ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	263
Number of 16mers from the input sequence	248
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	AEHIAAAGDAEPRLVR	200	0.92	
2	GTPVDTRAWFGRDAPV	64	0.89	
3	SGISKAQRETWERLWP	36	0.87	
3	PGVGLRPDTPVASGQL	11	0.87	
4	STSIRSRRSGISKAQR	28	0.86	
4	GGAVIELLWKKHGCSE	242	0.86	
5	GSGSGTSTLAMAKAEP	84	0.85	
5	HHGQMHAQPGVGLRPD	3	0.85	
6	HAATDHPGYAEHIAAA	191	0.83	
6	PDPWPKARHHKRRLLQ	158	0.83	
6	HVDVIAVDVYRRGLAQ	100	0.83	

7	QHLIAPDSLCGVRVFF	142	0.81	
8	AEPRLVRVDPDTELLP	209	0.80	
8	TPVASGQLPSTSIRSR	19	0.80	
9	QRETWERLWPELGLLA	42	0.79	
10	LAMAKAEPHVDVIAVD	92	0.78	
10	PELGLLALPQSPRGTP	51	0.78	
11	LQPATMALIADRLVPS	172	0.76	
12	DRLVPSGVLHAATDHP	182	0.75	
13	SVVRPATKYERKAQLG	226	0.73	
13	PDTELLPISVVRPATK	218	0.73	
14	RGLAQLLCAIDKVGSD	111	0.71	
15	KYERKAQLGGGAVIEL	233	0.69	
16	WFGRDAPVVLEIGSGS	72	0.66	
17	DKVGSDGINIRLILGN	121	0.64	
18	NIRLILGNAVDVLQHL	129	0.59	

OVERLAP DISPLAY

MVHHGQMHAQPGVGLRPDTPVASGQLPSTSIRSRRSGISKAQRETWERLWPELGLLALPQSPRGTPVDTRAWFGRDAPVVLEI
GSGSGTSTLAMAKAEPHVDVIAVDVYRRGLAQLLCAIDKVGSDGINIRLILGNAVDVLQHLIAPDSLCGVRVFFPDPWPKARH
HKRRLLQPATMALIADRLVPSGVLHAATDHPGYAEHIAAAGDAEPRLVRVDPDTELLPISVVRPATKYERKAQLGGGAVIELL
WKKHGCSERDLKIR^{263}

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AEHIAAAGDAEPRLVR------------------------------------------------
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GTPVDTRAWFGRDAPV-------------------------------------------------------------------
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SGISKAQRETWERLWP-------------------------------------------------------------------
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PGVGLRPDTPVASGQL-------------------------------------------------------------------
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STSIRSRRSGISKAQR-------------------------------------------------------------------
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GGAVIELLWKKHGCSE------
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GSGSGTSTLAMAKAEP-------------------------------------------------------------------
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HHGQMHAQPGVGLRPD-------------------------------------------------------------------
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HAATDHPGYAEHIAAA---------------------------------------------------------
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PDPWPKARHHKRRLLQ-------------------------------------------------------------------
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HVDVIAVDVYRRGLAQ-------------------------------------------------------------------
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QHLIAPDSLCGVRVFF-------------------------------------------------------------------
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AEPRLVRVDPDTELLP---------------------------------------
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TPVASGQLPSTSIRSR-------------------------------------------------------------------
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QRETWERLWPELGLLA-------------------------------------------------------------------
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LAMAKAEPHVDVIAVD-------------------------------------------------------------------
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PELGLLALPQSPRGTP-------------------------------------------------------------------
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LQPATMALIADRLVPS-------------------------------------------------------------------
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DRLVPSGVLHAATDHP------------------------------------------------------------------
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SVVRPATKYERKAQLG----------------------
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PDTELLPISVVRPATK------------------------------
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RGLAQLLCAIDKVGSD-------------------------------------------------------------------
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KYERKAQLGGGAVIEL---------------
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WFGRDAPVVLEIGSGS-------------------------------------------------------------------
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DKVGSDGINIRLILGN-------------------------------------------------------------------
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NIRLILGNAVDVLQHL-------------------------------------------------------------------
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