ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	524
Number of 16mers from the input sequence	509
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	PGSARPRTRFGAWLGR	37	0.94	
2	QGVAKWNYLPNAHNDF	297	0.93	
2	VSAGYRSDRVRSWLNP	252	0.93	
3	MGLPPRPGSPRTADPP	478	0.92	
4	RGTSDTDGSQTRGAEP	8	0.91	
5	DGSQTRGAEPVEGQRT	14	0.90	
6	PRTAPGQPARQMGLPP	467	0.88	
6	LPLISAGGTSTAATLS	385	0.88	
6	AEPVEGQRTGPEEASN	21	0.88	
7	RANPQPAQTQPARKTP	452	0.87	
7	TGMRIASRSADPFLRL	339	0.87	
8	PGSPRTADPPVRRSVH	484	0.86	
9	GLLWYAGLPLRVFLSS	224	0.85	

10	LRAGRDDKVNRLLRLP	419	0.83	
10	RMERASLREMLIPLVP	182	0.83	
11	QRYAGQRRTRRVRALE	504	0.82	
11	LPPRLEAFRDRKRANP	440	0.82	
12	MGIILLGLLWYAGLPL	218	0.81	
13	DPPVRRSVHHGAGQRY	491	0.79	
13	PVTGLQLPLISAGGTS	379	0.79	
13	QGGIFGDGLGQGVAKW	287	0.79	
13	NGSRGWFVVAGFSMQP	147	0.79	
13	LVPGIGKEANGSRGWF	138	0.79	
13	YVCLRMSVRFMRRIAF	109	0.79	
14	LGLIMVLSASAVRSYD	70	0.78	
15	SAVRSYDDDGSAWVIF	79	0.77	
15	TGPEEASNPGSARPRT	29	0.77	
16	RHEPEAVAALRAGRDD	410	0.76	
16	LALIVAQPDLGQTVSM	203	0.76	
16	VGLIGGYVCLRMSVRF	103	0.76	
17	DDDGSAWVIFGKQVLW	85	0.75	
18	AIIGEELGLVGALGLL	315	0.74	
18	AGFSMQPSELAKMAFA	156	0.74	
19	IGIIANAARHEPEAVA	402	0.72	
19	AFAIWGAHLLAARRME	169	0.72	
20	TTLWVLGQAFINIGYV	359	0.71	
21	GGTSTAATLSLIGIIA	391	0.70	
21	SWLNPENDPQDSGYQA	263	0.70	
22	AFRDRKRANPQPAQTQ	446	0.69	
23	DSGYQARQAKFALAQG	273	0.68	
24	AVAALLTTLGLIMVLS	62	0.66	
24	RFGAWLGRPMTSFHLI	45	0.66	
25	GYVIGLLPVTGLQLPL	372	0.63	
26	QVLWTLVGLIGGYVCL	97	0.61	
26	LREMLIPLVPAAVVAL	188	0.61	
27	VGALGLLGLFGLFAYT	324	0.57	
28	VNRLLRLPLPEPYLPP	427	0.54	
28	SGFAITIVMLVLVLVP	125	0.54	
29	FMRRIAFSGFAITIVM	118	0.52	

30	NYLPNAHNDFIFAIIG	303	0.51	

OVERLAP DISPLAY

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VLTRLLRRGTSDTDGSQTRGAEPVEGQRTGPEEASNPGSARPRTRFGAWLGRPMTSFHLIIAVAALLTTLGLIMVLSASAVRS
YDDDGSAWVIFGKQVLWTLVGLIGGYVCLRMSVRFMRRIAFSGFAITIVMLVLVLVPGIGKEANGSRGWFVVAGFSMQPSELA
KMAFAIWGAHLLAARRMERASLREMLIPLVPAAVVALALIVAQPDLGQTVSMGIILLGLLWYAGLPLRVFLSSLAAVVVSAAI
LAVSAGYRSDRVRSWLNPENDPQDSGYQARQAKFALAQGGIFGDGLGQGVAKWNYLPNAHNDFIFAIIGEELGLVGALGLLGL
FGLFAYTGMRIASRSADPFLRLLTATTTLWVLGQAFINIGYVIGLLPVTGLQLPLISAGGTSTAATLSLIGIIANAARHEPEA
VAALRAGRDDKVNRLLRLPLPEPYLPPRLEAFRDRKRANPQPAQTQPARKTPRTAPGQPARQMGLPPRPGSPRTADPPVRRSV
HHGAGQRYAGQRRTRRVRALEGQRYG$^{524}$
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