

# ABCpred Prediction Server

---

## INPUT INFORMATION

Sequence name	
Length of the sequence	644
Number of 16mers from the input sequence	629
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	PRDVGRTYEAVIRVNS	415	0.93	
2	TSILQRRVFRANRAE	172	0.92	
3	GEAGRHASDPVTIASP	584	0.91	
3	FAEEVEPIRLRNRTWP	49	0.91	
3	HTIVKPAGPPRVGQPS	17	0.91	
4	PVHERHPYGGDLVYTA	359	0.90	
4	VGEVIAPTPERPIIFN	235	0.90	
5	DRVIDRAPLWCAVDLR	65	0.87	
5	PIRLRNRTWPDRVIDR	55	0.87	
5	IDEIRRTVEYCNQLPV	345	0.87	
5	SRGVDPQIDFSNIDEI	333	0.87	

5	ADRIEGCLFGNGERTG	305	0.87	
6	GGEVSPKEMWDAFAEE	472	0.86	
6	SESPDAYTESFGAHTI	4	0.86	
6	KGLDAMKLDADAADCD	385	0.86	
6	RAEVQAIATDGARKCV	185	0.86	
7	ASPAQPGEAGRHASDP	597	0.85	
7	ASPAQPGEAGRHASDP	578	0.85	
7	GVAYIMKTDHGLSLPR	436	0.85	
7	AFSGSHQDAINKGLDA	374	0.85	
7	YSPESYTGTELEYAKQ	215	0.85	
7	GYKEIEVGFPSASQTD	106	0.85	
8	GRHASDPVTSKTVWGV	606	0.84	
8	GDDAQAAAYVEASVTI	562	0.84	
8	TVKINGVETEISGSGN	517	0.84	
8	TTSITATVKINGVETE	511	0.84	
8	EGTAGEGGEVSPKEMW	466	0.84	
8	PQRASSMPVNRYPFA	35	0.84	
9	AAAYVEASVTIASPAQP	568	0.83	
9	FVHALADVGFDAVAVLD	538	0.83	
9	TAVAAAELGFAAGADR	292	0.83	
10	RQHVDAADDDGGTTSI	499	0.82	
10	RPLERIRQHVDAADDD	493	0.82	
10	YPGTQWRFEYSPESYT	206	0.82	
11	DMLWQVPYLPIDPRDV	403	0.81	
11	SIEWMSRNLANRESVI	266	0.81	
11	LPATVEMTTPNVYADS	251	0.81	
11	TELEYAKQVCDVGEV	223	0.81	
11	RTFQACSGAPRAIVHF	153	0.81	
12	CLFGNGERTGNVCLVT	311	0.80	
12	SVILSLPHPHNDRGTAV	279	0.80	
12	TQCRPELIERTFQACS	144	0.80	
13	SGAPRAIVHFFYNSTSI	159	0.79	
13	PSASQTDFDFVREIIE	115	0.79	
14	PPRVGQPSWNPQRASS	25	0.78	

15	SGSGNGPLAAAFVHALA	528	0.77	
15	EIEQGAIPDDVTIQV	127	0.77	
16	DVTIQVLTQCRPELIE	137	0.76	
17	QALIDPMSARKRRMF	84	0.75	
17	APSITTASLRAVVSVA	624	0.75	
17	AEEYLAPVRPLERIRQ	485	0.75	
17	GGDLVYTAFIGSHQDA	367	0.75	
18	AVLDYYEHAMSAGDDA	550	0.74	
18	KQVCDVAVGEVIAPTPE	229	0.74	
19	DLLVRMGYKEIEVGFP	100	0.73	
20	APLWCAVDLRDGNQAL	71	0.72	
20	CLVTLGLNLFVSRGVDP	323	0.72	
20	ERPIIFNLPATVEMTT	244	0.72	
21	TSKTVWGVGIAPSITT	614	0.69	
21	YTESFGAHTIVKPAGP	10	0.69	
22	NSQSGKGGVAYIMKTD	429	0.68	
23	EAVIRVNSQSGKGGVA	423	0.66	
24	ATDGARKCVEQAAKYP	192	0.65	
25	ARKRRMFDLLVRMGYK	93	0.64	
26	EMWDAFAEEYLAPVRP	479	0.63	
27	VVFRANRAEVQAIATD	179	0.61	
28	SLPRRLQIEFSQVIQK	448	0.56	

