

ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	934
Number of 16mers from the input sequence	919
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	GGEADDAERRLPHLTP	480	0.94	
1	SDPDAAPPTFSARLTA	230	0.94	
2	YARRPYPPFMTSTLQQ	299	0.93	
3	AGDTGEPTPQRANLSD	671	0.91	
3	PAKYKSQPWARLGVNV	60	0.91	
3	ARTQARQLYGDEYVAP	358	0.91	
4	KPMVIKDGRFGPYVTD	865	0.90	
4	LDEIAAGNERRTNWLN	590	0.90	
4	AERRLPHLTPGQRDLI	486	0.90	
4	QQEASRKLRFSAERTM	313	0.90	
5	GRRVATGRDFDSLGLTL	248	0.89	

6	RGPAKRPARKAARKVP	911	0.88	
6	ALKIYAEPKRRGRQSA	834	0.88	
6	HEIVAREGRFGPYVTE	719	0.88	
6	FYFGGDHGVDPDSVARS	607	0.88	
6	YSSIIKTIQDRGYVHK	537	0.88	
6	RRELDGPNIDDFRLYE	406	0.88	
6	SGYIVESSRGHIRDLP	38	0.88	
6	NGYITYMRTDSTTLSE	337	0.88	
7	DGHATNPPARYTEASL	507	0.87	
7	GMTLSLRITGMSGHQE	437	0.87	
7	ATRIIVARERDRMAFR	199	0.87	
7	YGYEVSPVLWKKVAPK	174	0.87	
8	RQSASAPPLRELGTDP	846	0.86	
9	RELGTDPASGKPMVIK	855	0.85	
9	QLYGDEYVAPAPRQYT	364	0.85	
9	LVIVESPTKARKLASV	20	0.85	
10	GVNVDADFEPLYIISP	72	0.84	
10	KGRGSGGNGSGRRLVI	7	0.84	
10	LEGIDAREVNSIKLFD	633	0.84	
10	AGETFATPDVAVRELD	395	0.84	
10	ASAEKPYARRPYPPF	292	0.84	
11	FGPYVTDGETNASLRK	874	0.83	
11	LGIGRPSTYSSIIKTI	529	0.83	
11	HEAIRPAGETFATPDA	389	0.83	
11	RAAAEHPRDLIDLVD	147	0.83	
12	PARKAARKVPAKKAAS	917	0.82	
12	EPLYIISPEKRSTVSE	80	0.82	
12	PRVVGVDPASGEEITA	787	0.82	
12	PRTGSLLRSMDLQTVT	761	0.82	
12	LDIVELTPDGHATNPP	499	0.82	
12	ILAKLDASVSDPDAAP	221	0.82	
13	GPYLKRGNDSRSLVTE	808	0.81	
13	GEEITAQNGRYGPYLK	797	0.81	
13	DDTHGRPIYVRVGKNG	648	0.81	

13	SSRGHIRDLPRAASDV	44	0.81	
13	YELIWQRTVASQMADA	420	0.81	
14	TEDQIFTITLDEALKI	822	0.80	
15	DALRLLSLPRVVGVDP	779	0.79	
15	AEELFATPQQGRTLGL	698	0.79	
15	VETVDELVGGEADDAE	472	0.79	
15	SATALAAGLDGTQLTV	276	0.79	
15	FHEITEPAIRAAAEHP	138	0.79	
16	HGVPDSVARSGGLKKL	613	0.78	
16	GRTLTFPGFLKAYVET	459	0.78	
16	HQEVVFSATGRTLTFP	450	0.78	
16	TMSIAQRLYENGYITY	327	0.78	
17	DLPRAASDVPAKYKSQ	51	0.77	
18	FGPYVTEILPEPAADA	728	0.76	
18	RVGKNGPYLERLVAGD	658	0.76	
18	TAAMEDELDEIAAGNE	583	0.76	
18	LVDYDFTAAMEDELDE	577	0.76	
18	ASLVKALEELGIGRPS	520	0.76	
18	APAPRQYTRKVKNAQE	372	0.76	
18	ETRRILDRLYGYEVSP	165	0.76	
19	DDVASITDERAAELLA	891	0.75	
19	DGETNASLRKGDDVAS	880	0.75	
19	TVASQMADARGMTLSL	427	0.75	
19	PPTFSARLTAVAGR RV	236	0.75	
19	AWHLLLETLKPRIPVKR	120	0.75	
20	DERAAELLADRRARGP	898	0.74	
20	KRQKAAGPKPRTGSL	752	0.74	
20	PRIPVKRMVFEITEP	129	0.74	
21	AVTGLLEQHFGR LVDY	565	0.73	
21	DRMAFRSAAYWDILAK	209	0.73	
22	SMDLQTVTLEDALRLL	769	0.71	
22	LSDSITPDELTLQVAE	684	0.71	
22	QPWARLGVNVDADFEP	66	0.71	
22	MRTDSTTLSESAINAA	343	0.71	

22	YLATDGDREGEIAIWH	107	0.71	
23	GRTLGLDPETGHEIVA	708	0.70	
23	PARYTEASLVKALEEL	514	0.70	
23	IDLVDAQETRRLDRL	158	0.70	
24	AAAQGVKKRQKAAGP	744	0.69	
25	LRKGDEVIVLDEGSAT	263	0.68	
26	PKLSAGRVQSVATRII	188	0.66	
27	PGFLKAYVETVDELVG	465	0.65	
28	LWKKVAPKLSAGRVQS	182	0.62	
29	SPEKRSTVSELRGLLK	86	0.59	
29	KGSALVPSWVAFVTG	553	0.59	
30	PEPAADAAAAAQGVKK	737	0.58	
31	REVNSIKLFDDTHGRP	639	0.57	
31	QDRGYVHKKGSALVPS	545	0.57	
32	SELRGLLKDVDELYLA	94	0.54	
32	PDELTLQVAEELFATP	690	0.54	
33	GNERRTNWLNNFYFGG	596	0.53	

