ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	379
Number of 16mers from the input sequence	364
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	DVGRDSTRGLGAGADP	57	0.94	
2	LGAGADPEVGRKAAED	66	0.91	
3	ASLVQDAAHPDANIIF	276	0.90	
3	MGIGSARGEGRSLKAA	223	0.90	
4	GTVIDDSLGDEVRVTV	292	0.89	
5	AGEGGGTGTGGAPVVA	100	0.88	
6	ATLSIGGDDDDVDVPP	360	0.87	
6	TDLITTPGLINVDFAD	195	0.87	
7	AHRIESAKAGKLTSTL	329	0.86	
7	DVKGIMSGAGTALMGI	210	0.86	
7	TGTGGAPVVASIARKL	106	0.86	
8	LLMSDADVKLDVGRDS	47	0.85	
8	IEQGLKGVEFIAINTD	28	0.85	
9	PVMGETGGAHRIESAK	321	0.84	

10	TVIAAGFDVSGPGRKP	306	0.82	
11	PVDAVSVPLHTNGATL	347	0.81	
12	AKDEIEELLRGADMVF	82	0.80	
13	VVGIGGGGVNAVNRMI	13	0.79	
14	GVLMSIAGGSDLGLFE	256	0.78	
15	SPLLEASMEGAQGVLM	244	0.77	
16	VVTRPFSFEGKRRSNQ	128	0.75	
17	AGGSDLGLFEINEAAS	262	0.73	
18	VSLMDAFRSADEVLLN	174	0.71	
19	DTLIVIPNDRLLQMGD	156	0.69	
19	AALRESCDTLIVIPND	149	0.69	
20	RGEGRSLKAAEIAINS	229	0.68	
21	RKAAEDAKDEIEELLR	76	0.67	
21	GVEFIAINTDAQALLM	34	0.67	
21	AGKLTSTLFEPVDAVS	337	0.67	
21	ARKLGALTVGVVTRPF	118	0.67	
22	PGLINVDFADVKGIMS	201	0.66	
23	NTDAQALLMSDADVKL	41	0.65	
23	SMEGAQGVLMSIAGGS	250	0.65	
24	DRLLQMGDAAVSLMDA	164	0.64	
25	RRSNQAENGIAALRES	139	0.58	

OVERLAP DISPLAY

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MTPPHNYLAVIKVVGIGGGGVNAVNRMIEQGLKGVEFIAINTDAQALLMSDADVKLDVGRDSTRGLGAGADPEVGRKAAEDAK
DEIEELLRGADMVFVTAGEGGGTGTGGAPVVASIARKLGALTVGVVTRPFSFEGKRRSNQAENGIAALRESCDTLIVIPNDRL
LQMGDAAVSLMDAFRSADEVLLNGVQGITDLITTPGLINVDFADVKGIMSGAGTALMGIGSARGEGRSLKAAEIAINSPLLEA
SMEGAQGVLMSIAGGSDLGLFEINEAASLVQDAAHPDANIIFGTVIDDSLGDEVRVTVIAAGFDVSGPGRKPVMGETGGAHRI
ESAKAGKLTSTLFEPVDAVSVPLHTNGATLSIGGDDDDVDVPPFMRR379
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DVGRDSTRGLGAGADP-------------------------------------------------------------------
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LGAGADPEVGRKAAED-------------------------------------------------------------------
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ASLVQDAAHPDANIIF-------------------------------------------------------------------
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MGIGSARGEGRSLKAA-------------------------------------------------------------------
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GTVIDDSLGDEVRVTV-------------------------------------------------------------------
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AGEGGGTGTGGAPVVA-------------------------------------------------------------------
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---------------------------ATLSIGGDDDDVDVPP----
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TDLITTPGLINVDFAD-------------------------------------------------------------------
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AHRIESAKAGKLTSTL-----------------------------------
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DVKGIMSGAGTALMGI-------------------------------------------------------------------
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TGTGGAPVVASIARKL-------------------------------------------------------------------
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LLMSDADVKLDVGRDS-------------------------------------------------------------------
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IEQGLKGVEFIAINTD-------------------------------------------------------------------
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PVMGETGGAHRIESAK-------------------------------------------
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TVIAAGFDVSGPGRKP----------------------------------------------------------
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--------------PVDAVSVPLHTNGATL-----------------
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AKDEIEELLRGADMVF-------------------------------------------------------------------
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VVGIGGGGVNAVNRMI-------------------------------------------------------------------
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GVLMSIAGGSDLGLFE-------------------------------------------------------------------
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SPLLEASMEGAQGVLM-------------------------------------------------------------------
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VVTRPFSFEGKRRSNQ-------------------------------------------------------------------
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AGGSDLGLFEINEAAS-------------------------------------------------------------------
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VSLMDAFRSADEVLLN-------------------------------------------------------------------
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DTLIVIPNDRLLQMGD-------------------------------------------------------------------
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AALRESCDTLIVIPND-------------------------------------------------------------------
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RGEGRSLKAAEIAINS-------------------------------------------------------------------
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RKAAEDAKDEIEELLR-------------------------------------------------------------------
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GVEFIAINTDAQALLM-------------------------------------------------------------------
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----AGKLTSTLFEPVDAVS---------------------------
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ARKLGALTVGVVTRPF-------------------------------------------------------------------
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PGLINVDFADVKGIMS-------------------------------------------------------------------
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NTDAQALLMSDADVKL-------------------------------------------------------------------
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SMEGAQGVLMSIAGGS-------------------------------------------------------------------
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DRLLQMGDAAVSLMDA-------------------------------------------------------------------
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RRSNQAENGIAALRES-------------------------------------------------------------------
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