ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	651
Number of 14mers from the input sequence	638
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	RCGHIGALNEEAAK	368	0.91
2	SLAQLLLDPFFRTI	334	0.89
3	TITDYYKQLESSGW	281	0.88
4	EKNGRKRCWDRFNW	102	0.87
5	ATKQILIGSCKFRS	157	0.86
5	WKINDFNVDYRYCD	132	0.86
6	KCGRPVNIIDVFAF	85	0.85
6	NFLIAKDKDCQDLY	67	0.85
6	DEQLMNLIAKTNPS	205	0.85
6	FARQGIGIADKHLW	119	0.85
6	CWDRFNWQIEFARQ	109	0.85
7	LDACQRTKTITDYY	273	0.84
8	SDSGHSSTVSSGAQ	545	0.83
8	SDGWDRTSQTVSLA	323	0.83
9	IDVFAFENREKNGR	93	0.82
9	VTIATLEHIGVLEA	506	0.82
9	EKGNLSAIGTYLTI	45	0.82
9	SNIVGTIHITTSHF	10	0.82
10	VVWTAMYNRFDTGL	484	0.81
10	PLTGFTARCVEDEQ	194	0.81
11	VLIEKDWLGFGHKF	352	0.80
12	QANKFSYLANVDLH	466	0.79
12	SAVVHCSDGWDRTS	317	0.79
13	LAKRTLSLWSYIDD	440	0.78
13	IFRADNSSKEIWVA	24	0.78
13	QGKGYEDIKNYPNM	239	0.78
14	YQIMRLQPRAFEFN	395	0.77
14	RFHFFDIENIHVMR	253	0.77
14	NPSYQSLCLIDTRP	216	0.77
14	NVDYRYCDTYPEYL	138	0.77
15	KDRKDLNLAKRTLS	433	0.76
15	LIGSCKFRSRARLP	162	0.76
16	STVSSGAQPTTPLQ	551	0.75
16	QMASLQAVTFLAPS	520	0.75
17	APSFLFMKMISGVM	531	0.74
17	NYPNMRFHFFDIEN	248	0.74
17	KFRSRARLPVLTYW	167	0.74
18	HIGVLEAQMASLQA	513	0.73
18	VANALIGNIEKGNL	36	0.73
18	NIHVMRSSLNKLLD	261	0.73
19	YLCTPSSATKQILI	150	0.72
20	RSLLDCSAFLADLV	299	0.71
20	HRPNFGRFCRCAQP	181	0.71
21	KMISGVMSDSGHSS	538	0.70
21	FLADLVSRGISAVV	307	0.70
22	WSYIDDHDDYINP	448	0.69
22	FEFNERYLIDIHEH	405	0.69
22	FRTIRGFQVLIEKD	344	0.69
23	YNRFDTGLLPREST	490	0.68
23	HKFDDRCGHIGALN	363	0.68
24	LHPSAIVVWTAMYN	478	0.67
24	RFCRCAQPLTGFTA	187	0.67
25	DLYETLLKCGRPVN	78	0.66
25	GALNEEAAKEVSPI	373	0.66
26	QAVTFLAPSFLFMK	525	0.63
26	MMNKMQGKGYEDIK	234	0.63
26	ARLPVLTYWHRPNF	172	0.63
27	AKEVSPIFTQFLDC	380	0.62
27	RTSQTVSLAQLLLD	328	0.62
28	NSSKEIWVANALIG	29	0.58
29	HHDDYINPLYEFQA	454	0.57
30	GAQPTTPLQSLPEL	556	0.56
30	TIHITTSHFIFRAD	15	0.56
31	IDTRPLVNAMMNKM	225	0.53
32	HEHAYSCQYGTFLG	416	0.51