ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	414
Number of 16mers from the input sequence	399
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	ADRQVRPVAPGSKATM	25	0.93	
2	CEERGGDPRRPGKSDE	187	0.92	
3	DGHKMSKSRGNLVLVS	288	0.91	
3	YESGYDRDTMLRLCEE	174	0.91	
4	PGEPSWPSPFGPGRPG	213	0.90	
5	EATARLHRWRTATALP	337	0.88	
6	YVHAGMIGWDGHKMSK	279	0.87	
6	DATLQFGYESGYDRDT	167	0.87	
7	ITDIDDPLFERADRDG	82	0.86	
7	RYLADDLDTPKAIAAL	366	0.86	
7	LRLYDSADRQVRPVAP	19	0.86	

7	GEYQDIYFRADATLQF	157	0.86	
7	VELIEKMLACGAAYVI	137	0.86	
8	VVARVRRYLADDLDTP	360	0.85	
8	PGRPGWHVECAAIALS	224	0.85	
9	VTDAVEYGGHDAGAPK	385	0.84	
9	SDLIFPHHEFTAAHAE	252	0.84	
9	ECAAIALSRIGSGLDI	232	0.84	
9	PRRPGKSDELDALLWR	194	0.84	
9	AALRVLPPQDYVGATE	116	0.84	
10	VAPGSKATMYVCGITP	32	0.83	
11	LGHAATYVTFDLIHRL	53	0.81	
11	AGHYRADRFWSQQVLD	321	0.81	
11	YVGATEAIAEMVELIE	126	0.81	
12	GAAYVIDREMGEYQDI	147	0.80	
13	HRLWLDLGHELHYVQN	66	0.79	
14	PVPVLPGRGPQLRLYD	8	0.78	
14	YVCGITPYDATHLGHA	41	0.78	
14	HAECVSGERRFARHYV	265	0.78	
14	ALLWRAARPGEPSWPS	205	0.78	
15	QSWYCPPVPVLPGRGP	2	0.75	
16	AGPAAVDVVARVRRYL	353	0.74	
17	LSRIGSGLDIQGGGSD	238	0.73	
18	LFERADRDGVDWRDLA	89	0.72	
19	PYDATHLGHAATYVTF	47	0.71	
20	TPKAIAALDGWVTDAV	374	0.70	
21	LGHELHYVQNITDIDD	72	0.68	
22	PSAVRLGLLAGHYRAD	312	0.67	
23	RWRTATALPAGPAAVD	344	0.66	
24	VDWRDLAQAEVALFCE	98	0.65	
25	PKLVATAIDALLGVDL	399	0.64	
26	GGHDAGAPKLVATAID	392	0.60	
27	ALRAQDVEPSAVRLGL	304	0.57	
27	KSRGNLVLVSALRAQD	294	0.57	

OVERLAP DISPLAY

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MQSWYCPPVPVLPGRGPQLRLYDSADRQVRPVAPGSKATMYVCGITPYDATHLGHAATYVTFDLIHRLWLDLGHELHYVQNIT
DIDDPLFERADRDGVDWRDLAQAEVALFCEDMAALRVLPPQDYVGATEAIAEMVELIEKMLACGAAYVIDREMGEYQDIYFRA
DATLQFGYESGYDRDTMLRLCEERGGDPRRPGKSDELDALLWRAARPGEPSWPSPFGPGRPGWHVECAAIALSRIGSGLDIQG
GGSDLIFPHHEFTAAHAECVSGERRFARHYVHAGMIGWDGHKMSKSRGNLVLVSALRAQDVEPSAVRLGLLAGHYRADRFWSQ
QVLDEATARLHRWRTATALPAGPAAVDVVARVRRYLADDLDTPKAIAALDGWVTDAVEYGGHDAGAPKLVATAIDALLGVDL4
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CEERGGDPRRPGKSDE-------------------------------------------------------------------
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