ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	284
Number of 16mers from the input sequence	269
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	AVLIERAGTDGQDQTE	179	0.96	
2	SGELDFGITGRDLVCD	59	0.91	
2	AGMRIATAYPNLVRKD	108	0.91	
3	DWVAIRALVPRRDVNG	246	0.88	
4	AEAGYRRRTDSKDLTV	21	0.86	
5	SSFRYAAPAGRNWTTA	90	0.84	
5	ITPGLESPTIAPLADP	230	0.84	
6	APLADPDWVAIRALVP	240	0.82	
7	TLSQHDLVAFGEPLCD	161	0.80	
7	TKGIEATVIRLDGAVE	126	0.80	
8	QYLMLDYDCPRSALKK	211	0.79	

9	GTDGQDQTEARDQLVA	186	0.78	
9	WTTADLAGMRIATAYP	102	0.78	
10	DVVGSGRTLSQHDLVA	154	0.77	
11	GVADAIADVVGSGRTL	147	0.76	
12	YDCPRSALKKATAITP	217	0.75	
13	RPKDIAIYVGSGELDF	49	0.71	
14	RTDSKDLTVIDPVNNV	28	0.70	
15	QVRERLALGFGSSSFR	78	0.69	
15	VEISVQLGVADAIADV	140	0.69	
16	VNGIMDELAAIGAKAI	259	0.68	
17	TEARDQLVARVQGVVF	193	0.67	
18	AIGAKAILASDIRFCR	268	0.63	
19	RVAVPNKGALSEPATE	3	0.61	
20	VCDSGAQVRERLALGF	72	0.60	
21	LVARVQGVVFGQQYLM	199	0.57	
22	TVIRLDGAVEISVQLG	132	0.56	
23	VAFGEPLCDSEAVLIE	168	0.54	

OVERLAP DISPLAY

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MLRVAVPNKGALSEPATEILAEAGYRRRTDSKDLTVIDPVNNVEFFFLRPKDIAIYVGSGELDFGITGRDLVCDSGAQVRERL
ALGFGSSSFRYAAPAGRNWTTADLAGMRIATAYPNLVRKDLATKGIEATVIRLDGAVEISVQLGVADAIADVVGSGRTLSQHD
LVAFGEPLCDSEAVLIERAGTDGQDQTEARDQLVARVQGVVFGQQYLMLDYDCPRSALKKATAITPGLESPTIAPLADPDWVA
IRALVPRRDVNGIMDELAAIGAKAILASDIRFCRF$^{284}$
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AVLIERAGTDGQDQTE-------------------------------------------------------------------
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SGELDFGITGRDLVCD-------------------------------------------------------------------
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AGMRIATAYPNLVRKD-------------------------------------------------------------------
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DWVAIRALVPRRDVNG-----------------------
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AEAGYRRRTDSKDLTV-------------------------------------------------------------------
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SSFRYAAPAGRNWTTA-------------------------------------------------------------------
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ITPGLESPTIAPLADP---------------------------------------
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APLADPDWVAIRALVP-----------------------------
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TLSQHDLVAFGEPLCD-------------------------------------------------------------------
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TKGIEATVIRLDGAVE-------------------------------------------------------------------
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QYLMLDYDCPRSALKK----------------------------------------------------------
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GTDGQDQTEARDQLVA-------------------------------------------------------------------
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WTTADLAGMRIATAYP-------------------------------------------------------------------
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DVVGSGRTLSQHDLVA-------------------------------------------------------------------
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GVADAIADVVGSGRTL-------------------------------------------------------------------
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YDCPRSALKKATAITP----------------------------------------------------
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RPKDIAIYVGSGELDF-------------------------------------------------------------------
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RTDSKDLTVIDPVNNV-------------------------------------------------------------------
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QVRERLALGFGSSSFR-------------------------------------------------------------------
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VEISVQLGVADAIADV-------------------------------------------------------------------
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---------VNGIMDELAAIGAKAI----------
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TEARDQLVARVQGVVF-------------------------------------------------------------------
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------------------AIGAKAILASDIRFCR-
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RVAVPNKGALSEPATE-------------------------------------------------------------------
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VCDSGAQVRERLALGF-------------------------------------------------------------------
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LVARVQGVVFGQQYLM-------------------------------------------------------------------
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TVIRLDGAVEISVQLG-------------------------------------------------------------------
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VAFGEPLCDSEAVLIE-------------------------------------------------------------------
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