

ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	230
Number of 16mers from the input sequence	215
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	TRLKDAGVVPNARVTV	182	0.94
2	LGVGPEPGADDANLVR	138	0.92
3	NARVTVEETTPGGGTI	192	0.87
4	MYLRTIYDLEEGVTP	10	0.86
5	EVHAEACRWEHVMSED	96	0.85
5	DVIGLPWEEVHAEACR	88	0.85
5	DGLLRVAGDRHLELTE	51	0.85
5	GVTIVIPGHENVTLPH	204	0.85
5	HVMSEDVERRLVKVLN	106	0.85
6	TEHVQGDIDLITRLKD	171	0.82
7	TVSRMERDGLLRVAGD	44	0.80
8	GHENVTLPHEMAHAVK	211	0.77
9	VKVLNNPTTSPFGNPI	117	0.75
10	AVMRKHRLAERLLVDV	74	0.74
11	AVVVRQLTEHVQGDID	164	0.73
12	KGRALAIAVMRKHRLA	67	0.72
12	EEEGVTPILARIAERL	19	0.72
12	TSLPAGSPVAVVVRQL	155	0.72
13	DRHLELTKEKGRLALAIA	59	0.69
14	PGADDANLVRTELPA	144	0.65
15	RARIAERLDQSGPTVS	27	0.63

OVERLAP DISPLAY

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MNELVDTTEMYLRTIYDLEEGVTPLRARIAERLDQSGPTVSQTVSRMERDGLLRVAGDRHLELTEKGRALAIAVMRKHRLAERLLVDVIGLPWEEVHAEACRWEHVMSEDVERRLVKVLNNPTTSPFGNPIPGLVELGVGPEPGADDAN
-----LGVGPEPGADDANI-----
-----MYLRTIYDLEEGVTP-----
-----EVHAEACRWEHVMSED-----
-----DVIGLPWEEVHAEACR-----
-----DGLLRVAGDRHLELTE-----
-----HVMSEDVERRLVKVLN-----
-----TVSRMERDGLLRVAGD-----
-----AVMRKHRLAERLLVDV-----
-----VKVLNNPTTSPFGNPI-----
-----AVMRKHRLAERLLVDV-----
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----- EEEGVTPLRARIAERL -----
----- DRHLELTEKGRALAIA -----
----- RARIAERLDQSGPTVS -----
----- PGADDANI -----
