

ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	578
Number of 16mers from the input sequence	563
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	VERIETRLDMSIPAPQ	376	0.93	
2	AVRSMWPTVRDKVRLR	428	0.92	
3	ESVIDGGHDPRRFATD	269	0.91	
4	AGRINHAYLFSGPRGC	31	0.90	
5	AEVVQAGLGEMRGATA	333	0.89	
5	VALIDDAVDALAACDA	246	0.89	
6	PFRLLPRTMRALLAR	173	0.88	
7	LNCAQGPTANPCGVCE	59	0.87	
7	DAPEDALDRMREQAAR	308	0.87	
7	HVTAPLSVALDAGRIN	20	0.87	
7	LPTIRSRTTHHYPFRL	162	0.87	

8	VVELDAASHGGVDDTR	89	0.86	
8	AGRGDPSPRRDPEEVA	547	0.86	
8	PAAAASPVGGGANVAT	507	0.86	
8	RMREQAARIGRATLTR	316	0.86	
8	LIFIFATTEPEKVLPT	149	0.86	
9	RLRSRTTEVMLAGATV	441	0.84	
9	AGAADTHVTYTRALGL	225	0.84	
9	YPLVIRAGGGSPRDTL	202	0.84	
10	QSVPPDAASRGVVDAP	296	0.83	
11	GKTSSARILARSLNCA	47	0.82	
12	PRPVLAPTPASSEPTV	411	0.81	
12	EPKHQPAREPRVLAP	402	0.81	
13	PVGGGANVATAKAVNP	513	0.80	
14	AVPRPSAAAEPKHQP	392	0.79	
14	RICEQEGVVVDDAVYP	188	0.79	
15	WRVRCETGEPAAAASP	498	0.78	
15	ARIGRATLTRYAEVVQ	322	0.78	
16	PCGVCESECVSLAPNAP	69	0.77	
16	QRDEEEHMLAEAGRGD	536	0.77	
16	EVMLAGATVRALEDNT	448	0.77	
17	LAACDAAALFGAIESV	256	0.76	
18	SCVSLAPNAPGSIDVV	75	0.75	
18	HESAPLARRLSEQRNA	468	0.75	
18	RVFIVDEAHMVTTAGF	120	0.75	
19	LGEMRGATAPRLLLEV	340	0.74	
19	RALGLLGVTDVALIDD	236	0.74	
19	GVVVDDAVYPLVIRAG	194	0.74	
19	EAHMTTAGFNALLKI	126	0.74	
19	DTRELRDRAFYPVQS	102	0.74	
20	SGPRGCGKTSSARILA	41	0.72	
20	ALFGAIESVIDGGHDP	263	0.72	
20	DRAFYPVQSRVRFI	108	0.72	
21	LKIVEEPPEHLIFIFA	139	0.69	
22	TPASSEPTVA AVRSMW	418	0.68	

23	KAVNPAPTANSTQRDE	524	0.66	
23	ASDAESALLQRVERIE	365	0.66	
23	AGGGSPRDTLSVLDQL	208	0.66	
24	RPASFAEVVGQEHVTA	8	0.64	
24	ALYRKYPASFAEVVG	2	0.64	
25	PRRFATDLLERFRDLI	278	0.59	
26	VALELLQNELGARRID	561	0.58	
26	AEALKDALGVNWRVRC	487	0.58	
26	SEQRNADVLAELKDA	478	0.58	
26	TVRALEDNTLVLTHES	455	0.58	
26	EVVCARLLLPSASDAE	354	0.58	
27	PRRDPEEVALELLQNE	554	0.55	
28	TLSVLDQLLAGAADTH	216	0.53	

OVERLAP DISPLAY

MALYRKYPASFAEVVGQEHVTAPLSVALDAGRINHAYLFSGPRGCGKTSSARILARSLNCAQGPTANPCGVCESECVSLAPNA
PGSIDVVELDAASHGGVDDTRELDRDFYAPVQSRYSRVFIVDEAHMVTTAGFNALLKIVEEPPEHLIFIFATTEPEKVLPTIR
SRTHHYPFRLLPRTMRALLARICEQEGVVVDDAVYPLVIRAGGGSPRDTLSVLDQLLAGAADTHVYTRALGLLGVTDVALI
DDAVDALAACDAAALFGAIESVIDGGHDPRRFATDLLERFRDLIVLQSVDAASRGVVDAPEDALDRMREQAARIGRATLTRY
AEVVQAGLGEMRGATAPRLLLEVVVCARLLLPSASDAESALLQRVERIETRLDMSIPAPQAVPRPSAAAAEPKHQPAREPRPVL
APTPASSEPTVAAVRSMWPTVRDKVRLRSRTTEVMLAGATVRALEDNTLVLTHESAPLARRLSEQRNADVLAELKDALGVNW
RVRCEGTGEPAAAAASVGGGANVATAKAVNPAPTANSTQRDEEHMLAEAGRGDPSRRDPEEVALELLQNELGARRIDNA⁵⁷⁸

VERIETRLDMSIPAPQ-----

AVRSMWPTVRDKVRLR-----

ESVIDGGHDPRRFATD

AGRINHAYLFSGPRGC

AEVVQAGLGEMRGATA

VALIDDAVDALAACDA

PFRLLPRTMRALLAR

LNCAQGPTANPCGVCE

DAPEDALDRMREQAAR

HVTAPLSVALDAGRIN

LPTIRSRTHHYPFRLL

VVELDAASHGGVDDTR

AGRGDPSPRRDPEEVA

PAAAAAPVGGGANVAT

RMREQAARIGRATLTR

LIFIFATTEPEKVLPT

RLRSRTTEVMLAGATV

AGAADTHVTYTRALGL

YPLVIRAGGGSPRDTL

QSVFDAASRGVVDAPF

GKTSSARILARSLNCA

PRPVLAPTPASSEPTV

EPKHQPAREPRPVLAP

PVGGGANVATAKAVNP

AVPRPSAAAAEPKHQP

RICEQEGVVVDDAVYP

WRVRCETGEPAAAASP

ARIGRATLTRYAEVVQ

PCGVCEscvslapnap

QRDEEEHMLAEAGRGD

EVMLAGATVRALEDNT

LAACDAAALFGAIESV

SCVSLAPNAPGSIDVV

HESAPLARRLSEQRNA

RVFIVDEAHMVTTAGF

LGEMRGATAPRLLLEV

RALGLLGVTDVALIDD

GVVDDAVYPLVIRAG

EAHMVTTAGFNALLKI

DTRELDRAFYAPVQS

SGPRGCGKTSSARILA

ALFGAIESVIDGGHDP

DRAFYAPVQSRVRFI

LKIVEEPPEHLIFIFA

TPASSEPTVAAVRSMW

KAVNPAPTANSTQRDE

ASDAESALLQRVERIE

AGGGSPRDTLSVLDQL

RPASFAEVVGQEHVTA

ALYRKYPASFAEVVG

PRRFATDLLERFRDLI

VALELLQNELGARRID

AEALKDALGVNWRVRC

SEQRNADVLAELKDA

TVRALEDNTLVLTHER

EVV CARLLLPSASDAE

PRRDPEEVALELLQNE

TL SVLDQLLAGAADTH