OVERLAP DISPLAY

LADPKTKGRGSGGNGSGRRLVIVESPTKARKLASYLGSYIVESSRGHIRDLPRAASDVPAKYKSPWARLGVNVDADFEPLY
IISPEKRSTVSELRGLLKDVDELYLATDGDREGEIAWHLLETLPRI PVKRMVFHEITTEPAIRAAAEHPRDLIDLVDAQET
RRLDRLYGYEVSPVLWKKVAPKLSAGRVQSVATRIIVARERDRMAFRSAAAYWDILAKLDASVSDPDAAPPTFSARLTAVAGR
RVATGRDFDSLGLTRKGDEVIVLDEGSATALAAGLDGTQLTVASAEKPYARRPYPPFMTSTLQQEASRKLRFSAERTMSIAQ
RLYENGYITYMRTDSTTLESASAINAARTQARQLYGDEYVAPAPRQYTRKVKNAQEAHEAIRPAGETFATPDAVRRELDGPNID
DFRLYELIWQRTVASQADARGMTLSLRITGMSGHQEVVFSATGRTLTFPGFLKAYVETVDELVGGEADDAERRLPPLTPGQR
LDIVELTPDGHATNPPARYTEASLVKALEELGIGRPSTYSSIIKTIQDRGYVHKKGSALVPSWVAFVTGLLEQHFGRLLVDYD
FTAAMEDELDEIAAGNERRTNWLNNFYFGGDHGVDPDSVARSGGLKLVGINLEGLDAREVNSIKLFDDTHGRPIYVRVGKNGP
YLERLVAGDTGEPTPQRANLSDSITPDELTLQVAEELFATPQQGRTLGLDPETGHEIVAREGRFGPYVTEILPEPAADAAAA
QGVKKRQKAAGPKPRTGSLRSMDLQTVTLEDALRLLSLPRVVGVDPASGEEITAQNGRYGPYLKRGNDSRSLVTEQIFITIT
LDEALKIYAEPKRRGRQSASAPPLRELGTDPASGKPMVIKDGRFGPYVTDTGETNASLRKGDVASITDERAAELLADRRARGP
AKRPARKAARKVPAKKAARD⁹³⁴

SDPDAAPPTFSARLTA

YARRPYPPFMTSTLQQ

AGDTGEPTPQRANLSD

PAKYKSQPWARLGVNV

ARTQARQLYGDEYVAP

KPMVIKDGREFGPYVTD

LDEIAAGNERRTNWLN

AEERLPHLTPGQRLDI

QQEASRKLRFSAERTM

GRRVATGRDFDSLGLT

RGPAKRPARKAARKVP

ALKIYAEPKRRGRQSA

HEIVAREGRFGPYVTE

FYFGGDHGVPSVARS

YSSIKTIQDRGYVHK

RRELDGPNIDDFRLYE

SGYIVESSRGHIRDLP

NGYITYMRTDSTTLSE

DGHATNPPARYTEASL

GMTLSLRITGMSGHQE

ATRIIVAREDRMAFR

YGYEVSPVLWKKVAPK

RQSASAPPLRELGTDP

RELGTDPASGKPMVIK

QLYGDEYVAPAPRQYT

LVIVESPTKARKLASV

GVNVDADFEPLYIISP

KGRGSGGNGSGRRLVI

LEGIDAREVNSIKLFD

AGETFATPDAVRRELD

ASAEKPYARRPYPPF

FGPYVTDGETNASLRK

LGIGRPSTYSSIIKTI

HEAIRPAGETTFATPDA

RAAAEHPRDLIDLVD

---PARKAARKVPAKKAAK---

EPLYIISPEKRSTVSE

PRVVGVDPASGEEITA

DDTHGRPIYVRVGKNG

SSRGHIRDLPRAASDV

YELIWQRTVASQMADA

TEDQIFTITLDEALKI

DALRLLSLPRVVGVDP

AEELFATPQQGRTLGL

VETVDELVGGEADDAE

SATALAAGLDGTQLTV

FHEITEPAIRAAAHP

HGVPDSVARSGGLKKL

FGPYVTEILPEPAADA

RVGKNGPYLERLVAGD

TAAMEDELDEIAAGNE

LVDYDFTAAMEDELDE

ASIVKALEELGIGRPS

APAPRQYTRKVKNAQE

ETRRILDRLYGYEVSP

DDVASITDERAAELLA

DGETNASLRKGDDVAS

TVASQADARGMTLSL

PPTFSARLTAVAGRRV

AWHLETLKPRIPVKR

DERAAELLADRRARGP

KRQKAAGPKPRTGSL

PRIPVKRMVFHEITEP

AVTGLLEQHFGRLLVDY

DRMAFRSAAYWDILAK

SMDLQTVTLEDALRLL

LSDSITPDELTLQVAE

QPWARLGVNVDADFEP

MRTDSTTLSESAINAA

YLATDGDREGEIAWH

GRTLGLDPETGHEIVA

PARYTEASLVKALEEL

IDLVDAQETRRILDRL

SPEKRSTVSELRGLLK

KGSALVPSWVAFVVG

PEPAADAAAAAQGVKK

REVNSIKLFDDTHGRP

