ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	439
Number of 16mers from the input sequence	424
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	TGLAIAATSRRKDQAW	323	0.92	
1	PGSWERPWSFAEFLDA	173	0.92	
2	GVMQQLATFCAGGKCP	76	0.89	
2	APLPIGPRGRAACSDI	305	0.89	
2	AGHWRYQTFDRADGLD	286	0.89	
3	HGFANAHRRVGNLAVL	370	0.88	
4	AVQFYADLTNKHKVAP	247	0.87	
5	AADDDDALTFFFAANP	31	0.86	
5	GRSGRDRQWGFVNAWV	196	0.86	
6	GVPWSVPRMNPTHLNF	224	0.84	
7	AWELTYAELADRGVLL	96	0.82	

7	CAGGKCPDVLMAWELT	85	0.82	
7	MDRYFGPVLRGSRPAT	408	0.82	
7	HDGFLEAVQFYADLTN	241	0.82	
7	FLFYNKQLFDDAGVPP	156	0.82	
8	EGPAYSEGLPVTPAWE	387	0.81	
8	QSMSTADLFSVGKAGI	268	0.81	
8	PRMNPTHLNFDHDGFL	230	0.81	
8	IGALYETFTFNGGQYA	132	0.81	
9	AACSDIGVTGLAIAAT	315	0.80	
10	RALLSGPGVMQQLATF	69	0.79	
10	TFDRADGLDFDVAPLP	293	0.79	
10	DDAGVPPPPGSWERPW	165	0.79	
11	QALIGESRLFVPVLRS	350	0.78	
12	KPFERRSLLRGAGALT	4	0.77	
12	VSFYAAGLFAMNNGVP	211	0.77	
13	TAASLAPWAAGCAADD	19	0.76	
14	VGKAGIALAGHWRYQT	278	0.75	
14	GFVNAWVSFYAAGLFA	205	0.75	
15	FAANPDELRPRMRVVN	42	0.74	
16	FQRRYPDIKVRALLSG	59	0.72	
16	RSAINSHGFANAHRRV	364	0.72	
16	EQWSGNFLFYNKQLFD	150	0.72	
16	NGGQYAFPEQWSGNFL	142	0.72	
17	PAWEKIAALMDRYFGP	399	0.71	
17	HKVAPSAAEQQSMSTA	258	0.71	
18	AELKSDSIGALYETFT	125	0.69	
19	NTLLARDQAFAAELKS	114	0.68	
20	SRRKDQAWEFVKFATG	331	0.67	
21	GSRPATSLTGLSQAVD	418	0.64	
21	AELADRGVLLDLNTLL	102	0.64	
22	SLTGLSQAVDEVLRNP	424	0.63	
23	SLLRGAGALTAASLAP	10	0.60	

OVERLAP DISPLAY

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MVNKPFERRSLLRGAGALTAASLAPWAAGCAADDDDALTFFFAANPDELRPRMRVVNEFQRRYPDIKVRALLSGPGVMQQLAT
FCAGGKCPDVLMAWELTYAELADRGVLLDLNTLLARDQAFAAELKSDSIGALYETFTFNGGQYAFPEQWSGNFLFYNKQLFDD
AGVPPPPGSWERPWSFAEFLDAAQALTKQGRSGRDRQWGFVNAWVSFYAAGLFAMNNGVPWSVPRMNPTHLNFDHDGFLEAVQ
FYADLTNKHKVAPSAAEQQSMSTADLFSVGKAGIALAGHWRYQTFDRADGLDFDVAPLPIGPRGRAACSDIGVTGLAIAATSR
RKDQAWEFVKFATGPVGQALIGESRLFVPVLRSAINSHGFANAHRRVGNLAVLSEGPAYSEGLPVTPAWEKIAALMDRYFGPV
LRGSRPATSLTGLSQAVDEVLRNP^439
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TGLAIAATSRRKDQAW-------------------------------------------------------------------
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PGSWERPWSFAEFLDA-------------------------------------------------------------------
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APLPIGPRGRAACSDI-------------------------------------------------------------------
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AGHWRYQTFDRADGLD-------------------------------------------------------------------
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HGFANAHRRVGNLAVL------------------------------------------------------
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AVQFYADLTNKHKVAP-------------------------------------------------------------------
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AADDDDALTFFFAANP-------------------------------------------------------------------
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GRSGRDRQWGFVNAWV----------------------------------------------------------------
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GVPWSVPRMNPTHLNF----------------------------------------------------------------
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AWELTYAELADRGVLL----------------------------------------------------------------
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MDRYFGPVLRGSRPAT---------------
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HDGFLEAVQFYADLTN----------------------------------------------------------------
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FLFYNKQLFDDAGVPP----------------------------------------------------------------
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EGPAYSEGLPVTPAWE-----------------------------------
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QSMSTADLFSVGKAGI----------------------------------------------------------------
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IGALYETFTFNGGQYA-------------------------------------------------------------------
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FAANPDELRPRMRVVN-------------------------------------------------------------------
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HKVAPSAAEQQSMSTA-------------------------------------------------------------------
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AELKSDSIGALYETFT-------------------------------------------------------------------
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NTLLARDQAFAAELKS-------------------------------------------------------------------
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