ABCpred Prediction Server

Sequence name	
Length of the sequence	314
Number of 16mers from the input sequence	299
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	EHPEFEGPRRRARRER	37	0.90	
2	TQPGRTYDVSSPDLPT	297	0.89	
2	RVVIWGTTDRCEEKAE	275	0.89	
3	AAKRRARGQIVSEQNP	71	0.88	
3	VGRIAAPSVASITLTL	256	0.88	
4	YFDVDNPGPSDPTTKA	225	0.86	
4	LLQIDTQQVADRVATI	154	0.86	
5	RRERAERRAAQARATA	49	0.82	
5	SITLTLADGRVVIWGT	266	0.82	
5	TEHNEDPQIERVADDA	2	0.82	
6	QIERVADDAADEEAVT	9	0.81	

6	DRCEEKAEKLAALLTQ	283	0.81	
6	GAVSREEVLDAARVRP	135	0.81	
7	GPHLFDRDGVDFATDP	203	0.80	
7	EEAVTEPLATESKDEP	20	0.80	
7	IVIIGIGAVSREEVLD	129	0.80	
8	ATAIEQARRAAKRRAR	62	0.79	
8	TESKDEPAEHPEFEGP	29	0.79	
8	RITIVERVPVVVKDFS	186	0.79	
8	DRVATIRRVASARVQR	164	0.79	
9	GPRRRARRERAERRAA	43	0.78	
9	VDFATDPPPPALPYFD	212	0.78	
10	IVSEQNPAKPAARGVV	80	0.77	
11	AKPAARGVVRGLKALL	87	0.74	
12	SARVQRQYPSALRITI	174	0.72	
13	LHPEVASQVGRIAAPS	248	0.68	
14	PGPSDPTTKAALQVLT	231	0.62	
15	GLALYFTPAMSAREIV	115	0.59	
16	VRPATPLLQIDTQQVA	148	0.56	
17	EVLDAARVRPATPLLQ	141	0.55	

OVERLAP DISPLAY

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MTEHNEDPQIERVADDAADEEAVTEPLATESKDEPAEHPEFEGPRRRARRERAERRAAQARATAIEQARRAAKRRARGQIVSE
QNPAKPAARGVVRGLKALLATVVLAVVGIGLGLALYFTPAMSAREIVIIGIGAVSREEVLDAARVRPATPLLQIDTQQVADRV
ATIRRVASARVQRQYPSALRITIVERVPVVVKDFSDGPHLFDRDGVDFATDPPPPALPYFDVDNPGPSDPTTKAALQVLTALH
PEVASQVGRIAAPSVASITLTLADGRVVIWGTTDRCEEKAEKLAALLTQPGRTYDVSSPDLPTVK
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EHPEFEGPRRRARRER-----------------------------------------------------------------
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---------------------------------------------------TQPGRTYDVSSPDLPT--
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-----------------------RVVIWGTTDRCEEKAE-----------------------
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AAKRRARGQIVSEQNP-------------------------------------------------
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------VGRIAAPSVASITLTL-------------------------------------------
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YFDVDNPGPSDPTTKA--------------------------------------------------------
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LLQIDTQQVADRVATI-------------------------------------------------------
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RRERAERRAAQARATA-------------------------------------------------------
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---------------SITLTLADGRVVIWGT----------------------------------
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TEHNEDPQIERVADDA-------------------------------------------------------
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QIERVADDAADEEAVT-------------------------------------------------------
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---------------------------DRCEEKAEKLAALLTQ----------------
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GAVSREEVLDAARVRP-------------------------------------------------------
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GPHLFDRDGVDFATDP-------------------------------------------------------
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EEAVTEPLATESKDEP-------------------------------------------------------
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IVIIGIGAVSREEVLD---------------------------------------------------------
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ATAIEQARRAAKRRAR---------------------------------------------------------
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TESKDEPAEHPEFEGP---------------------------------------------------------
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RITIVERVPVVVKDFS---------------------------------------------------------
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DRVATIRRVASARVQR---------------------------------------------------------
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GPRRRARRERAERRAA---------------------------------------------------------
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VDFATDPPPPALPYFD---------------------------------------------------------
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IVSEQNPAKPAARGVV---------------------------------------------------------
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AKPAARGVVRGLKALL---------------------------------------------------------
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SARVQRQYPSALRITI---------------------------------------------------------
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LHPEVASQVGRIAAPS-----------------------------------------------------
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PGPSDPTTKAALQVLT---------------------------------------------------------
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GLALYFTPAMSAREIV---------------------------------------------------------
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VRPATPLLQIDTQQVA-------------------------------------------------------------------
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EVLDAARVRPATPLLQ-------------------------------------------------------------------
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