

ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	874
Number of 16mers from the input sequence	859
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	PGMDSSPPSEDYGRQP	9	0.97
2	PEPIDTQRMPSESELIS	499	0.91
3	MMDIQLHEPTMWKHSP	739	0.90
4	LHRPDAFDRDDPRGGE	827	0.89
4	GGSVRWDPTNGQGRVY	624	0.89
5	GDRIAAPRRVPEPIDT	489	0.88
6	AGLGLFTKRSHEKCVV	587	0.87
6	GRMSDDWTRLARRMS	282	0.87
7	DRAIHELARGDAYWDT	768	0.86
7	PHRAEARIEDRAIHEL	759	0.86
7	QGRVYVGSTSRRLIDD	635	0.86
7	FYRPAHQNVYDAIIDL	57	0.86
7	MSEISEAPLFIDDSPN	296	0.86
7	GQMVIVAARPGVGKST	219	0.86
7	YGYAGABEGADVAEVVD	142	0.86
8	QPIRYEPVDEANLAAV	528	0.85
9	RRIGGAPYLHTLISTV	95	0.84
9	ADFI LAKHRNGPTKT V	843	0.84
9	GISLHNSLEQDADVVI	810	0.84
9	TMWKHSPSRSPHRAE	748	0.84
9	HDSWRLHIHGAKDQVR	673	0.84
9	SLARMIGDGSCLKNQP	514	0.84
9	VGKSTLGLDFMRSCSI	230	0.84
10	RGEPADAVTVAAELDR	75	0.83
10	MLRQLKGPVRNPNLDS	706	0.83
10	QRLPRGRCTPIAAWLA	572	0.83
10	GELMRSGERPMVWSLD	419	0.83
10	DLLQPTMDEIDAIASS	180	0.83
11	ITSIGDQHVFDGTVSG	787	0.82
11	YDAILDLYGRGEPADA	66	0.82
11	HEKCVPEAVFRAPNDQ	597	0.82
11	GAEVAFGELMRSGERP	413	0.82
11	ESGCLTASTRILRADT	397	0.82
12	SLRPARQLRPRGRCTP	566	0.81
12	MTSGKKYESRQVEVSE	341	0.81
13	PKKVVAQVRNRLSAKQ	723	0.80
13	GREVEATGSHPPMKFE	463	0.80

13	MVARPMINVFPSSGRKE	439	0.80
13	FSLEMSKSEIVMRLLS	254	0.80
14	AELDRRGLLRRIGGAP	86	0.79
14	RVGIFSWITHAPKLG	657	0.79
14	PFMKFEGWTPLAQLKV	473	0.79
14	SVLGGMLLSKDAIADV	33	0.79
14	ATGFTELDEVNGLHP	203	0.79
15	DGTVSGTHNFVANGIS	797	0.78
15	RCTPIAAWLAGLGLFT	578	0.78
15	VFPSGRKEVFRRLAS	447	0.78
15	DKKPLADLRESGCLT	387	0.78
15	YDVADRRLSEDFVALE	164	0.78
16	GPVRNPNDLSDAPKVV	712	0.77
16	AVTVSAAHSDRAAIRD	542	0.77
16	PMVWSLDERLRMVARP	428	0.77
16	TMMEIRAKARRLRQKA	313	0.77
17	THAPKLGHDSWRLHI	665	0.76
17	VVAISQLNRGPEQRTD	372	0.76
17	GGLARGVATGFTELDE	196	0.76
18	RAQAEIYDVADRLSE	158	0.75
18	TLISTVPTAANAGYYA	105	0.75
19	PPSEYGRQPQDLAA	15	0.74
20	KDAIADVLERLRPGDF	42	0.73
20	ASTRILRADTGAEVAF	403	0.73
21	DAYWDTVVEITSIGDQ	778	0.72
21	DFMRSCSIRHRMASVI	238	0.72
22	SDRAAIRDDYLAARVP	550	0.71
22	IRHRMASVIFSLEMSK	245	0.71
22	DAIASSGGLARGVATG	190	0.71
23	VLERLRPGDFYRPAHQ	48	0.70
23	AKELEVVPVAISQLNR	365	0.70
23	DWTRLARRMSEISEAP	288	0.70
23	LDEVNGLHHPGQMVIV	209	0.70
24	RRLVEAGTRVVQYGYA	130	0.68
25	TVTVAHQHLHSRFANM	857	0.67
26	ESRQVEVSEFSRHLKL	348	0.66
26	AGYYASIVAEKALLRR	116	0.66
27	KSEIVMRLLSAEAKIK	260	0.65
28	AVVDDLAPGMDSSPPS	2	0.64
29	SLEQDADVILLHRPD	816	0.63
29	DLAAEQSVLGGMLLSK	27	0.63
30	DRDDPRGGADFILAK	834	0.62
30	RHVGVHGAEVAAQEM	691	0.62
30	VFRLRLASGREVEATG	455	0.62
31	HRNGPTKTVTVAHQH	850	0.61
32	EAVFRAPNDQVALFLR	603	0.60
32	RDDYLAARVPSLRPAR	556	0.60
33	IVAEKALLRRLVEAGT	122	0.59
34	GSTSRRLLIDVAQLLL	641	0.58
35	DEANLAAVTVSAHSD	536	0.57
36	IHGAKDQVRFLRHVGV	680	0.56
36	AKARRLRQKANLKLIV	319	0.56
37	DDVAQLLRLVGVFSWI	649	0.55

OVERLAP DISPLAY

MAVVDDLAPGMDSSPPSEYGRQPQDLAAEQSVLGGMLLSKDAIADVLERLRPGDFYRPAHQNVYDAIILDLYGRGEPADAVTVAAELDRRGLLRRIGGAPYLHTLISTVPTAANAGYYASIVAEKALLRRLVEAGTRVVQYGYAGAEGAI
 -----PGMDSSPPSEYGRQP-----

