

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	PASIGFPPYHPPMRTF	140	0.94	
2	YEGIDEETVRRIGHLP	100	0.91	
3	IQEIRTTIYDLHGASQ	436	0.88	
4	DGLVEAMLVVTAGLDL	49	0.86	
4	GLLIEDPKPLRLDDVS	122	0.86	
5	IETVGSAVASIVGRTI	273	0.85	
6	GGEFTLASVPGASGTV	554	0.84	
6	DRDRIARDLHDHVIQR	386	0.84	
7	VVTAGLDLEATLRAIV	57	0.83	
7	TGSGLTNLRQRAEQAG	539	0.83	
7	ESFGTLYLTDKTNGQP	165	0.83	

8	HGASQGITRLRQRIDA	447	0.82	
8	DGAAMRPLRHTLSQLR	11	0.82	
9	PGASGTVLRWSAPLSQ	563	0.81	
10	QSWIEATRDIA TELLS	213	0.80	
11	NGRGLPDEFTGSGLTN	530	0.79	
11	DRVDLEGLDELADAGP	308	0.79	
11	PVRVRDESEFGTLYLTD	159	0.79	
12	DSGLRTSVQFVGPLSV	469	0.78	
12	WQLATSQRMRRELDVL	369	0.78	
13	TVRVKVDDDLCEVTD	514	0.77	
13	RQRIDAAVAQFADSGL	457	0.77	
14	DDLCEVTDNGRGLPD	521	0.76	
14	SIVGRTIPVAGAVLRE	282	0.76	
14	AALVAVPVDEDMPAAD	251	0.76	
15	VREAVSNAVRHAKAST	497	0.74	
15	ALQGAVPHERNPEVQQ	408	0.74	
15	VLSQGGPGAFTDEQLE	341	0.74	
15	PMRTFLGVPVRVRDES	151	0.74	
16	VEQIVEGRDRDLGLVE	38	0.73	
17	LSVVDALADQAEAVV	482	0.72	
17	MRELDVLTDRDRIARD	378	0.72	
18	TSLVDARYGAMEVHDR	76	0.71	
18	QRAEQAGGEFTLASVP	548	0.71	
19	AIVHSATSLVDARYGA	70	0.70	
19	AVAQFADSGLRTSVQF	463	0.70	
19	GIPRRVDRVDLEGLDE	302	0.70	
19	LSGTEPATVFRLVAAE	227	0.70	
20	IQRLFAIGLALQGAVP	399	0.69	
20	LVEVQDRVEQIVEGRD	31	0.69	
20	AVLREVFVNGIPRRVD	293	0.69	
20	AAEALKLTAADAALVA	240	0.69	
21	RDIA TELLSGTEPATV	220	0.68	
22	PEVQQRLSDVVDDLQD	419	0.67	
23	GAMEVHDRQHRVLHFV	84	0.66	

23	LADQAEAVVREAVSNA	489	0.66	
24	AFTDEQLEMMAAFADQ	349	0.63	
25	DVVDDLQDVIQEIRTT	427	0.62	
26	TVRRIGHLPKGLGVIG	107	0.60	
27	DEMPAADVGELLVIE	259	0.59	
27	HTLSQLRLHELLVEVQ	20	0.59	
27	YLTDKTNGQPFSDDE	171	0.59	
28	PLRARGTVAGVVVLS	328	0.58	
29	AFADQAALAWQLATSQ	360	0.57	
29	ADAGPALLPLRARGT	319	0.57	
29	LVQALAAAAGIAVANA	188	0.57	
29	NGQPFSDDEVLVQAL	177	0.57	
30	AAGIAVANARLYQQAK	195	0.54	
31	PLRLDDVSAHPASIGF	130	0.51	

OVERLAP DISPLAY

MTTGGLVDENDGAAMRPLRHTLSQLRLHELLVEVQDRVEQIVEGRDRLDGLVEAMLVVTAGLDLEATLRRAIVHSATSLVDARY
GAMEVHDRQHRVLHFVYEGIDEETVRRIGHLPKGLGVIGLLIEDPKPLRLDDVSAHPASIGFPPYHPPMRTFLGVPVRVRDES
FGTLYLTDKTNGQPFSDDEVLVQALAAAAGIAVANARLYQQAKARQSWIEATRDIAATELLSGTEPATVFRLVAAEALKLTAA
DAALVAVPVDEDMPAADVGELLVIE TVGSAVASIVGRTIPVAGAVLREVFVNGIPRRVDRVDLEGLDELADAGPALLPLRAR
GTVAGVVVLSQGGPGAFTDEQLEMMAAFADQAALAWQLATSQRMRRELDVLTDRDRIARDLHDHVIQRLFAIGLALQGAVPH
ERNPEVQQRLSDVVDDLQDVIQEIRTTIYDLHGASQGITRLRQRIDAAVAQFADSGLRITSVQFVGPLSVVDSALADQAEAVR
EAVSNAVRHAKASTLTVRVKVVDDDLCEVTDNGRGLPDEF'TGSGLTNLRQRAEQAGGEFTLASVPGASGTVLRWSAPLSQ⁵⁷⁸

PASIGFPPYHPPMRTF-----

YEGIDEETVRRIGHL-----

IQEIRTTIYDLHGASQ

DGLVEAMLVVTAGLDL

GLLIEDPKPLRLDDVS

IETVGSAVASIVGRTI

GGEFTLASVPGASGTV

DRDRIARDLHDHVIQR

VVTAGLDLEATLRAIV

TGSGLTNLRQRAEQAG

ESFGTLYLTDKTNQQP

HGASQGITRLRQRIDA

DGAAMRPLRHTLSQLR

PGASGTVLRWSAPLSQ

QSWIEATRDIAPELLS

NGRGLPDEFTGSGLTN

DRVDLEGLDELADAGP

PVRVRDESEFGTLYLTD

DSGLRTSVQFVGPLSV

WQLATSQRRMRELDVL

TVRVKVVDDDLCEVTD

RQRIDAAVAQFADSGL

DDLCIEVTDNNGRGLPD

SIVGRTIPVAGAVLRE

AALVAVPVDEEDMPAAD

VREAVSNAVRHAKAST

ALQGAVPHERNPEVQQ

VLSQGGPGAFTDEQLE

PMRTFLGVPVRVRDES

VEQIVEGRDRLDGLVE

LSVDSALADQAEAVV

MRELDVLTDRDRIARD

TSLVDARYGAMEVHDR

QRAEQAGGEFTLASVP

AIVHSATSLVDARYGA

AVAQFADSGLRTSVQF

GIPRRVDRVDLEGLDE

LSGTEPATVFRLVAAE

IQRLF AIGLALQGAVP

LVEVQDRVEQIVEGRD

AVLREVFVNGIPRRVD

AAEALKLTAADAALVA

RDIAPELLSGTEPATV

PEVQQRLSDVVDDLQD

GAMEVHDRQHRVLHFV

LADQAEAVVREAVSNA

AFTDEQLEMMAAFADQ

DVVDDLQDVIQEIRTT

TVRRIGHLPKGLGVIG

DEMPAADVGELLVIE

HTLSQLRLHELLVEVQ

YLTDKTNGQPFSDDE

PLRARGTVAGVVVLS

AFADQAALAWQLATSQ

ADAGPALLLPLRARGT

LVQALAAAAGIAVANA-----

NGQPFSDDEVLVQAL-----

AAGIAVANARLYQQA-----

PLRLDDVSAHPASIGF-----

