ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	494
Number of 16mers from the input sequence	479
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	AGTNAHHGSGDCFVAE	155	0.91	
2	AGRTTLMVTGTHGKTT	113	0.90	
3	AREQPLAGVSGASVAE	415	0.89	
3	LATAQGPRVMRLSVPG	280	0.89	
4	HVTVPMRYVPDFSAVA	431	0.88	
4	ADEVFVLDVYGAREQP	404	0.88	
5	GPEILTALRVRANRSA	471	0.86	
5	ASPGDVIVTMGAGDVT	453	0.86	
5	GMSGIARILLDRGGLV	22	0.86	
6	QQVAAAASPGDVIVTM	447	0.85	
6	VLEQGDGGRCMVVFQP	369	0.85	

7	GTHGKTTTTSMLIVAL	122	0.84	
8	MGAGDVTLLGPEILTA	462	0.83	
8	SRTKAFAAEFGRALNA	388	0.83	
8	ALVVCTDDPGGAALAQ	221	0.83	
8	PSFAVGGELGEAGTNA	144	0.83	
9	PELVEARRRGIPVVLR	89	0.82	
9	AALAQRATELGIRVLR	232	0.82	
9	CFVAEADESDGSLLQY	166	0.82	
10	VMRLSVPGRHMALNAL	288	0.80	
10	RVLRYGSVPGETMAAT	244	0.80	
10	GSLLQYTPHVAVITNI	176	0.80	
11	AGVSGASVAEHVTVPM	421	0.79	
12	PTEISATLAAARMVLE	356	0.77	
13	LVSGSDAKESRGVHAL	36	0.76	
14	VAHIRLASELATAQGP	271	0.75	
14	PGETMAATLVSWQQQG	252	0.75	
14	FVERIVPGGALVVCTD	212	0.75	
14	HVAVITNIESDHLDFY	184	0.75	
15	VSTEQLPPDLRRVHMV	1	0.74	
16	LGALLAAVQIGAPADE	303	0.73	
16	VHMVGIGGAGMSGIAR	13	0.73	
17	SVRVFDDYAHHPTEIS	345	0.72	
18	DASSLDLLPGGATAVV	63	0.71	
18	PGRHMALNALGALLAA	294	0.71	
18	LQHCGLDPSFAVGGEL	137	0.71	
19	GVRRRFELVGTCGVGK	328	0.70	
20	ATAVVTTHAAIPKTNP	74	0.67	
20	ALIRIGHDASSLDLLP	56	0.67	
20	GLAGFEGVRRRFELVG	322	0.67	
21	RRRGIPVVLRPAVLAK	95	0.66	
21	SMLIVALQHCGLDPSF	131	0.66	
22	MVVFQPHLYSRTKAFA	379	0.65	
22	GSVEAYVAVFDSFVER	200	0.65	
23	ILLDRGGLVSGSDAKE	29	0.64	

23	TLVSWQQQGVGAVAHI	259	0.64	
24	RVRANRSAPGRPGVLG	479	0.62	
25	QIGAPADEVLDGLAGF	311	0.61	
26	AVLAKLMAGRTTLMVT	106	0.58	
27	KESRGVHALRARGALI	43	0.57	
27	SDHLDFYGSVEAYVAV	193	0.57	

OVERLAP DISPLAY

VSTEQLPPDLRRVHMVGIGGAGMSGIARILLDRGGLVSGSDAKESRGVHALRARGALIRIGHDASSLDLLPGGATAVVTTHAA
IPKTNPELVEARRRGIPVVLRPAVLAKLMAGRTTLMVTGTHGKTTTTSMLIVALQHCGLDPSFAVGGELGEAGTNAHHGSGDC
FVAEADESDGSLLQYTPHVAVITNIESDHLDFYGSVEAYVAVFDSFVERIVPGGALVVCTDDPGGAALAQRATELGIRVLRYG
SVPGETMAATLVSWQQQGVGAVAHIRLASELATAQGPRVMRLSVPGRHMALNALGALLAAVQIGAPADEVLDGLAGFEGVRRR
FELVGTCGVGKASVRVFDDYAHHPTEISATLAAARMVLEQGDGGRCMVVFQPHLYSRTKAFAAEFGRALNAADEVFVLDVYGA
REQPLAGVSGASVAEHVTVPMRYVPDFSAVAQQVAAAASPGDVIVTMGAGDVTLLGPEILTALRVRANRSAPGRPGVLG^{494}

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