

ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	941
Number of 16mers from the input sequence	926
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	ASDWDHPYTREQAAYP	890	0.96	
2	AGALGDALVHDKYFDT	372	0.95	
3	QGYDTHTPPVLLRNI	88	0.93	
3	GGPGVGPVAVRAHLAP	701	0.93	
4	VRRIDGAYGDRNLVCS	918	0.92	
4	EWPVDDNPLRGAPHTA	870	0.92	
4	GVSVDSDGTPAYRLAL	303	0.92	
5	ALMITYPSTHGVYEHD	632	0.91	
6	PGHPFAPELPKGYPVS	719	0.90	
6	EMESITWPEFGRQHPF	505	0.90	
7	QAAAYPLGTAFRPKVWP	901	0.89	

7	PVLYTGENGMAHECI	782	0.89	
7	TSEFLTHPAFTQYRTE	454	0.89	
7	FGVPMGFGGPHAGYLA	273	0.89	
7	TLMHRAARGPVKRVVV	160	0.89	
8	HRDICLIPSSAHGTNA	578	0.87	
8	YHASRGEPHRDICLIP	570	0.87	
8	GVIAQLPGASGRITDW	214	0.87	
8	YQPEISQGRLEALLNF	116	0.87	
8	WYTAYTPYQPEISQGR	109	0.87	
9	AVSMIGQGYDTHTPP	82	0.86	
9	GYPVSSAPYGSASILP	730	0.86	
9	VVVVDCHDNGDVLDD	603	0.86	
9	TVLARVPGRADVLAR	387	0.86	
9	LTLIAPPGEIGADVAF	252	0.86	
10	RAEIDKVGAGEWPVDD	860	0.85	
10	DSLPPAASEAEALAE	57	0.85	
10	PGEIGADVAFGTTQRF	258	0.85	
11	HLAPFLPGHPFAPELP	713	0.84	
11	KTFCIPHGGGGPGVGP	692	0.84	
11	HDAGGQVYVDGANLNA	656	0.84	
11	AHTDIARTSEFLTHP	446	0.84	
11	KPLGIEIVTADLRAGL	192	0.84	
12	LMVEPTESESLAEVDA	836	0.83	
12	APTMSFPVAGTLMVEP	825	0.83	
13	AHECILDLRGITKLTG	793	0.82	
13	DIAEICAAVHDAGGQV	647	0.82	
13	RNIENPAWYTAYTPY	101	0.82	
14	ADYGFHAPTMSFPVAG	819	0.81	
14	DLRGITKLTGITVDDV	799	0.81	
14	PGASGRITDWSALVQQ	220	0.81	
14	FQTLVTDLTGLEIANA	131	0.81	
15	APYGSASILPITWAYI	736	0.80	
15	ASEAEALAEALRALADA	63	0.80	
15	VPAGILDTLTDGTAAP	39	0.80	

15	AAAEAMTLMHRAARGP	154	0.80	
16	PHTAQCLLASDWDHPY	882	0.79	
16	PITWAYIRMMGAEGLR	745	0.79	
16	GGDVSHLNLHKTF CIP	682	0.79	
16	YRLALQTTREQHIRRDK	314	0.79	
17	ACDEATTDTHVAVVLD	421	0.78	
17	AVIGVDSLDDLAVKAV	24	0.78	
17	ARGPVKRVVVDADVFT	166	0.78	
18	EGLRAASLTAITSANY	757	0.77	
18	SMIPLGSCTMKNAAA	489	0.77	
18	ETSMMRYLRALADKDI	469	0.77	
18	VLAAMYASYHGAGGLT	343	0.77	
19	RLDEYYPVLYTGNGM	776	0.76	
19	PVAVRAHLAPFLPGHP	707	0.76	
19	APASDTAGLRQLVADL	521	0.76	
20	PSTHGVYEHDAEICA	638	0.75	
20	SWLV LITGYDAVSLQP	538	0.75	
20	TMKLNAAAEMESITWP	497	0.75	
20	VAAAAPAHTDIATRTS	440	0.75	
21	DRHIGLDSQAVATMLA	9	0.74	
21	TNAASAALAGMRVVVV	591	0.74	
21	GAGGLTAIARRVHAHA	353	0.74	
21	HIRRDKATSNICTAQV	324	0.74	
21	HARQLPGRLVGVSVDS	293	0.74	
21	ASMLDEGTAAAEAMTL	146	0.74	
21	TGLEIANASMLDEGTA	139	0.74	
22	LWRVDADHVSACDEA	410	0.73	
23	LTAITSANYIARRLDE	764	0.72	
23	AKVGEHAERLSALMIT	621	0.72	
23	TGYDAVSLQPNAGSQG	544	0.72	
23	AVATMLAVIGVDSLDD	18	0.72	
24	KLTGITVDDVAKRLAD	805	0.71	
24	NALVGLARPGKFGGDV	670	0.71	
24	SALVQQAHDRGALVAV	230	0.71	

