

ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	478
Number of 16mers from the input sequence	463
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	EFYIFDSVSFDSRANG	135	0.96
2	KIEPQAPVKDLYELP	394	0.91
2	PASAFDKSVFDDGLAF	38	0.91
3	SDMLLLPDPETARIDP	67	0.88
3	STGIADTAYFGAEAEF	121	0.88
4	ETARIDPFRAAKTLNI	76	0.87
4	LDGIKKNKIEPQAPVVK	388	0.87
5	LEPYSRDPNRNIARKAE	101	0.86
6	SACVRIPITGSNPKAK	348	0.85
6	YKYIIKNTAWQNGKTV	245	0.85
7	HEYLTEGGVFTNDLIE	434	0.84
7	TVNSYKRLVPGYEAPI	323	0.84
7	TEADGSPNRGYKVRHK	168	0.84
8	LSDVIDRLEADHEYLT	423	0.83
8	SAMLMAGLDGIKKNKIE	381	0.83
8	DETYAGLSDTARHYI	291	0.83
8	HEVGGGQAEINYQFN	218	0.83
9	EAAASIPQPTQLSDV	411	0.82
9	HKGGYFPVAPNDQYVD	182	0.82
10	IETWISFKRENEIEPV	448	0.81
10	KDLYELPPEAAASIPQ	403	0.81
10	GKTVTFMPKPLFGDNG	257	0.81
10	SGFILEKGGHHEVGGSGG	209	0.81
11	PVNIRPHPYEFALYYD	462	0.80
11	KAKRLEFRSPDSSGNP	361	0.80
11	GGLLHHAPSLLAFTNP	307	0.80
11	GAPLMYDETYAGLSD	285	0.80
12	SDTARHYIGGLLHHAP	299	0.79
12	APNDQYVLDLRDKMLTN	190	0.79
12	EVDAISGWNTGAATE	154	0.79
13	DSSGNPYLAFSAMLMA	371	0.78
14	SRANGSFYEVDASGW	146	0.77
15	RGFQSIHESDMLLLPD	59	0.76
15	KSVFDDGLAFDGSIR	44	0.76
15	LPGIMQHFTIPASAFD	28	0.76
15	HQSLWKDGAPLMYDET	278	0.76
16	PLFGDNGSGMHCHQSL	266	0.73

