

ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	586
Number of 16mers from the input sequence	571
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	AGEADLGGTMRLGSYP	437	0.96	
1	DGVISTPDAPSIYDIP	245	0.96	
2	EGKIGAIAYARARGLP	373	0.93	
3	PVIATMPDQEEIVAGE	424	0.91	
3	VITEIGGTVGDIESQP	149	0.91	
4	PVEIPEIPEHTPNGSS	555	0.89	
4	NSAEFDPDTPDPVIAT	413	0.89	
4	AQPDADGNRPDVVITE	137	0.89	
4	KRRILAMAQPDADGNR	130	0.89	
4	YSTVIAKERRGEYLGD	102	0.89	
5	EHTPNGSSHRDGVGQP	563	0.88	

5	LILRCDRDVPEALKNK	220	0.88	
6	VEFVEYPPDRHPFVVG	505	0.86	
6	PYLNVDPGTMNPFQHG	49	0.86	
6	LGSYPAVLEPDSVVAQ	448	0.86	
6	CWVASDGCETTSGAAA	338	0.86	
6	RSIGITPDALILRCDR	211	0.86	
7	LHVTMQKLDPYLNVDP	40	0.85	
7	REELDAFVVRRLNLPF	265	0.85	
8	SGLRFSGTSPDGHLVE	491	0.84	
8	YQTTQVSEHRHRYEV	465	0.84	
8	ARSVGLTNANSAEFD	404	0.84	
9	CIVIEAARSVGLTNAN	398	0.83	
9	YVELSDAYLSVAEALR	310	0.83	
10	PGTMNPFQHGEVFT	55	0.82	
10	ERHRHRYEVNNAYRDK	472	0.82	
10	HITDEIKRRILAMAQP	124	0.82	
11	RDKIAESGLRFSGTSP	485	0.81	
11	IAYARARGLPVLGLCL	379	0.81	
12	DQEEIVAGEADLGGTM	431	0.80	
12	GGFGIRGIEGKIGAI	365	0.80	
12	FVVRRLNLPFRDVDWT	271	0.80	
13	PELKSRLPTRLPLFVA	525	0.79	
13	FVSGGVASSLGKGLTA	13	0.79	
14	ERFLDRNLPGSANVTT	83	0.78	
14	WTEWDDLLRRVHEPHE	285	0.78	
14	TQHSVAALRSIGITPD	203	0.78	
14	LVPYLAPSGELKTKPT	188	0.78	
14	KERRGEYLGDTVQVIP	108	0.78	
15	PFVVGTAHPELKSRLP	516	0.76	
16	SGAAAALGDVHGVLIP	349	0.74	
16	EALRAGGFKHRAKVEI	322	0.74	
16	SSLGQLLTARGLHVTM	29	0.74	
16	VGDIESQPFLEAARQV	157	0.74	
17	RVHEPHETVRIALVGK	294	0.73	

18	FQHGEVFTEDGAETD	61	0.72	
18	GELKTKPTQHSVAALR	196	0.72	
19	SSHRDGVGQPLPEPAS	569	0.71	
19	PQTATKHLFVSGGVAS	5	0.71	
19	PEALKNKIALMCDVDI	229	0.71	
19	AARQVRHYLGREDVFF	168	0.71	
20	YEVNNAYRDKIAESGL	478	0.70	
21	SIYDIPKVLHREELDA	255	0.69	
22	VAFVGAAIDYKAGELL	539	0.68	
23	VTEDGAETDLDVGHYE	68	0.67	
24	YKAGELLPVEIPEIPE	548	0.65	
25	ASSLGKGLTASSLGQL	19	0.64	
26	HYLGREDVFFLHVSLV	174	0.60	

OVERLAP DISPLAY

MRKHPQTATKHLFVSGGVASSLGKGLTASSLGQLLTARGLHVTMQKLDPYLNVDPGTMNPFQHGEVFTEDGAETDLDVGHYE
RFLDRNLPGSANVTTGQVYSTVIAKERRGEYLGDTVQVIPHITDEIKRRILAMAQPDADGNRPDVVITEIGGTVDIESQPFL
EAARQVRHYLGREDVFFLHVSLVLPYLAPSGELKTKPTQHSVAALRSIGITPDALILRCRDVPEALKNKIALMCDVDIDGVIS
TPDAPSIYDIPKVLHREELDAFVVRRLNLPFRDVDWTEWDDLRRVHEPHETVRIALVGKYVELSDAYLSVAEALRAGGFKHR
AKVEICWVASDGCETTSGAAAALGDVHGVLI PGGFGIRGIEGKIGAIAYARARGLPVLGLCLGLQCIVIEAARSVGLTNANSA
EFDPDTPDPVIAATMPDQEEIVAGEADLGGTMRLGSPAVLEPDSVVAQAYQTTQVSERHRHRYEVNNAYRDKIAESGLRFSGT
SPDGHLVEFVEYPPDRHPFVVGTAHPELKSRRPTRPHPLFAFVGAAIDYKAGELLPVEIPEIPEHTPNGSSHRDGVGQPLPE
PASRG⁵⁸⁶

AGEADLGGTMRLGSPY-----

DGVISTPDAPSIYDIP-----

EGKIGAIAYARARGLP

PVIATMPDQEEIVAGE

VITEIGGTVGDIESQP

PVEIPEIPEHTPNGSS

NSAEFDPDTPDPVIAT

AQPDADGNRPDVVITE

KRRILAMAQPDADGNR

YSTVIAKERRGEYLGD

EHTPNGSSHRDGVGQP

LILRCDRDVPEALKNK

VEFVEYPPDRHPFVVG

PYLNVDPGTMNPFQHG

LGSYPAVLEPDSVVAQ

CWVSDGCETTSGAAA

RSIGITPDALILRCDR

LHVTMQKLDPYLNVDP

REELDAFVRRRLNLPF

SGLRFSGTSPDGHLVE

YQTTQVSEHRHRYEV

ARSVGLTNANSAEFD

CIVIEAARSVGLTNAN

YVELSDAYLSVAEALR

PGTMNPFQHGVEFVTE

ERHRHRYEVNNAYRDK

HITDEIKRRILAMAQP

RDKIAESGLRFSGTSP

IAYARARGLPVLGLCL

DQEEIVAGEADLGGTM

GGFGIRGIEGKIGAIA

FVVRRLNLPFRDVDWT

PELKSRPTRPHPLFVA-----

FVSGGVASSLGKGLTA-----

ERFLDRNLPGSANVTT-----

WTEWDDLLRRVHEPHE-----

TQHSVAALRSIGITPD-----

LVPYLAPSGELKTKPT-----

KERRGEYLGDTVQVIP-----

PFVVGTQAHPELKSRP

SGAAAAALGDVHGVLIIP

EALRAGGFKHRAKVEI

SSLGQLLTARGLHVTM

VGDIESQPFLEAARQV

RVHEPHETVRIALVGK

FQHGEVFTEDGAETD

GELKTKPTQHSVAALR

SSHRDGVGQPLPEPAS--

PQTATKHLFVSGGVAS--

PEALKNKIALMCDVDI--

AARQVRHYLGREDVFF--

YEVNNAYRDKIAESGL--

SIYDIPKVLHREELDA--

VAFVGAALDYKAGELL-----

VTEDGAETDLLDVGHYE-----

YKAGELLPVEIPEIPE-----

ASSLGKGLTASSLGQL-----

HYLGREDVFFLHVSIV-----

