

# ABCpred Prediction Server

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## INPUT INFORMATION

Sequence name	
Length of the sequence	577
Number of 16mers from the input sequence	562
Threshold setting (Default value is 0.5)	0.51

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## 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	LRTWQTAHVMKARRGA	379	0.94	
1	TTIIGGGTGPAGTK	158	0.94	
1	NPDIMTGVHRDLVVGP	106	0.94	
2	GGAIAWAAMGDANASI	460	0.92	
2	TGFVEDTIGAIAGRSI	260	0.92	
2	GGASGFKLHEDWGSTP	218	0.92	
3	PSIEVDPDTFTVRIDG	542	0.91	
4	GGTGPAGTKATTVTP	164	0.90	
5	ISMIGSDSQAMGRVGE	361	0.88	
5	GRSIHAYHTEGAGGGH	272	0.88	
6	PQSIDARLADRLAVNR	504	0.87	

6	SVHFVAPQSIDARLAD	498	0.87	
7	PSGSQAADNNNRVRRYI	399	0.86	
7	LVEVTEDRCGGPGLAG	29	0.86	
8	KVLRESMGQGRASRAD	53	0.85	
8	GALEGDPGSQAADNN	393	0.85	
8	AGGGHAPDIITVAAQP	283	0.85	
8	IVTAGTVDCHVHLICP	132	0.85	
9	MGQGRASRADGAPDTV	59	0.84	
9	TVRIDGQVWQPQPAAE	552	0.84	
9	AAAATAAATSVHFVAP	489	0.84	
9	EGTKATTVTPGEWHLA	170	0.84	
10	TGAVIIDYWGIKADI	76	0.83	
10	RGLAPVADVRAVGKTD	519	0.83	
10	KLHEDWGSTPAAIDTC	224	0.83	
11	AESRIRPSTIAAEDVL	340	0.82	
11	STEIISGNRRIVTAGT	122	0.82	
12	IVGIGKAGNPDIMTGV	98	0.80	
12	PGLAGDEAVFGGGKVL	40	0.80	
13	AVGKTDLPLNDALPSI	529	0.79	
13	VLPSSTNPTRPHTVNT	300	0.79	
13	YGPTTGDRIRLADTNL	13	0.79	
14	MDHLIGSVEVGKLADL	427	0.78	
14	CPAIAHGMDHLIGSVE	420	0.78	
15	IGIRDGRIVGIGKAGN	91	0.77	
15	TIGAIAGRISHAYHTE	266	0.77	
16	PTPQPVLPRLPMFGAAA	476	0.75	
16	AVFGGGKVLRESMGQG	47	0.75	
16	RMLESLDGWPVNFAALL	186	0.75	
17	SRADGAPDTVITGAVI	65	0.74	
17	SRERYAQLYGPTTGDR	5	0.74	
17	PTRPHTVNTLDEHLD	307	0.74	
17	PQIIIVEALAAGTTII	147	0.74	
18	WGIIKADIGIRDGRIV	84	0.73	
18	PAAIDTCLAVADVAGV	233	0.73	

18	FALLGKGNTVNPDALW	198	0.73
19	GDANASIPTPQPVLP	469	0.72
19	TVAAQPNVLPSSTNPT	293	0.72
19	RDLVVGPSTEIISGNR	115	0.72
20	VNTLDEHLDMLMVCHH	313	0.71
20	ALHSDTLNETGFVEDT	251	0.71
21	MLMVCHHLNPRIPEDL	322	0.67
22	VTPGEWHLARMLES LD	177	0.66
22	HVHLICPQIIVEALAA	141	0.66
23	STIAAEDVLHDMGAIS	347	0.65
24	GVRPHVVLKGGAIAWA	451	0.63
24	DSQAMGRVGEVVLRTW	367	0.63
24	NPRIPEDLAFAESRIR	330	0.63
25	WQPQPAEELPMTQRYF	560	0.62
26	WEPAFFGVRPHVVLKG	445	0.60
27	PRPMFGAAAATAAATS	483	0.58
28	VAGVQVALHSDTLNET	245	0.57
29	GKLADLVWEPAFFGV	437	0.55
30	NNRVRRYIAKYTICPA	407	0.52

