ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	640
Number of 16mers from the input sequence	625
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	HWAEIGNDVENAIATA	403	0.94
2	LRTRFRTVTEDAERQI	380	0.91
2	GGLGQPHLSATLGLLP	180	0.91
3	TVTEDAERQIDSCDPT	386	0.90
3	LSVVNDPNLRDRLASD	328	0.90
4	IVELIDHTIAIAKLNE	36	0.89
5	DNFVWAYQRSEALADD	421	0.88
5	GDTVTQPDDPRRVGVI	21	0.88
6	AEEITRSLTESLQATI	578	0.87
6	GRMESKPLRRGHKMII	470	0.87
6	AGLCAYRDLRRKRARK	4	0.87
6	LRRKRARKWGDTVTQP	12	0.87
7	HKMIIGMRGSYGGVVM	481	0.86
8	RQRITDPQVRVVIAGL	63	0.85
8	QRLLRDHYREIAEEIT	567	0.85
9	QVLSRATERVRAGVLG	296	0.84
9	ATKTDLYPRWREIVNA	232	0.84
10	VVSYSAQPSARLVLAA	109	0.83
11	QATIAAAQVAETERDN	590	0.82
11	DISTDVRRAPHAGGRE	139	0.82
12	RQLGILSQVNDNLAGL	612	0.81
12	PLSVGAGLILGRMAYK	511	0.81
12	MRGSYGGVVMIGMLSS	487	0.81
12	SPHVMGTDFGRLKALG	455	0.81
12	HTIAIAKLNERGDLVQ	42	0.81
12	LGEIRSATEQLAVSLG	310	0.81
12	TEPEMWFVRQAHQICP	211	0.81
13	VRSEAKANVRRFVDDI	536	0.80
14	VENAIATAVGDNFVWA	411	0.79
14	QIDSCDPTAHWAEIGN	394	0.79
14	DRLASDLERRKREAQQ	338	0.79
14	LLRSHAVTLNDKELNE	267	0.79
14	AGPDGTTAAVDIPVDD	124	0.79
15	GDLVQRLTRARQRITD	53	0.78
15	TERVRAGVLGEIRSAT	302	0.78
15	AHLQRARVPMPIIAVS	250	0.78
15	LAFIDTPGVGGLGQPH	171	0.78

16	APHAGGREVLRVEVGA	147	0.77
17	LILGRMAYKEDKQNRL	518	0.76
18	LGDGFNDLTADVDHDL	365	0.75
19	AHQICPVGAVVATKTD	221	0.74
20	LAGLEPTLTPRASLGR	624	0.73
20	RSEALADDVARSFADA	429	0.73
20	EVGAPSPLLRGGLAFI	159	0.73
21	DSVLSAELSPHVMGTD	447	0.71
21	TADVDHDLRTRFRTVT	373	0.71
21	YPRWREIVNANAAHLQ	238	0.71
21	GLLPEADAVLVVSDTS	192	0.71
22	QQTALWQQVLGDGFND	356	0.69
23	RVVIAGLLKQGKSQLL	72	0.68
23	SKQSRDRLKMIQRLLR	556	0.68
23	KREAQQAVQQTALWQQ	348	0.68
24	FADAGLDSVLSAELSP	441	0.67
25	AQVAETERDNRIRELQ	596	0.66
26	TDFGRLKALGRMESKP	461	0.65
27	ARVGDDEATVVITVVS	96	0.64
27	GVVMIGMLSSVVGLGL	493	0.64
27	LNDKELNEESNFPAIV	275	0.64
28	VRRFVDDISFVVSKQS	544	0.63
28	PIIAVSSLLRSHAVTL	260	0.63
29	LLKQGKSQLLNSLLNL	78	0.62
30	LLNLPAARVGDDEATV	90	0.60
31	KQNRLLRVRSEAKANV	529	0.55
32	EATVVITVVSYSAQPS	102	0.54
33	SSVVGLGLFNPLSVGA	501	0.52

OVERLAP DISPLAY

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MVPAGLCAYRDLRRKRARKWGDTVTQPDDPRRVGVIVELIDHTIAIAKLNERGDLVQRLTRARQRITDPQVRVVIAGLLKQGKSQLLNSLLNLPAARVGDDEATVVITVVSYSAQPSARLVLAAGPDGTTAAVDIPVDDISTDVRRAPHA(
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------------------------------------------------------------LLKQGKSQLLNSLLNL-----------------------------------------------
--------------------------------------------------------------------LLNLPAARVGDDEATV--------------------------------------
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------------------------------------------------------------------------EATVVITVVSYSAQPS----------------------------------
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