

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	EFYIFDSVSDSRANG	135	0.96
2	KIEPQAPVDKDLYELP	394	0.91
2	PASAFDKSVFDDGLAF	38	0.91
3	SDMLLLPDPETARIDP	67	0.88
3	STGIADTAYFGAEAEF	121	0.88
4	ETARIDPFRRAKTLNI	76	0.87
4	LDGIKNKIEPQAPVDK	388	0.87
5	LEPYSRDPRNIAKRAE	101	0.86
6	SACVRIPITGSNPKAK	348	0.85
6	YKYIICKNTAWQNGKTV	245	0.85
7	HEYLTEGGVFTNDLIE	434	0.84
7	TVNSYKRLVPGYEAPI	323	0.84
7	TEADGSPNRRGYKVRHK	168	0.84
8	LSDVIDRLEADHEYLT	423	0.83
8	SAMLMAGLDGINKNIE	381	0.83
8	DETGYAGLSDTARHYI	291	0.83
8	HEVGSGGGQAEINYQFN	218	0.83
9	EEAASIPQTPTQLSDV	411	0.82
9	HKGGYFPVAPNDQYVD	182	0.82
10	IETWISFKRENIEIPV	448	0.81
10	KDLYELPPEEAASIPQ	403	0.81
10	GKTVTMPKPLFGDNG	257	0.81
10	SGFILEKGHHEVGS GG	209	0.81
11	PVNIRPHPYEFALYYD	462	0.80
11	KAKRLEFRSPDSSGNP	361	0.80
11	GGLLHHAPSLLAFTNP	307	0.80
11	GAPLMYDETGYAGLSD	285	0.80
12	SDTARHYIGGLHHAP	299	0.79
12	APNDQYVDLRKMLTN	190	0.79
12	EVDAISGWNTGAATE	154	0.79
13	DSSGNPYLAFSAMLMA	371	0.78
14	SRANGSFYEVDAISGW	146	0.77
15	RGFQSIHESDMLLL PD	59	0.76
15	KSVFDGGLAFDGSSIR	44	0.76
15	LPGIMQHFTIPASA FD	28	0.76
15	HQSLWKDGAPL MYDET	278	0.76
16	PLFGDNGSGMHCHQSL	266	0.73

16	LHAADDMQLYKYIICKN	236	0.73
17	AFDGSSIRGFQSIHES	52	0.71
17	KDEKVEYVDVRCDLDP	14	0.71
18	YVDVRCDLPGIMQHF	20	0.70
18	ARKAENYLISTGIADT	112	0.70
19	EAPINLVYSQRNRSAC	335	0.67
19	SLLAFTNPTVNSYKRL	315	0.67
20	VTEKTPDDVFKLAKDE	1	0.64
21	RENEIEPVNIRPHPYE	456	0.61
22	QAEINYQFNSLLHAAD	225	0.60

OVERLAP DISPLAY

VTEKTPDDVFKLAKDEKVEYVDVRCDLPGIMQHTIPASAFDKSVFDDGLAFDGSSIHEGQSIHESDMLLLPDPE TARIDPFRAAKTLNINFFVHDPTLEPYSRDPRNIARKAENYLISTGIADTAYFGAEAEFYIFDSVSFDSRANG-----EFYIFDSVSFDSRANG-----

-PASAFDKSVPDDGLAF-

-SDMLLLPDPE TARIDP-

-STGIADTAYFGAEAEF-

-ETARIDPFRAAKTLNI-

-LEPYSRDPRNIARKAE-

-RGFQSIHESDMLLLPD-

-SRANG-

-KSVFDDGLAFDGSSIR-

-LPGIMQHTIPASAFD-

-AFDGSSIRGFQSIHES-

-KDEKVEYVDVRCDLP-

-YVDVRCDLPGIMQHF-

-ARKAENYLISTGIADT-

VTEKTPDDVFKLAKDE-----