

ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	624
Number of 16mers from the input sequence	609
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	TNGSQIPRECDVLYT	387	0.94	
2	AEEGDETVRPHYADHLI	563	0.93	
3	AVTIVIAEEGDETVRP	557	0.91	
4	HGRPTDRNAHPRDAA	80	0.90	
4	PVEVELASEFRYRDPV	333	0.90	
4	AARRSTPLVLGIGDNE	179	0.90	
5	SGETADTLEAVRHAKA	361	0.89	
5	YVVVMDALRRMEYRGY	14	0.89	
5	RELETAGVEFASDTDT	114	0.89	
6	AHLVARAYRHGETADD	133	0.87	
7	DGYRISDFDGNDGLQA	225	0.86	
8	LVLGIGDNEMFVGSDV	186	0.85	
9	RARGYDVKPRNLAKS	605	0.84	

9	GPEIGVASTKTFLAQI	405	0.84	
9	GGTLTVRRRAGRLANL	39	0.84	
9	AVVITADGYRISDFDG	219	0.84	
9	AAFIEHTREAVELGQD	202	0.84	
9	YRHGETADDFVGSVLA	140	0.84	
10	AVLYTRAGPEIGVAST	398	0.83	
10	IEHWTRLPVEVELASE	326	0.83	
11	AEMPSTALSGTTGLGH	59	0.81	
11	CGTAYHSGLLAKYAIE	312	0.81	
11	FMLKEIAEQPAAVADT	264	0.81	
12	SPKGSATLHAKLLSNI	534	0.80	
12	TREAVELGQDQAVVIT	208	0.80	
13	PLQVFAASVARARGYD	595	0.79	
13	ADHLIEIPAVSTLLQP	574	0.79	
13	CGIVGYVGRRPAYVVV	2	0.79	
14	HPhRDAAGKIAVVHNG	89	0.78	
14	VIVVMPSPKGSATLHA	528	0.78	
14	HVGYPVALEGALKLKE	485	0.78	
14	VIAATGPVAELAHRFA	459	0.78	
14	AEKGGYEFMLKEIAE	256	0.78	
15	ALSGTTGLGHTRWATH	65	0.77	
15	ELEAMPDLVARVIAAT	448	0.77	
15	ARGTKYPDEVEREYHE	433	0.77	
16	LSNIREIQTRGAVTIV	546	0.76	
16	RIVLDEQRLSDQELRE	288	0.76	
16	ALRRMEYRGYDSSGIA	20	0.76	
16	RLEGHFTLVFANADDP	159	0.76	
17	DFDGNLQAGRDFRP	231	0.75	
18	HGPIALIEDGLPVIVV	516	0.73	
18	ELAYMHAEGFAAGELK	500	0.73	
19	AQIAANYLLGLALAQA	418	0.71	
19	PFHIDWDLAAEKGGY	246	0.71	
19	LQAGRDFRPFHIDWDL	238	0.71	
20	DSSGIALVDGGTLTVR	30	0.70	
21	ANLEEAVAEMPSTALS	52	0.69	
21	EFASDTDTEVA AHLVA	122	0.69	
22	EGFAAGELKHGPIALI	507	0.68	

22	QELREIDKVFVACGT	299	0.68	
23	AKEQKAKVLAICNTNG	374	0.67	
23	EFRYRDPVLDRLSTLVV	341	0.67	
24	LEAVRHAKAQKAKVLA	368	0.66	
25	VGSVLAVLRRLEGHFT	150	0.65	
26	HRFAQSSTVFLGRHV	471	0.63	
27	VSTLLQPLLSTIPLQV	583	0.60	
27	ADTLLGHFVGGRIVLD	277	0.60	
28	GIIENFAVLRRELETA	104	0.59	
29	PVAELAHRFAQSSTVL	465	0.52	
30	ALEGALKKELAYMHA	491	0.51	

OVERLAP DISPLAY

VCGIVGYVGRRPAYVVMDALRRMEYRGYDSSGIALVDGGTLTVRRRAGRLANLEEEVAEMPSTALS GTTGLGHTRWATHGRP
TDRNAHPHRDAAGKIAVVHNGI IENFAVLRRELETAGVEFASD TDTEVA AHLVARAYRHGETADDFVGSVLAVLRRLEGHFTL
VFANADDPGTLVAARRSTPLVLGIGDNEMFVGS DVAAFIEHTREAVELGQDQAVVITADGYRISDFD GNDGLQAGRDFRPFHI
DWDLAAAEEKGGYEFMLKEIAEQPAAVADTLLGHFVGGRIVLD EQRLSDQELREIDKVFVACGTAYHSGLLAKYAIEHWTRL
PVEVELASEFRYRDPVLDRLSTLVVAISQSGETADTLEAVRHAKAQKAKVLAICNTNGSQIPRECDAVLYTRAGPEIGVASTKT
FLAQIAANYLLGLALA QARGTKYPDEVEREYHELEAMPDLVARVIAATGPVAELAHRFAQSSTVFLGRHVGY PVALEGALKL
KELAYMHAEGFAAGELKHGPIALIEDGLPVIVVMPSPKGSATLHAKLLSNIREIQTRGAVTIVIAEEGDETVRPPYADHLIEIP
AVSTLLQPLLSTIPLQVFAASVARARGYDVKPRNLAKSVTVE⁶²⁴

TNGSQIPRECDAVLYT

AEEGDETVRPPYADHLI

AVTIVIAEEGDETVRP

HGRPTDRNAHPHRDAA

PVEVELASEFRYRDPV

AARRSTPLVLGIGDNE

SGETADTLEAVRHAKA

YVVVMDALRRMEYRGY

RELETAGVEFASDTDT

AHLVARAYRHGETADD

DGYRISDFDGNGLQA

LVLGIGDNEMFVGS DV

RARGYDVKPRNLAKS

GPEIGVASTKTFLAQI

GGTLTVRRRAGRLANL

AVVITADGYRISDFDG

AAFIEHTREAVELGQD

YRHGETADDFVGSVLA

AVLYTRAGPEIGVAST

IEHWTRLPEVELASE

AEMPSTALSGTTGLGH

CGTAYHSGLLAKYAIE

FMLKEIAEQPAAVADT

SPKGSATLHAKLLSNI

TREAVELGQDQAVVIT

PLQVFAASVARARGYD

ADHLIEIPAVSTLLQP

CGIVGYVGRRPAYVVV

HPHRDAAGKIAVVHNG

VIVVMPSPKGSATLHA

HVGYPVALEGALKLKE

VIAATGPVAELAHRFA

AEKGGYEYFMLKEIAE

ALSGTTGLGHTRWATH

ELEAMPDLVARVIAAT

ARGTKYPDEVEREYHE

LSNIREIQTRGAVTIV

RIVLDEQRLSDQELRE

ALRRMEYRGYDSSGIA

RLEGHFTLVFANADDP

DFDGNDGLQAGRDFRP

HGPIALIEDGLPVIVV

ELAYMHAEGFAAGELK

AQIAANYLLGLALAQA

PFHIDWDLAAAEEKGGY

LQAGRDFRPFHIDWDL

DSSGIALVDGGTLTVR

ANLEEVAEMPSTALS

EFASDTDTEVAAHLVA

EGFAAGELKHGPIALI

QELREIDKVFVVACGT

AKEQKAKVLAICNTNG

EFRYRDPVLDLDRSTLVV

LEAVRHAKAQKAKVLA

VGSVLAVLRRLEGHFT

