ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	214
Number of 16mers from the input sequence	199
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	AGVIRKDTDRDKILTA	176	0.96	
2	YGIIDTVLEYRKLSAQ	197	0.95	
3	GVQVDDASANDIMAQL	45	0.90	
4	PSFIEHSSFGVKESNP	17	0.89	
5	LLAAGTPGKRMALPNA	115	0.87	
6	RDITMYINSPGGGFTS	70	0.85	
7	QLLVLESLDPDRDITM	59	0.84	
7	RVLIHQPSLSGVIQGQ	131	0.84	
8	ILTAEEAKDYGIIDTV	188	0.82	
9	RHTGKDAGVIRKDTDR	170	0.81	
10	MAIYDTMQYVRADIQT	87	0.78	

11	ANDIMAQLLVLESLDP	53	0.77	
12	SQNSQIQPQARYILPS	3	0.75	
13	SFGVKESNPYNKLFEE	24	0.74	
14	DLEIQAAEIERMRTLM	149	0.73	
14	GKRMALPNARVLIHQP	122	0.73	
15	SPGGGFTSLMAIYDTM	78	0.72	
16	PQARYILPSFIEHSSF	10	0.71	
17	TLMETTLARHTGKDAG	162	0.69	
18	RADIQTVCLGQAASAA	97	0.68	
19	AEIERMRTLMETTLAR	155	0.66	
19	GQAASAAAVLLAAGTP	106	0.66	
20	LSGVIQGQFSDLEIQA	139	0.53	

OVERLAP DISPLAY

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MNSQNSQIQPQARYILPSFIEHSSFGVKESNPYNKLFEERIIFLGVQVDDASANDIMAQLLVLESLDPDRDITMYINSPGGGF
TSLMAIYDTMQYVRADIQTVCLGQAASAAAVLLAAGTPGKRMALPNARVLIHQPSLSGVIQGQFSDLEIQAAEIERMRTLMET
TLARHTGKDAGVIRKDTDRDKILTAEEAKDYGIIDTVLEYRKLSAQTA214
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---------AGVIRKDTDRDKILTA------------------------
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-----------------------------------------------------------------------------------
------------------------------YGIIDTVLEYRKLSAQ--
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GVQVDDASANDIMAQL-------------------------------------------------------------------
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PSFIEHSSFGVKESNP-------------------------------------------------------------------
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LLAAGTPGKRMALPNA-------------------------------------------------------------------
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RDITMYINSPGGGFTS-------------------------------------------------------------------
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QLLVLESLDPDRDITM-------------------------------------------------------------------
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RVLIHQPSLSGVIQGQ-------------------------------------------------------------------
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---------------------ILTAEEAKDYGIIDTV-----------
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---RHTGKDAGVIRKDTDR-----------------------------
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MAIYDTMQYVRADIQT-------------------------------------------------------------------
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ANDIMAQLLVLESLDP-------------------------------------------------------------------
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SQNSQIQPQARYILPS-------------------------------------------------------------------
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SFGVKESNPYNKLFEE-------------------------------------------------------------------
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DLEIQAAEIERMRTLM--------------------------------------------------
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GKRMALPNARVLIHQP-------------------------------------------------------------------
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SPGGGFTSLMAIYDTM-------------------------------------------------------------------
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PQARYILPSFIEHSSF-------------------------------------------------------------------
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TLMETTLARHTGKDAG-------------------------------------
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RADIQTVCLGQAASAA-------------------------------------------------------------------
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AEIERMRTLMETTLAR--------------------------------------------
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GQAASAAAVLLAAGTP-------------------------------------------------------------------
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LSGVIQGQFSDLEIQA------------------------------------------------------------
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