ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	291
Number of 16mers from the input sequence	276
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	AELARAIIESRSGADT	268	0.93	
2	GNMISGRDVRKVYITD	80	0.91	
2	GGVVMAGDRRSTQGNM	67	0.91	
3	IESRSGADTFGSDGGE	275	0.88	
4	EALYDAADDDSATGGP	226	0.87	
4	EKLEGVPLTFAGKINR	124	0.87	
5	SISGGAPLAGGDAQLP	40	0.86	
5	DGAVDVPESRIAELAR	257	0.86	
6	KVYITDDYTATGIAGT	90	0.84	
7	HGTTIVALKYPGGVVM	56	0.83	
7	AVIIDADGAVDVPESR	251	0.83	

8	SGSLFAKSSMKKLYSQ	198	0.82	
9	AVDLSSFTDFLRRQAP	19	0.81	
10	DIHASDPQSAGRIVSF	165	0.80	
11	PELLPASISGGAPLAG	34	0.79	
11	AGTAAVAVEFARLYAV	103	0.79	
12	QVTDGDSGLRVAVEAL	213	0.78	
13	GDRRSTQGNMISGRDV	73	0.75	
14	DDSATGGPDLVRGIFP	234	0.74	
15	EEEGYQAVGSGSLFAK	189	0.70	
15	DAAGGWNIEEEGYQAV	181	0.70	
16	NSLSGTPAVDLSSFTD	12	0.69	
17	VELEHYEKLEGVPLTF	118	0.67	
18	PQSAGRIVSFDAAGGW	171	0.66	
19	AMQGLLALPLLAGYDI	151	0.65	
20	DLVRGIFPTAVIIDAD	242	0.63	
21	TWPLPDRLSINSLSGT	2	0.61	
21	NRLAIMVRGNLAAAMQ	138	0.61	
22	FLRRQAPELLPASISG	28	0.51	

OVERLAP DISPLAY

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VTWPLPDRLSINSLSGTPAVDLSSFTDFLRRQAPELLPASISGGAPLAGGDAQLPHGTTIVALKYPGGVVMAGDRRSTQGNMI
SGRDVRKVYITDDYTATGIAGTAAVAVEFARLYAVELEHYEKLEGVPLTFAGKINRLAIMVRGNLAAAMQGLLALPLLAGYDI
HASDPQSAGRIVSFDAAGGWNIEEEGYQAVGSGSLFAKSSMKKLYSQVTDGDSGLRVAVEALYDAADDDSATGGPDLVRGIFP
TAVIIDADGAVDVPESRIAELARAIIESRSGADTFGSDGGEK291
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------------------AELARAIIESRSGADT--------
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GNMISGRDVRKVYITD-------------------------------------------------------------------
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GGVVMAGDRRSTQGNM-------------------------------------------------------------------
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-------------------------IESRSGADTFGSDGGE-
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EALYDAADDDSATGGP--------------------------------------------------
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EKLEGVPLTFAGKINR-------------------------------------------------------------------
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SISGGAPLAGGDAQLP-------------------------------------------------------------------
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-------DGAVDVPESRIAELAR-------------------
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KVYITDDYTATGIAGT-------------------------------------------------------------------
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HGTTIVALKYPGGVVM-------------------------------------------------------------------
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-AVIIDADGAVDVPESR-------------------------
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SGSLFAKSSMKKLYSQ-------------------------------------------------------------------
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AVDLSSFTDFLRRQAP-------------------------------------------------------------------
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DIHASDPQSAGRIVSF-------------------------------------------------------------------
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PELLPASISGGAPLAG-------------------------------------------------------------------
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AGTAAVAVEFARLYAV-------------------------------------------------------------------
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QVTDGDSGLRVAVEAL------------------------------------------------------------
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GDRRSTQGNMISGRDV----------------------------------------------------------------
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DDSATGGPDLVRGIFP----------------------------------------
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EEEGYQAVGSGSLFAK----------------------------------------------------------------
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DAAGGWNIEEEGYQAV----------------------------------------------------------------
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NSLSGTPAVDLSSFTD----------------------------------------------------------------
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VELEHYEKLEGVPLTF----------------------------------------------------------------
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PQSAGRIVSFDAAGGW----------------------------------------------------------------
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AMQGLLALPLLAGYDI----------------------------------------------------------------
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DLVRGIFPTAVIIDAD--------------------------------
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TWPLPDRLSINSLSGT----------------------------------------------------------------
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NRLAIMVRGNLAAAMQ----------------------------------------------------------------
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FLRRQAPELLPASISG----------------------------------------------------------------
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