ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	270
Number of 16mers from the input sequence	255
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	RVNALAPTVFRSAVTE	195	0.92	
2	AAEWGGHGIRVNALAP	186	0.91	
2	PITEMAVEDFDAVMDA	112	0.91	
3	AVTEWMFTDDPKGRAT	207	0.89	
3	AAGYSAYCPSKAGTDL	165	0.89	
4	NSAGLAELVNGAGIDD	55	0.88	
5	DPKGRATREAMLARIP	216	0.87	
6	AAVVTCRPDSLADAQQ	71	0.86	
7	DAVMDANVRGAWLVCR	122	0.83	
8	QQMVEAALGRYGRLDG	85	0.80	
8	EEMALAQQVPNLGLAR	2	0.80	

8	GVLVASGSNHVAPITE	100	0.80	
9	RVAARALADAGARLTL	36	0.78	
10	AMLARIPLRRFAEPED	225	0.77	
11	SILITGATGSLGRVAA	24	0.73	
12	GARLTLAGGNSAGLAE	46	0.72	
13	RGAWLVCRAAGRVLLE	130	0.69	
14	LGLARFSVQDKSILIT	13	0.66	
15	SSFYTGQVMYLDGGYT	253	0.65	
16	PSKAGTDLLAKTLAAE	173	0.64	
17	GALIYLLSDASSFYTG	243	0.63	
18	VLLEQGQGGSVVLVSS	142	0.62	
19	GRYGRLDGVLVASGSN	93	0.61	
20	AEPEDFVGALIYLLSD	236	0.60	

OVERLAP DISPLAY

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VEEMALAQQVPNLGLARFSVQDKSILITGATGSLGRVAARALADAGARLTLAGGNSAGLAELVNGAGIDDAAVVTCRPDSLAD
AQQMVEAALGRYGRLDGVLVASGSNHVAPITEMAVEDFDAVMDANVRGAWLVCRAAGRVLLEQGQGGSVVLVSSVRGGLGNAA
GYSAYCPSKAGTDLLAKTLAAEWGGHGIRVNALAPTVFRSAVTEWMFTDDPKGRATREAMLARIPLRRFAEPEDFVGALIYLL
SDASSFYTGQVMYLDGGYTAC270
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RVNALAPTVFRSAVTE------------------------------------------------------------
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AAEWGGHGIRVNALAP-------------------------------------------------------------------
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PITEMAVEDFDAVMDA-------------------------------------------------------------------
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AVTEWMFTDDPKGRAT------------------------------------------------
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AAGYSAYCPSKAGTDL-------------------------------------------------------------------
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NSAGLAELVNGAGIDD-------------------------------------------------------------------
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DPKGRATREAMLARIP---------------------------------------
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AAVVTCRPDSLADAQQ-------------------------------------------------------------------
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DAVMDANVRGAWLVCR-------------------------------------------------------------------
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QQMVEAALGRYGRLDG-------------------------------------------------------------------
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EEMALAQQVPNLGLAR-------------------------------------------------------------------
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GVLVASGSNHVAPITE-------------------------------------------------------------------
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RVAARALADAGARLTL-------------------------------------------------------------------
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AMLARIPLRRFAEPED------------------------------
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SILITGATGSLGRVAA-------------------------------------------------------------------
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GARLTLAGGNSAGLAE-------------------------------------------------------------------
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RGAWLVCRAAGRVLLE-------------------------------------------------------------------
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LGLARFSVQDKSILIT-------------------------------------------------------------------
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---SSFYTGQVMYLDGGYT--
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PSKAGTDLLAKTLAAE-------------------------------------------------------------------
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GALIYLLSDASSFYTG------------
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VLLEQGQGGSVVLVSS-------------------------------------------------------------------
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GRYGRLDGVLVASGSN-------------------------------------------------------------------
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AEPEDFVGALIYLLSD-------------------
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