ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	359
Number of 16mers from the input sequence	344
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	VGQITSAVLFGVLVLQ	121	0.93	
2	IREDGPPSHHTKRGTP	35	0.90	
3	DDLIKIRRSRNLGLNK	101	0.89	
4	NACVTAPGLGCYNVRD	212	0.88	
4	YVLITFWQYRNACVTA	202	0.88	
5	RMFRMAPFHHHFELVG	309	0.85	
6	ILTFRTTGRRMFRMAP	300	0.84	
7	CVVIVSAWSNAVNFTD	170	0.83	
8	HHTKRGTPSMGGVAIL	43	0.81	
9	PVLIRLFTKQGFGHQI	20	0.80	
9	ATVTLAPVLFVLFCVV	157	0.80	

10	AGLAFDGEGIGASGLL	71	0.79	
10	AGYLGAHLAGLAFDGE	63	0.79	
10	AGACIGFLWWNAAPAK	239	0.79	
10	FGVLVLQFRNAAGLTP	130	0.79	
11	VGWAETTVIIRFWLLT	323	0.77	
11	GVIAGLSVTSRTEILA	267	0.77	
12	PAKIFMGDTGSLALGG	252	0.76	
13	GEGIGASGLLVLGLAT	77	0.74	
14	QFRNAAGLTPGSADLS	136	0.73	
15	LGLATALGGVGFIDDL	88	0.72	
15	AAGTMAMVTAAYVLIT	191	0.72	
16	GSADLSYVREIATVTL	146	0.71	
17	LIAVAVAVTVSILLTP	5	0.70	
17	TVSILLTPVLIRLFTK	13	0.70	
18	CGLGVALFYGEWLAAV	342	0.67	
18	SRTEILAVVLGALFVA	276	0.67	
19	RFWLLTAITCGLGVAL	333	0.65	
20	GSLALGGVIAGLSVTS	261	0.61	
21	FLWWNAAPAKIFMGDT	245	0.57	
22	PGLGCYNVRDPLDLAL	218	0.56	
23	LFVAEITSVVLQILTF	288	0.55	

OVERLAP DISPLAY

MRQILIAVAVAVTVSILLTPVLIRLFTKQGFGHQIREDGPPSHHTKRGTPSMGGVAILAGIWAGYLGAHLAGLAFDGEGIGASGLLVLGLATALGGVGFIDDLIKIRRSRNLGLNKTAKTVGQITSAVLFGVLVLQFRNAAGLTPGSADLSYVREIATVTLAPVLFVLFCVVIVSAWSNAVNFTDGLDGLAAGTMAMVTAAYVLITFWQYRNACVTAPGLGCYNVRDPLDLALIAAATAGACIGFLWWNAAPAKIFMGDTGSLALGGVIAGLSVTSRTEILAVVLGALFVAEITSVVLQILTFRTTGRRMFRMAPFHHHFELVGWAETTVIIRFWLLTAITCGLGVALFYGEWLAAVGA^{359}

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VGQITSAVLFGVLVLQ-------------------------------------------------------------------
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IREDGPPSHHTKRGTP-------------------------------------------------------------------
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DDLIKIRRSRNLGLNK-------------------------------------------------------------------
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NACVTAPGLGCYNVRD-------------------------------------------------------------------
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YVLITFWQYRNACVTA-------------------------------------------------------------------
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RMFRMAPFHHHFELVG-----------------------------------
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ILTFRTTGRRMFRMAP--------------------------------------------
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CVVIVSAWSNAVNFTD-------------------------------------------------------------------
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HHTKRGTPSMGGVAIL-------------------------------------------------------------------
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PVLIRLFTKQGFGHQI-------------------------------------------------------------------
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ATVTLAPVLFVLFCVV-------------------------------------------------------------------
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AGLAFDGEGIGASGLL-------------------------------------------------------------------
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AGYLGAHLAGLAFDGE-------------------------------------------------------------------
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AGACIGFLWWNAAPAK--------------------------------------------------------------------
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FGVLVLQFRNAAGLTP--------------------------------------------------------------------
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VGWAETTVIIRFWLLT---------------------
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GVIAGLSVTSRTEILA--------------------------------------------------------------------
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PAKIFMGDTGSLALGG--------------------------------------------------------------------
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GEGIGASGLLVLGLAT--------------------------------------------------------------------
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QFRNAAGLTPGSADLS--------------------------------------------------------------------
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LGLATALGGVGFIDDL--------------------------------------------------------------------
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AAGTMAMVTAAYVLIT--------------------------------------------------------------------
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GSADLSYVREIATVTL--------------------------------------------------------------------
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LIAVAVAVTVSILLTP--------------------------------------------------------------------
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TVSILLTPVLIRLFTK-------------------------------------------------------------------
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RFWLLTAITCGLGVAL-----------
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GSLALGGVIAGLSVTS-------------------------------------------------------------------
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FLWWNAAPAKIFMGDT-------------------------------------------------------------------
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PGLGCYNVRDPLDLAL-------------------------------------------------------------------
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LFVAEITSVVLQILTF--------------------------------------------------------
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