## OVERLAP DISPLAY

VTTSESPDAYTESFGAHTIVKPAGPPRVGQPSWNPQRASSMPVNRYPFAEEVEPIRLRNRTWPDRVIDRAPLWCAVDLRDGN  
QALIDPMSARKRRMFDLLVRMGYKEIEVGFPASQTDVDFVREIIEQGAIPDDVTIQVLTQCRPELIERTFQACSGAPRAIV  
HFYNSTSIQRRVVFRANRAEVQAIATDGARKCVEQAAKYPGTQWRFEYSPESYTGTELEYAKQVCDVAVGEVIAPTPEPIIF  
NLPATVEMTTPNVYADSIWMSRNLNRESVILSLPHNDRGTAVAAAELGFAAGADRIEGCLFNGERTGNVCLVTLGLNLF  
SRGVDPQIDFSNIDEIRRTVEYCNQLPVHERHPYGGDLVYTAFIGSHQDAINKGLDAMKLDADAADCDDMLWQVPYLPIDP  
RDVGRTYEAVIRVNSQSGKGGVAYIMKTDHGLSLPRRLQIEFSQVIQKIAEGTAGEGGEVSPKEMWDAFAEEYLAPVRPLERI  
RQHVDAAADDGGTTSITATVKINGVETEISGSGNGPLAAAFVHALADVGFVAVLDYYEHAMSAGDDAQAAYVEASVTIASPA  
QPGEAGRHASDPVTIASPAQPGEAGRHASDPVTSKTVWGVGIAPSITTASLRAVVSVAVNRAAR<sup>644</sup>

PRDVGRTYEAVIRVNS

TSILQRRVFRANRAE

GEAGRHASDPVTIASP

FAEEVEPIRLRNRTWP

HTIVKPAGPPRVGQPS

PVHERHPYGGDLVYTA

VGEVIAPTPERPIIFN

DRVIDRAPLWCAVDLR

PIRLRNRTWPDRVIDR

IDEIRRTVEYCNQLPV

SRGVDPQIDFSNIDEI

ADRIEGCLFGNGERTG

GGEVSPKEMWDAFAEE

SESPDAYTESFGAHTI

KGLDAMKLDADAADC

RAEVQAIATDGARKCV

ASPAQGEAGRHASDP

ASPAQGEAGRHASDP

GVAYIMKTDHGLSLPR

AFSGSHQDAINKGLDA

YSPESYTGTELEYAKQ

-----  
-----  
-----  
-----  
**GYKEIEVGFPSASQTD**-----  
-----  
-----  
-----  
-----  
-----  
-----  
-----

-----  
-----  
-----  
-----  
-----  
-----  
-----  
-----  
**GRHASDPVTSKTVWGV**-----  
-----  
-----  
-----  
-----  
-----  
-----  
-----

-----  
-----  
-----  
-----  
**GDDAQAAAYPEASVTI**-----  
-----  
-----  
-----  
-----  
-----  
-----  
-----

-----  
-----  
-----  
-----  
**TVKINGVETEISGSGN**-----  
-----  
-----  
-----  
-----  
-----  
-----  
-----

-----  
-----  
-----  
-----  
**TTSITATVKINGVETE**-----  
-----  
-----  
-----  
-----  
-----  
-----  
-----

-----  
-----  
-----  
-----  
**EGTAGEGGEVSPKEMW**-----  
-----  
-----  
-----  
-----  
-----  
-----  
-----

-----  
-----  
-----  
-----  
**PQRASSMPVNRYPFA**-----  
-----  
-----  
-----  
-----  
-----  
-----  
-----





DMLWQVPYLPIDPRDV

SIEWMSRNLANRESVI

LPATVEMTTPNVYADS

TELEYAKQVCDVGEV

RTFQACSGAPRAIVHF

CLFGNGERTGNVCLVT

SVILSLHPHNDRGTAV

TQCRPELIERTFQACS

SGAPRAIVHFYNSTSI

PSASQTDFFVREIIE

PPRVGQPSWNPQRASS

SGSGNGPLAAFVHALA

EIIEQGAI PDDVTIQV

DVTIQVLTQCRPELIE

QALIDPMS PARKRRMF

APSITTASLRAVVS AV

AEEYLAPVRPLERIRQ

GGDLVYTA FSGSHQDA

AVLDYEHAMSAGDDA

KQVCD AVGEVIAPTPE

DLLVRMGYKEIEVGFP

APLWCAVDLIRDGNQAL

CLVTLGLNLFSRGVDP

ERPIIFNLPATVEMTT

TSKTVWGVGIAPSITT

YTESFGAHTIVKPAGP

NSQSGKGGVAYIMKTD

EAVIRVNSQSGKGGVA

ATDGARKCQEQAAYP

ARKRRMFDLLVRMGYK

EMWDAFAEEYLAPVRP

VVFRANRAEVQAIATD

SLPRRLQIEFSQVIQK