ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	582
Number of 16mers from the input sequence	567
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	SGAIWRPVDPAPRLLP	186	0.97	
2	ALASNGPSLIDCELDP	541	0.92	
2	NRPIVAPLTGDIGSVM	317	0.92	
2	IRTATSGRPGGVYLDI	156	0.92	
3	ARNIIDMHLPRHRLDS	408	0.91	
3	IQVDIEASEFDSNRPI	305	0.91	
4	SAAWTGELADRKARNS	347	0.89	
4	YGVVGIPITDLARAAQ	32	0.89	
5	GYHVSTPTELESALTD	525	0.88	
6	PEAIDRALDVLAQAQR	203	0.87	
7	QASGIRYIGFRHEASA	47	0.86	

7	TGIPFLPMSMAKGLLP	243	0.86	
8	PLTGDIGSVMSALLEA	323	0.85	
9	PSLIDCELDPADGVES	547	0.84	
9	EATIFRSAAPVWRHDP	488	0.84	
10	AAAGFLTARPGVCLTT	67	0.83	
10	GFSGMEFETICRYRLP	457	0.83	
11	GVMGIGMGYAIAAAVE	427	0.82	
11	GESPQWSADAKFIQVD	293	0.82	
11	IGQVQDIGRGVARAIR	142	0.82	
12	RRLADDHHPMRFYNAL	367	0.81	
12	PMSMAKGLLPDSHPQS	249	0.81	
13	GVCLTTSGPGFLNGLP	77	0.80	
13	PADGVESGHLAKLNTT	556	0.80	
13	AVETGRPVVAIEGDSA	440	0.80	
13	QSAAAARSLAMARADV	263	0.80	
14	LGAIRSVLQRNPDVYV	382	0.79	
14	MARADVVLLVGARLNW	273	0.79	
14	PRLLPAPEAIDRALDV	197	0.79	
14	GQAVEASAASGAIWRP	177	0.79	
14	CHLVVDALKANDVDTI	16	0.79	
14	PMIQISGSSSRPMVDL	103	0.79	
15	HELIAEAFGGKGYHVS	514	0.78	
15	VILNNGGVYRGDEATI	476	0.78	
15	RGDYQDLDQLNAARPF	120	0.78	
16	TELESALTDALASNGP	532	0.77	
16	AAPVWRHDPAPTVLNA	495	0.77	
16	FETICRYRLPVTVVIL	463	0.77	
17	PGGVYLDIPGDVLGQA	164	0.76	
18	VVAIEGDSAFGFSGME	447	0.73	
18	RKARNSAKMRRRLADD	357	0.73	
19	RHRLDSGTWGVMGIGM	418	0.72	
20	GLLPDSHPQSAAAARS	255	0.71	
20	AAYAQADNVIREFVEH	227	0.71	
21	GFLNGLPALANATTNC	86	0.70	

21	ASPCTVLTDGCHLVVD	6	0.70	
21	LQRNPDVYVVNEGANA	389	0.70	
22	ASEFDSNRPIVAPLTG	311	0.69	
22	NDVDTIYGVVGIPITD	26	0.69	
23	RHEASAGNAAAAAGFL	57	0.67	
24	PTVLNAHARHELIAEA	505	0.66	
24	YVVNEGANALDLARNI	396	0.66	
24	RPFVKAAYRIGQVQDI	133	0.66	
25	VGARLNWLLGNGESPQ	282	0.64	
26	EAAADRSSVASAAWTG	337	0.62	
26	GSVMSALLEAAADRSS	329	0.62	
27	ANATTNCFPMIQISGS	95	0.60	
27	GHLAKLNTTSAATPAI	563	0.60	
28	LDQLNAARPFVKAAYR	126	0.58	
29	PLLVLSKGAAYAQADN	219	0.56	
30	TDLARAAQASGIRYIG	40	0.51	

OVERLAP DISPLAY

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MTTRSASPCTVLTDGCHLVVDALKANDVDTIYGVVGIPITDLARAAQASGIRYIGFRHEASAGNAAAAAGFLTARPGVCLTTS
GPGFLNGLPALANATTNCFPMIQISGSSSRPMVDLQRGDYQDLDQLNAARPFVKAAYRIGQVQDIGRGVARAIRTATSGRPGG
VYLDIPGDVLGQAVEASAASGAIWRPVDPAPRLLPAPEAIDRALDVLAQAQRPLLVLSKGAAYAQADNVIREFVEHTGIPFLP
MSMAKGLLPDSHPQSAAAARSLAMARADVVLLVGARLNWLLGNGESPQWSADAKFIQVDIEASEFDSNRPIVAPLTGDIGSVM
SALLEAAADRSSVASAAWTGELADRKARNSAKMRRRLADDHHPMRFYNALGAIRSVLQRNPDVYVVNEGANALDLARNIIDMH
LPRHRLDSGTWGVMGIGMGYAIAAAVETGRPVVAIEGDSAFGFSGMEFETICRYRLPVTVVILNNGGVYRGDEATIFRSAAPV
WRHDPAPTVLNAHARHELIAEAFGGKGYHVSTPTELESALTDALASNGPSLIDCELDPADGVESGHLAKLNTTSAATPAISGD
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