

# ABCpred Prediction Server

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## INPUT INFORMATION

Sequence name	
Length of the sequence	358
Number of 16mers from the input sequence	343
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	DGHAQQALRAGQGATT	230	0.94	
2	AGCSSNPLANFAPGYP	24	0.89	
3	HGTAFLAARGGYFVAD	122	0.88	
4	TVQQPNSLAFDETSDT	322	0.87	
5	IEPAQPAVSPPTSQDP	42	0.86	
5	TTMAADPLGRVLIADT	244	0.86	
5	YFVALLSSGHTARVNV	133	0.86	
6	ADGAVYTLAKNPNAVDP	172	0.85	
6	APRVIFLPGPAAALTS	104	0.85	
7	GYDLTTGIPVEKVRYP	306	0.84	
7	PGPAAALTSDDHGTAF	111	0.84	

8	GQTSVTTIGADGHAQQ	220	0.82	
9	LILRQAYPVRQAPYGL	272	0.80	
10	AAPASIMVFDDVHVAP	90	0.79	
10	GAVRPLSGHPRAALFD	59	0.79	
11	WVSQTASNTVIGYDLT	295	0.78	
12	NFAPGYPPTEPAQPA	33	0.76	
12	YGLAGSRELAWVSQTA	285	0.76	
13	SGHPRAALFDNGTRQL	65	0.75	
13	RVLIADTRGGQLLVYG	253	0.75	
13	VTQGNNTVVLDRGQTS	208	0.75	
14	AVSPPTSQDPAGAVRP	48	0.74	
14	LRAGQQGATTMAADPLG	237	0.74	
14	ASRTKIFARVDALVTQ	195	0.74	
14	DGKLVLGSADGAVYTL	164	0.74	
15	AVDPASGAATVASRTK	184	0.73	
15	TLAKNPAVDPASGAAT	178	0.73	
15	SGHTARVNADAAHTD	140	0.73	
16	AHTDFTAIARRSDGKL	152	0.72	
17	GIPVEKVRYPPTVQQPN	312	0.70	
18	SDTLYVVSGSGAGVQV	335	0.69	
19	TVVLDRGQTSVTTIGA	214	0.68	
20	TRQLVALRPGADSAAP	77	0.63	
21	MVFDDVHVAPRVIFLP	96	0.58	
21	FARVDALVTQGNNTVV	201	0.58	
22	VQRRFIGLLMLSVLVA	9	0.57	
23	GQLLVYGVDPPLILRQA	262	0.54	
24	VSGSGAGVQVIEHAAG	341	0.51	

## OVERLAP DISPLAY

LLTGNKPAVQRRFIGLLMLSVLVAGCSSNPLANFAPGYPPTEPAQPAVSPPTSQDPAGAVRPLSGHPRAALFDNGTRQLVAL  
RPGADSAAPASIMVFDDVHVAPRVIFLPGPAAALTSDDHGTAFLAARGGYFADLSSGHTARVNADAAHTDFTAIARRSDGK

LVLGSADGAVYTLAKNPAVDPASGAATVASRTKIFARVDALVTQGNTTVVLDRGQTSVTTIGADGHAQQALRAGQQGATTMAAD  
PLGRVLIADTRGGQLLVYGVDPPLILRQAYPVRQAPYGLAGSRELAWVSQTASNTVIGYDLTTGIPVEKVRYP  
TQQPNSLAFD  
ETSDTLYVVSGSGAGVQVIEHAAGTR<sup>358</sup>

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DGHAQQALRAGQQGATT

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AGCSSNPLANFAPGYP

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HGTAFIAARGGYFVAD

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TVQQPNSLAFDETSDT

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IEPAQPAVSPPTSQDP

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TTMAADPLGRVLIADT

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YFVADLSSGHTARVNV

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ADGAVYTLAKNPAVDP

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APRVIFLPGPAAALTS

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GYDLTTGIPVEKVRYP

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PGPAAALTSDDHGTAF

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GQTSVTTIGADGHAQQ

LILRQAYPVRQAPYGL

AAPASIMVFDDHVAP

GAVRPLSGHPRAALFD

WVSQTASNTVIGYDLT

NFAPGYPPTEPAQPA

YGLAGSRELAWVSQTA

SGHPRAALFDNGTRQL

RVLIADTRGGQLLVYG

VTQGNNTVVLDRGQTS

AVSPPTSQDPAGAVRP

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**LRAGQQGATTMAADPLG**  
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**ASRTKIFARVDALVTQ**  
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**DGKLVLGSADGAVYTL**  
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**AVDPASGAATVASRTK**  
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**TLAKNPAVDPASGAAT**  
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**SGHTARVNADAHTD**  
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**AHTDFTAIARRSDGKL**  
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**GIPVEKRYPTVQQPN**  
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**SDTLYVVSGSGAGVQV**  
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**TVVLDRGQTSVTTIGA**  
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**TRQLVALRPGADSAAP**  
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MVFDDVHVAPRVIFLP

FARVDALVTQGNNTVV

VQRFIGLLMLSVLVA

GQLLVYGVDPPLILRQA

VSGSGAGVQVIEHAAG