## OVERLAP DISPLAY

MARLSRERYAQLYGPTTGDRIRLADTNLLVEVTEDRCGGPGLAGDEAVFGGGKVLRESMGQGRASRADGAPDTVITGAVIIDY  
 WGI IKADIGIRDGRIVGIGKAGNPDIMTVHRLVVPSTEIISGNRRIVTAGTVDCVHHLICPQIIVEALAAGTTIIGGGT  
 GPAEGTKATTVPGEWHLARMLES LDGWPVN FALLKGNTVNPDALWEQLRGGASGFKLHEDWGSTPAAIDTCLAVADVAGVQ  
 VALHSDTLNETGFVEDTIGAIAGRSIHAYTEGAGGGHAPIITVAAQPNLPSSTNPTRPHTVNTLDEHLDMLMVCHHLNPR  
 IPEDILAFAESRIRPSTIAEDVLHDMGAISMIGSDSQAMGRVGEVVLRTWQTAHVMKARRGALEGDPGSQAADNNRVRRYIA  
 KYTICPAIAHGMMDHLIGSVEVGKLADLVWEPAFFGVRPHVVLKGGAIAWAAMGDANASIPTPQPVLP prmfgaaaataaats  
 VHFVAPQSIDARLADRLAVNRGLAPVADVR AVGKTDLPLNDALPSIEVD PDTFTVRIDGQWQ P QPAAELPMTQRYFLF<sup>577</sup>

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LRTWQTAHVMKARRGA

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TTTIIIGGGTGP<sub>A</sub>E<sub>G</sub>TK

NPDIMTGVH<sub>R</sub>D<sub>L</sub>V<sub>V</sub>GP

GGAI<sub>A</sub>AMGDANASI

TGFVEDTIGAIAGRSI

GGASGFKLHEDWGSTP

PSIEVDPDTFTVRIDG

GGTGPAEGTKATTVTP

ISMIGSDSQAMGRVGE

GRSIHAYHTEGAGGGH

-PQSIDARLADRLAVNR

SVHFVAPQSIDARLAD

PSGSQAADNNRVRRYI

LVEVTEDRCGGPGLAG

KVLRESMGQGRASRAD

GALEGDPSGSQAADNN

AGGGHAPDIITVAAQP

IVTAGTVDCHVHLICP

MGQGRASRADGAPDTV

TVRIDGQVWQPQPAAE

AAAATAAATSVHFVAP

EGTKATTVTPGEWHLA

TGAVIIDYWGIIKADI

RGLAPADVRAVGKTD

KLHEDWGSTPAAIDTC

AESRIRPSTIAAEDVL

STEIIISGNRRIVTAGT

IVGIGKAGNPDIMTGV

PGLAGDEAVFGGGKVL

AVGKTDLPLNDALPSI

VLPSSTNPTRPHTVNT

YGPTTGDRIRLADTNL

MDHLIGSVEVGKLADL

CPAIAHGMDHLIGSVE

IGIRDGRIVGIGKAGN

TIGAIAGRSIHAYHTE

PTPQPVLPROMFGAAA

AVFGGGKVLRESMGQG

RMLESLDGWPVNFAALL

SRADGAPDTVITGAVI

SRERYAQLYGPTTGDR

PTRPHTVNTLDEHLD

PQIIVEALAAAGTTII

WGIIKADIGIRDGRIV

PAAIDTCLAVADVAGV

FALLGKGNTVNPDALW

GDANASIPTPQPVLPR

TVAAQPNVLPSSTNPT

RDLVVGPSTEIISGNR

VNTLDEHLDMLMVCHH

ALHSDTLN NETGFVEDT

MLMVCHHLPRIPEDL

VTPGEWHLARMLESLD

HVHLICPQIIIVEALAA

STIAAEDVLHDMGAIS

GVRPHVVLKGGAIAWA

DSQAMGRVGEVVLRTW

NPRIPEDLAFAESRIR

WQPQPAEELPMTQRYF-

WEPAFFGVRPHVVLKG

PRPMFGAAAATAAATS

VAGVQVALHSDTLNET

GKLADLVLWEPAFFGV

NNRVRYYIAKYTICPA