ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	449
Number of 16mers from the input sequence	434
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	LDTWQAAVRPNTKAFF	149	0.94
2	AGGIEAGKAFVNALKL	358	0.93
2	AGLPSSPWHERAKRLA	330	0.93
3	GIEGIDDILADLELGF	418	0.91
3	AGVIVDGGNFDWTQGR	230	0.91
3	TKQIHAGQHPDPTTNA	20	0.91
4	TPDPSYHGVVFAELGP	251	0.88
5	FGLEIPGNIYTRIGNP	58	0.87
6	VSFVDDPDDLDTWQAA	140	0.86
7	LSSGQAAETFAILNLA	94	0.85
7	DHIVSSPRLYGGTYNL	113	0.85
8	HGVVFAELGPPAFALK	257	0.84
9	YTRIGNPTTDVVEQRI	67	0.83
9	DWTQGRFPGFTTPDPS	240	0.83
10	PIYATTSYTFDDTAHA	39	0.82
10	SLVIHPASTTHAQLSP	385	0.82
10	RDYGSAASPFNAFLVA	279	0.82
10	VVHSATKYLGGHGAAI	214	0.82
11	HRNGVPLIVDNTIATP	186	0.80
12	YSLAKLGIEVSFVDDP	131	0.79
13	VEQRIAALEGGVAALF	78	0.78
13	SLRIERHVANAQRVAE	301	0.78
13	FAETISNPQIDLLDTP	164	0.78
13	GGTYNLFHYSLAKLGI	123	0.78
14	ADSNSTDADPTAHWSF	3	0.77
14	KARVQLLRDYGSAASP	272	0.77
15	QPLAQGADIVVHSATK	205	0.75
16	PWHERAKRLAPKGTGA	336	0.74
16	FLAARDDVLSVNYAGL	317	0.74
17	DLELGFAAARRFSADP	428	0.72
18	ASTTHAQLSPAEQLAT	391	0.71
19	DNTIATPYLIQPLAQG	195	0.70
20	AHWSFETKQIHAGQHP	14	0.69
21	SHVANIGDVRSLVIHP	375	0.65
22	PGLVRLAVGIEGIDDI	410	0.64
23	LATGVSPGLVRLAVGI	404	0.63
23	VLSVNYAGLPSSPWHE	324	0.63

24	LEGGVAALFLSSGQAA	85	0.62
25	DPTTNARALPIYATTS	30	0.59
26	AQRVAEFLAARDDVLS	311	0.58
26	VRPNTKAFFAETISNP	156	0.58
27	KAFVNALKLHSHVANI	365	0.53
28	SYTFDDTAHAAALFGL	45	0.52
28	LGPPAFALKARVQLLR	264	0.52
29	AAAARRFSADPQSVAAF	434	0.51

OVERLAP DISPLAY

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MSADSNSTDADPTAHWSFETKQIHAGQHPDPTTNARALPIYATTSYTFDDTAHAAALFGLEIPGNIYTRIGNPTTDVVEQRIAALEGGVAALFLSSGQAAETFAILNLAGAGDHIVSSPRLYGGTYNLFHYSLAKLGIEVSFVDDPDDLD
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----------------TKQIHAGQHPDPTTNA------------------------------------------------------------------------------------------------------------------------------
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-----------------------------------------------------FGLEIPGNIYTRIGNP---------------------------------------------------------------------------------------
-------------------------------------------------------------------------------------------------------------------------------------------VSFVDDPDDLD
---------------------------------------------------------------------------------LSSGQAAETFAILNLA-----------------------------------------------------------
-------------------------------------------------------------------------------------------DHIVSSPRLYGGTYNL-------------------------
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---------------------------------------------------------------YTRIGNPTTDVVEQRI------------------------------------------------------------------------------
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----------------------------PIYATTSYTFDDTAHA-----------------------------------------------------------------------------------------------------------------
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------------------------------------------------------------------------------------------------------------------------YSLAKLGIEVSFVDDP----
--------------------------------------------------------------------VEQRIAALEGGVAALF-------------------------------------------------------------------------
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------------------------------------------------------------------------------------------------------------------GGTYNLFHYSLAKLGI-----------
--ADSNSTDADPTAHWSF--------------------------------------------------------------------------------------------------------------------------------------------
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-----------AHWSFETKQIHAGQHP-----------------------------------------------------------------------------------------------------------------------------------
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------------------------------------------------------------------LEGGVAALFLSSGQAA------------------------------------------------------------------------
------------------------DPTTNARALPIYATTS--------------------------------------------------------------------------------------------------------------------
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--------------------------------------SYTFDDTAHAAALFGL-----------------------------------------------------------------------------------------------------
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