25	HVAVVLDAFGVAAAAP	430	0.70	
25	RAGLPDGEFFGVIAQL	204	0.70	
26	RALADKDIALDRSMIP	477	0.68	
26	ARRVHAHAEEIAGALG	361	0.68	
27	DTLTDGTGAAPGLDLSL	45	0.67	
27	HAGYLAVHAKHARQLP	283	0.67	
28	LARAKANGINLWRVDA	400	0.66	
28	QGRLEALLNFQTLVTD	122	0.66	
29	LAEVDAFCEAMIGIRA	846	0.65	
30	SDHSTFADRHIHGLDSQ	2	0.64	
30	VFTQTA AVLATRAKPL	179	0.64	
31	VLATRAKPLGIEIVTA	186	0.63	
32	PSSAHGTNAASAALAG	585	0.62	
33	PNAGSQGEYAGLLAIH	553	0.61	
34	PGRADEVLARAKANGI	393	0.60	
34	AHDRGALVAVGADLLA	236	0.60	
35	LAELRALADANTVAVS	69	0.56	
35	TSNICTAQVLLAVLAA	331	0.56	
35	LVAVGADLLALTLIAP	242	0.56	

OVERLAP DISPLAY

VSDHSTFADRHIHGLDSQAVATMLAVIGVDSLDDLAVKAVPAGILDTLTDGTGAAPGLDLSLPPAASEAEALAEELRALADANTVAV
SMIGQGYDTHTPPVLLRNI IENPAWYTAYTPYQPEISQGRLEALLNFQTLVTDLTGLEIANASMLDEGTAAAEAMTLMHRAA
RGPVKRVVVDADVFTQTA AVLATRAKPLGIEIVTADLRAGLPDGEFFGVIAQLPGASGRITDWSALVQQAHDRGALVAVGADL
LALTLIAPPGEIGADVAFGTTQRFVPMGFGGPHAGYLAVHAKHARQLPGRVLVGSVSDSGTPAYRLALQTREQHIRRDKATS
NICTAQVLLAVLAAMYASYHGAGGLTAIARRVHAHAEEIAGALGDALVHDKYFDTVLARVPGRADEVLARAKANGINLWRVDA
DHVSVACDEATTDTHVAVVLDAFGVAAAAPAHTDIATRTSEFLTHPAFTQYRTETSMMRYLRALADKDIALDRSMIPLGSCTM
KLNAAEMESITWPEFGRQHPFAPASDTAGLRQLVADLQSWLVLITGYDAVSLQPNAGSQGEYAGLLAIHEYHASRGEPHRDI
CLIPSSAHGTNAASAALAGMRVVVDCHDNGDVLDDLRAKVGEHAERLSALMITYPSTHGVYEHDAEICAAVHDAGGQVYV
DGANLNALVGLARPGKFGGDVSHLNLHKTFCIPHGGGGPGVGPVAVRAHLAPFLPGHPFAPELPGKYPVSSAPYGSASILPIT
WAYIRMMGAEGLRAASLTAITSANYIARRLDEYYPVLYTGENGMVAHECILDLRGITKLTGITVDDVAKRLADYGFHAPTMSF
PVAGTLMVEPTESESLAEVDAFCEAMIGIRAEIDKVGAGEWPVDDNPLRGAPHTAQCLLASDWDHPYTREQAAYPLGTAFRPK
VWPAVRRIDGAYGDRNLVCSCPPVEAFA⁹⁴¹

