

ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	248
Number of 16mers from the input sequence	233
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	DGSIADEPHFVVMGGT	144	0.90
2	FVVMGGTTEPIANALK	153	0.89
3	RGGIQFADTRGYAYDR	76	0.88
4	ANALKESYAENASLTD	164	0.87
4	IFTEQAKPYEVELCVA	110	0.87
5	AGSADTSGGDQPTLGV	190	0.85
5	RERSELARKGIARAKS	14	0.85
6	YGETKRPELYRITYDG	130	0.84
7	RVGFAAAGKFNEFDNL	59	0.80
7	PELYRITYDGSIADEP	136	0.80
8	PRRAFRRITGSALQAL	218	0.79

9	RGYAYDRRDVTRQLA	85	0.78	
10	LRIAVAALRAGSADTS	181	0.77	
11	ALAYAGGVLFVAENPS	32	0.76	
11	VYAQTLGTIFTEQAKP	102	0.76	
12	RRDVTRQLANVYAAQT	91	0.75	
13	PYEVELCVAEVAHYGE	117	0.73	
14	ISELYDRVGFAGKFAAAGKF	53	0.72	
15	GVASLEVAVLDANRPR	204	0.68	
16	ISPEQAMRERSELARK	7	0.67	
16	GVLFVAENPSRSLSQKI	38	0.67	
17	GKFNEFDNLRRGGIQF	66	0.65	
18	RKGIAKSVVALAYA	21	0.61	
19	LLVDQESPQSDGESSG	233	0.60	
19	AVLDANPRRAFRRT	211	0.60	
20	TGSALQALLVDQESPO	226	0.55	
20	SYAENASLTDALRIAV	170	0.55	

OVERLAP DISPLAY

VSFPYFISPEQAMRERSELARKGIARAKSVVALAYAGGVLFVAENPSRSLSQKISELYDRVGFAGKFAEFDNLRRGGIQFAD
 TRGYAYDRRDVTRQLANVYAAQTGTIFTEQAKP
 PYEVELCVAEVAHYGETKRPELYRITYDGSIADEPHFVVMGGTTEPIANA
 LKESYAENASLTDALRIAVAALRAGSADTSQQDQPTLGVASLEVAVLDANPRRAFRRT
 TGSALQALLVDQESPO
 SDGESSG²
 48

DGSIADEPHFVVMGGT-----

FVVMGGTTEPIANALK-----

RGGIQFADTRGYAYDR-----

ANALKESYAENASLTD-----

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IFTEQAKPYEVELCVA-----

AGSADTSGGDQPTLGV-----

RERSELARKGIARAKS-----

YGETKRPELYRITYDG-----

RVGFAAAGKFNEFDNL-----

PELYRITYDGSIADEP-----

-----PRRAFRRITGSALQAL-----

RGYAYDRRDVTGRQLA-----

-----LRIAVAALRAGSAHTS-----

ALAYAGGVLFVAENPS-----

VYAQTILGTIFTEQAKP-----

RRDVTGRQLANVYAQ-----

PYEVELCVAEVAHYGE-----

ISELYDRVGFAAAGKF-----

-----GVASLEVAVLDANRPR-----

ISPEQAMRERSELARK-----

GVLFVAENPSRSIQLKI

GKFNEFDNLRRGGIQF

RKGIAKSVVALAYA

LLVDQESPQSDGESSG

AVLDANRPRRAFRRIT

TGSALQALLVDQESPO

SYAENASLTDALRIAV