.79	
13	YGPTTGDRIRLADTNL	13	0.79	
14	MDHLIGSVEVGKLADL	427	0.78	
14	CPAIAHGMDHLIGSVE	420	0.78	
15	IGIRDGRIVGIGKAGN	91	0.77	
15	TIGAIAGRSIHAYHTE	266	0.77	
16	PTPQPVLPRPMFGAAA	476	0.75	
16	AVFGGGKVLRESMGQG	47	0.75	
16	RMLESLDGWPVNFALL	186	0.75	
17	SRADGAPDTVITGAVI	65	0.74	
17	SRERYAQLYGPTTGDR	5	0.74	
17	PTRPHTVNTLDEHLDM	307	0.74	
17	PQIIVEALAAGTTTII	147	0.74	
18	WGIIKADIGIRDGRIV	84	0.73	
18	PAAIDTCLAVADVAGV	233	0.73	

18	FALLGKGNTVNPDALW	198	0.73	
19	GDANASIPTPQPVLPR	469	0.72	
19	TVAAQPNVLPSSTNPT	293	0.72	
19	RDLVVGPSTEIISGNR	115	0.72	
20	VNTLDEHLDMLMVCHH	313	0.71	
20	ALHSDTLNETGFVEDT	251	0.71	
21	MLMVCHHLNPRIPEDL	322	0.67	
22	VTPGEWHLARMLESLD	177	0.66	
22	HVHLICPQIIVEALAA	141	0.66	
23	STIAAEDVLHDMGAIS	347	0.65	
24	GVRPHVVLKGGAIAWA	451	0.63	
24	DSQAMGRVGEVVLRTW	367	0.63	
24	NPRIPEDLAFAESRIR	330	0.63	
25	WQPQPAAELPMTQRYF	560	0.62	
26	WEPAFFGVRPHVVLKG	445	0.60	
27	PRPMFGAAAATAAATS	483	0.58	
28	VAGVQVALHSDTLNET	245	0.57	
29	GKLADLVLWEPAFFGV	437	0.55	
30	NNRVRRYIAKYTICPA	407	0.52	

OVERLAP DISPLAY

MARLSRERYAQLYGPTTGDRIRLADTNLLVEVTEDRCGGPGLAGDEAVFGGGKVLRESMGQGRASRADGAPDTVITGAVIIDY
WGIIKADIGIRDGRIVGIGKAGNPDIMTGVHRDLVVGPSTEIISGNRRIVTAGTVDCHVHLICPQIIVEALAAGTTTIIGGGT
GPAEGTKATTVTPGEWHLARMLESLDGWPVNFALLGKGNTVNPDALWEQLRGGASGFKLHEDWGSTPAAIDTCLAVADVAGVQ
VALHSDTLNETGFVEDTIGAIAGRSIHAYHTEGAGGGHAPDIITVAAQPNVLPSSTNPTRPHTVNTLDEHLDMLMVCHHLNPR
IPEDLAFAESRIRPSTIAAEDVLHDMGAISMIGSDSQAMGRVGEVVLRTWQTAHVMKARRGALEGDPSGSQAADNNRVRRYIA
KYTICPAIAHGMDHLIGSVEVGKLADLVLWEPAFFGVRPHVVLKGGAIAWAAMGDANASIPTPQPVLPRPMFGAAAATAAATS
VHFVAPQSIDARLADRLAVNRGLAPVADVRAVGKTDLPLNDALPSIEVDPDTFTVRIDGQVWQPQPAAELPMTQRYFLF[577]

LRTWQTAHVMKARRGA----------

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VAGVQVALHSDTLNET--------------------------------------------------------
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GKLADLVLWEPAFFGV--------------------------------------------------------
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NNRVRRYIAKYTICPA--------------------------------------------------------
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