ASDWDHPYTREQAAYP

AGALGDALVHDKYFDT

QGYDTHTPPVLLRNI

GGPGVGPVAVRAHLAP

VRRIDGAYGDRNLVCS

EWPVDDNPLRGAPHTA

GVSVDSGTPAYRLAL

ALMITYPSTHGVEHD

PGHPFAPELPGYPVS

EMESITWPEFGRQHPF

HRDICLIPSSAHGTNA

YHASRGEPHRDICLIP

GVIAQLPGASGRITDW

YQPEISQGRLEALLNF

WYTAYTPYQPEISQGR

AVSMIGQGYDTHTPP

GYPVSSAPYGSASILP

VVVVDCHDNGDVLDD

TVLARVPGRADEVLAR

LTLIAPPGEIGADVAF

RAEIDKVGAGEWPVDD

DSLPPAASEAEALAEI

PGEIGADVAFGTTQRF

HLAPFLPGHPFAPELP

KTFCIPHGGGGPGVGP

HDAGGQVYVDGANLNA

AHTDIATRTSEFLTHP

KPLGIEIVTADLRAGL

LMVEPTESESLAEVDA

APTMSFPVAGTLMVEP

AHECILDRLRGITKLTG

DIAEICAAVHDAGGQV

RNI IENPAWYTAYTPY

ADYGFHAPTMSFPVAG

DLRGITKLTGITVDDV

PGASGRITDWSALVQQ

FQTLVTDLTGLEIANA

APYGSASILPITWAYI

ASEAEALAE LRALADA

VPAGLLDTLTDGAA

AAAEAMTLMHRAARGP

PHTAQCLLASDWDHPY

PITWAYIRMMGAEGLR

GGDVSHLNLHKTFCIP

YRLALQTRQHIRRDK

ACDEATTDTHVAVVLD

AVIGVDSLDDLAVKAV

ARGPVKRVVVDADVFT

EGLRAASLTAITSANY

SMIPLGSCTMKLNAAA

ETSMMRYLRALADKDI

VLAAMYASYHGAGGLT

RLDEYYPVLTYGENGM

PVAVRAHLAPFLPGHP

APASDTAGLRQLVADL

PSTHGVYEHDAEICA

SWLVLITGYDAVSLQP

TMKLNAAAEMESITWP

VAAAAPAHTDIATRTS

DRHIGLDSQAVATMLA

TNAASAALAGMRVVVV

GAGGLTAIARRVHAHA

HIRRDKATSNICTAQV

HARQLPGRLVGVSVDS

ASMLDEGTAAAEAMTL

TGLEIANASMLDEGTA

LWRVDADHVSACDEA

LTAITSANYIARRLDE

AKVGEHAERLSALMIT

TGYDAVSLQPNAGSQG

AVATMLAVIGVDSLDD

KLTGITVDDVAKRLAD

NALVGLARPGKFGGDV

SALVQQAHDRGALVAV

HVAVVLDAFGVAAAAAP

RAGLPDGEFFGVIAQL

RALADKDIALDRSMIP

ARRVHAHAEAIAGALG

DTLTDTGAAPGLDSL

HAGYLAVHAKHARQLP

LARAKANGINLWRVDA

QGRLEALLNFQTLVTD

LAEVDAFCEAMIGIRA

-
SDHSTFADRHI GLDSQ

VFTQTAAVLATRAKPL

VLATRAKPLGIEIVTA

PSSAHGTNAASAALAG

PNAGSQGEYAGLLAIH

PGRADVLARAKANGI

AHDRGALVAVGADLLA

LAELRALADANTVAVS

