ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	461
Number of 16mers from the input sequence	446
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	ALTWQLPAEPGGGAAP	396	0.95	
1	PAWAIGPPVVDAAAQP	22	0.95	
2	VAIIDTGVQPGPRLPN	91	0.93	
2	PSWWQPYVLSVASLTS	275	0.93	
3	AKPVADPPVPAPKDTT	412	0.92	
4	WVGIAAPGENIASVSN	303	0.90	
4	DLSRPDDPRNWAGVTS	256	0.90	
4	VVAGWWTPPAWAIGPP	14	0.90	
4	HGTLVAGIVAGQPGND	126	0.90	
5	IVAGQPGNDGFSGVAP	133	0.89	
5	VDAGGDFVESTDGLTD	107	0.89	

6	SGSVSASCDSNPLTDL	242	0.88	
7	VIPGTDPGVPTPSQTM	59	0.87	
7	RTSGGDPQLAQATLDV	165	0.87	
7	GNDGFSGVAPAARLLS	139	0.87	
8	PVPAPKDTTPRNVAFA	419	0.86	
8	AEPGGGAAPAKPVADP	403	0.86	
8	DAAAQPPSGDPGPVAP	32	0.86	
8	PSKFSMPGPWVGIAAP	294	0.86	
9	APMEQRGACSVSGVIP	46	0.84	
9	NVSTITCLPADRMVDQ	199	0.84	
9	MSTKFSPRTSGGDPQL	158	0.84	
10	RGEGQLVAIIDTGVQP	85	0.83	
10	PAAWQFSRGEGQLVAI	78	0.83	
10	AGAIVHAADLGAKVIN	184	0.83	
11	DGLTDCDGHGTLVAGI	118	0.82	
12	RGARESSNIVGAGNLD	377	0.81	
13	RLTATAHRGARESSNI	370	0.80	
13	PGLNATEVVRRLTATA	360	0.80	
13	NGLPDAHQKLVALSGT	326	0.80	
14	AFACLAATVVVAGWWT	5	0.79	
15	GDGALANGLPDAHQKL	320	0.78	
15	AAIRYAAVDKDAVIVA	219	0.78	
16	GTSYAAGYVSGVAALV	340	0.77	
16	LLSIRAMSTKFSPRTS	152	0.77	
17	DPRNWAGVTSVSIPSW	262	0.76	
18	SGVAALVRSRYPGLNA	349	0.75	
18	ASVSNSGDGALANGLP	314	0.75	
19	TPSQTMLNLPAAWQFS	69	0.74	
20	DRMVDQAALGAAIRYA	209	0.71	
21	AVDKDAVIVAAAGNTG	225	0.70	
21	PQLAQATLDVAVLAGA	171	0.70	
22	NIVGAGNLDAVAALTW	384	0.66	
23	TAATVAIARRRREPTE	446	0.64	
24	NLDAVAALTWQLPAEP	390	0.63	

24	YVLSVASLTSAGQPSK	281	0.63	
24	GVAPAARLLSIRAMST	145	0.63	
25	VQPGPRLPNVDAGGDF	98	0.60	
25	DLGAKVINVSTITCLP	192	0.60	
26	AGAAALSVLVGLTAAT	434	0.56	

OVERLAP DISPLAY

MIRAAFACLAATVVVAGWWTPPAWAIGPPVVDAAAQPPSGDPGPVAPMEQRGACSVSGVIPGTDPGVPTPSQTMLNLPAAWQF
SRGEGQLVAIIDTGVQPGPRLPNVDAGGDFVESTDGLTDCDGHGTLVAGIVAGQPGNDGFSGVAPAARLLSIRAMSTKFSPRT
SGGDPQLAQATLDVAVLAGAIVHAADLGAKVINVSTITCLPADRMVDQAALGAAIRYAAVDKDAVIVAAAGNTGASGSVSASC
DSNPLTDLSRPDDPRNWAGVTSVSIPSWWQPYVLSVASLTSAGQPSKFSMPGPWVGIAAPGENIASVSNSGDGALANGLPDAH
QKLVALSGTSYAAGYVSGVAALVRSRYPGLNATEVVRRLTATAHRGARESSNIVGAGNLDAVAALTWQLPAEPGGGAAPAKPV
ADPPVPAPKDTTPRNVAFAGAAALSVLVGLTAATVAIARRRREPTE^{461}

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