

ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	491
Number of 16mers from the input sequence	476
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	AISETYPPGSTFKVIT	213	0.92
2	YSVATDGRFRFLRVYP	64	0.91
2	PGVQIASKTGTAEHGT	417	0.91
2	EPTVSLREAFVKSCNT	269	0.91
2	FFTGRDPRGGNVDTTI	123	0.91
3	GGITMRPYLVGSLKGP	359	0.90
3	NPEVQAQAWQLGDNP	190	0.90
4	DAMQQGCYGPCKGAVV	148	0.89
5	SKTGTAEHGTDRHPT	423	0.87
6	PVTGFYSLRYSSTALE	86	0.86
7	IRTGADALRSMARAFG	291	0.85
8	DGLRADPRNQVLLDE	32	0.84
8	AESTVGP IPDSAALGM	319	0.84
8	AFGLDSPRPRTPLQVA	304	0.84
9	PLPGSTAQLENYGGAP	250	0.83
9	ALAAGATEQEQLTAAP	232	0.83
10	FKVITTAALAAGATE	224	0.82
10	TGKILALVSSPSYDPN	169	0.82
11	NPEVYAPVTGFYSLRY	80	0.81
12	ALGMTSIGQKDALTP	331	0.79
13	AVVALEPSTGKILALV	161	0.78
14	AAPIGRAVIEAALQGE	475	0.77
14	ATMTQVFTADGLRADP	23	0.77
15	PIPDSAALGMTSIGQK	325	0.75
15	PPRPTPLQVAESTVGP	310	0.75
16	RGQITAGGQLLAYSVA	52	0.74
16	FAPAQAPKVAVAVLVE	446	0.74
16	PRHTPPHAWYIAFAPA	434	0.74
16	GGNVDTTINPRIQQAG	131	0.74
17	LTAAPTIPLPGSTAQL	243	0.73
18	GRFRFLRVYPNPEVYA	70	0.72
18	NGADRLSATGGALAAP	462	0.72
18	RVLLDEYSRQRGQITA	42	0.72
18	ISTTVGYQQRRVSPQ	379	0.72
18	NLLASHNPEVQAQAWQ	184	0.72
19	SLRYSSTALERAEDPI	92	0.71
19	IGQKDALTPLANAÆI	337	0.71

19	GDNPASPLTNRAISET	202	0.71
19	ILNGSDRRLFGRRRLAD	107	0.71
20	VSSPSYDPNLLASHNP	176	0.70
21	LMVGAEKVAQQKGAIP	402	0.69
21	LERAEDEPILNGSDRRL	100	0.69
22	VGSLKGPDLANISTTV	368	0.68
23	ASLRRI SVTVMALIVL	3	0.65
23	CNTAFVQLGIRTGADA	282	0.65
24	QQKGAIPGVQIASKTG	411	0.64
25	QQRRAVSPQVAAKLTE	386	0.62
26	ANAELAAATIANGGITM	348	0.61
27	QVAAKLTELMVGAEKV	394	0.58
28	VMALIVLLLLLNATMTQ	12	0.57

OVERLAP DISPLAY

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MNASLRRI SVTVMALIVLLLLLNATMTQVFTADGLRADPRNQRVLLDEYSRQRGQITAGGQLLAYSVA TDGRFRFLRVYPNPEVYAPVTGFYSLRYSSTALERAEDPILNGSDRRLFGRRRLADFFTGDRDPRGGNVDTTIINPRIQQAGWDAM
-----
                                     YSVATDGRFRFLRVYP
-----
                                                     FFTGRDPRGGNVDTTI
-----
                                                                DAM
-----
                                  PVTGFYSLRYSSTALE
-----
          DGLRADPRNQRVLLDE
-----
                                     NPEVYAPVTGFYSLRY
-----
          ATMTQVFTADGLRADP
-----
                                  RGQITAGGQLLAYSVA
-----
                                                                GGNVDTTIINPRIQQAG
-----
                                  GRFRFLRVYPNPEVYA
-----
          RVLLDEYSRQRGQITA
-----
                                  SLRYSSTALERAEDPI
-----
                                  ILNGSDRRLFGRRRLAD
-----
                                  LERAEDPILNGSDRRL
-----
--ASLRRI SVTVMALIVL
-----
          VMALIVLLLLLNATMTQ
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