ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	345
Number of 16mers from the input sequence	330
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	GATGQVGQVMRTLLDE	9	0.93	
2	AAGVDESLVGRIRRDP	294	0.92	
3	MSKVQAPRFAAAGVTV	76	0.90	
4	LFVSGDNLRKGAALNT	319	0.89	
5	GRIRRDPGVPDGRGLA	303	0.87	
6	GGAEQLVYDGGALEFP	179	0.86	
6	AHRRPKGIIANPNCTT	117	0.86	
7	AGVTVIDNSSAWRKDP	87	0.85	
7	EIEVEDAETADPSGLD	51	0.85	
8	DGGALEFPPPNTYVAP	187	0.82	
9	SSAWRKDPDVPLVVSE	95	0.81	

9	GSLVDDGSGETDEDQK	212	0.81	
10	LVVSEVNFERDAHRRP	106	0.77	
11	IALFSAGSAMSKVQAP	67	0.76	
11	QAVSGSGLAGVAELAE	157	0.76	
12	QVMRTLLDERDFPASA	16	0.74	
13	DEDQKLRFESRKILGI	223	0.72	
14	LGIPDLLVSGTCVRVP	236	0.71	
14	KVLHDEARLVRLVVSS	140	0.71	
15	VPDGRGLALFVSGDNL	311	0.68	
15	SGTCVRVPVFTGHSLS	244	0.68	
16	INAEFAQPLSPERARE	260	0.67	
16	PVFTGHSLSINAEFAQ	251	0.67	
17	ARSQGRKLAFRGQEIE	38	0.66	
17	ARELLDGATGVQLVDV	273	0.66	
17	FPPPNTYVAPIAFNVV	193	0.66	
18	GLAGVAELAEQARAVI	163	0.65	
18	AAMPVLKVLHDEARLV	134	0.65	
19	VRLVVSSYQAVSGSGL	149	0.63	
20	DPSGLDIALFSAGSAM	61	0.62	
21	GVQLVDVPTPLAAAGV	282	0.61	
22	LAEQARAVIGGAEQLV	170	0.59	
23	RFESRKILGIPDLLVS	229	0.57	
24	RDFPASAVRFFASARS	25	0.52	
24	VAPIAFNVVPLAGSLV	200	0.52	

OVERLAP DISPLAY

MGLSIGIVGATGQVGQVMRTLLDERDFPASAVRFFASARSQGRKLAFRGQEIEVEDAETADPSGLDIALFSAGSAMSKVQAPR
FAAAGVTVIDNSSAWRKDPDVPLVVSEVNFERDAHRRPKGIIANPNCTTMAAMPVLKVLHDEARLVRLVVSSYQAVSGSGLAG
VAELAEQARAVIGGAEQLVYDGGALEFPPPNTYVAPIAFNVVPLAGSLVDDGSGETDEDQKLRFESRKILGIPDLLVSGTCVR
VPVFTGHSLSINAEFAQPLSPERARELLDGATGVQLVDVPTPLAAAGVDESLVGRIRRDPGVPDGRGLALFVSGDNLRKGAAL
NTIQIAELLTADL^{345}

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GATGQVGQVMRTLLDE-------------------------------------------------------------------
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AAGVDESLVGRIRRDP------------------------------------
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MSKVQAPRFAAAGVTV-------------------------------------------------------------------
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LFVSGDNLRKGAALNT-----------
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GRIRRDPGVPDGRGLA---------------------------
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GGAEQLVYDGGALEFP-------------------------------------------------------------------
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AHRRPKGIIANPNCTT-------------------------------------------------------------------
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AGVTVIDNSSAWRKDP-------------------------------------------------------------------
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EIEVEDAETADPSGLD-------------------------------------------------------------------
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DGGALEFPPPNTYVAP-------------------------------------------------------------------
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SSAWRKDPDVPLVVSE-------------------------------------------------------------------
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GSLVDDGSGETDEDQK-------------------------------------------------------------------
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LVVSEVNFERDAHRRP-------------------------------------------------------------------
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IALFSAGSAMSKVQAP-------------------------------------------------------------------
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QAVSGSGLAGVAELAE-------------------------------------------------------------------
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QVMRTLLDERDFPASA-------------------------------------------------------------------
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DEDQKLRFESRKILGI-------------------------------------------------------------------
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LGIPDLLVSGTCVRVP-------------------------------------------------------------------
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KVLHDEARLVRLVVSS-------------------------------------------------------------------
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VPDGRGLALFVSGDNL-------------------
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SGTCVRVPVFTGHSLS-------------------------------------------------------------------
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INAEFAQPLSPERARE-------------------------------------------------------------------
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PVFTGHSLSINAEFAQ-------------------------------------------------------------------
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ARSQGRKLAFRGQEIE-------------------------------------------------------------------
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ARELLDGATGVQLVDV---------------------------------------------------------
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FPPPNTYVAPIAFNVV-------------------------------------------------------------------
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GLAGVAELAEQARAVI-------------------------------------------------------------------
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AAMPVLKVLHDEARLV-------------------------------------------------------------------
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VRLVVSSYQAVSGSGL-------------------------------------------------------------------
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DPSGLDIALFSAGSAM-------------------------------------------------------------------
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GVQLVDVPTPLAAAGV------------------------------------------------
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LAEQARAVIGGAEQLV-------------------------------------------------------------------
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RFESRKILGIPDLLVS-------------------------------------------------------------------
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RDFPASAVRFFASARS-------------------------------------------------------------------
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VAPIAFNVVPLAGSLV-------------------------------------------------------------------
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