ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	316
Number of 16mers from the input sequence	301
Threshold setting (Default value is 0.5)	0.55

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	ASTIDHPGHVVSLAGV	162	0.94	
2	TRQVRARWEGRAGAGL	24	0.90	
3	VIVIVAETGRLPVDNP	184	0.89	
3	LAGIDTGTSFGGMGAS	113	0.89	
4	PLVIGMTRQVRARWEG	18	0.85	
5	GAAQIGGVMVGAPLVI	6	0.83	
6	APLVATGSPLDPSADL	82	0.82	

7	AGAGLLQPWRDLLKQL	35	0.77
7	EITIAALVEPTILLAV	130	0.77
8	GVMVGAPLVIGMTRQV	12	0.75
9	AMVLEYAGPRLALVEW	211	0.74
9	SFGGMGASREITIAAL	121	0.74
10	TIVFAAAPVIVAGTTL	61	0.73
10	LGKQQITPAGTTIVFA	50	0.73
10	GIAGAAPTALDVLTGV	247	0.73
10	ATHLELTMVHEAMVLE	200	0.73
11	AVFALSIPAGSANLGA	144	0.72
12	LLANLFLPWGIAGAAP	238	0.71
13	AGPRLALVEWAAGMRL	217	0.66
14	GRLPVDNPATHLELTM	192	0.64
15	PVIVAGTTLLIAAIAP	68	0.62
15	AVAAKVAILAVLLATF	264	0.62
15	GVLAFVALVIVIVAET	176	0.62
16	AVLLATFEVFLAKLRL	273	0.61
17	LGTVALTLAGIDTGTS	106	0.57

| 18 | PLDPSADLFAVVGLLF | 90 | 0.55 | |

OVERLAP DISPLAY

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MSYLAGAAQIGGVMVGAPLVIGMTRQVRARWEGRAGAGLLQPWRDLLKQLGKQQITPAGTTIVFAAAPVIVAGTTLLIAAIAPLVATGSPLDPSADLFAVVGLLFLGTVALTLAGI
DTGTSFGGMGASREITIAALVEPTILLAVFALSIPAGSANLGALVASTIDHPGHVVSLAGVLAFVALVIVIVAETGRLPVDNPATHLELTMVHEAMVLEYAGPRLALVEWAAGMRL
TVLLALLANLFLPWGIAGAAPTALDVLTGVVAVAAKVAILAVLLATFEVFLAKLRLFRVPELLAGSFLLALLAVTAANFFTVGA³¹⁶
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ASTIDHPGHVVSLAGV--------------------------------------------------------------------------------------------------
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TRQVRARWEGRAGAGL--------------------------------------------------------------------------------------------------
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VIVIVAETGRLPVDNP--------------------------------------------------------------------------------------------------
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LAGIDTGTSFGGMGAS--------------------------------------------------------------------------------------------------
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PLVIGMTRQVRARWEG--------------------------------------------------------------------------------------------------
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GAAQIGGVMVGAPLVI--------------------------------------------------------------------------------------------------
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APLVATGSPLDPSADL--------------------------------------------------------------------------------------------------
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AGAGLLQPWRDLLKQL--------------------------------------------------------------------------------------------------
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EITIAALVEPTILLAV--------------------------------------------------------------------------------------------------
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GVMVGAPLVIGMTRQV--------------------------------------------------------------------------------------------------
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AMVLEYAGPRLALVEW----------------------------------------------------------------
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SFGGMGASREITIAAL----------------------------------------------------------------
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TIVFAAAPVIVAGTTL----------------------------------------------------------------
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LGKQQITPAGTTIVFA----------------------------------------------------------------
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-------------GIAGAAPTALDVLTGV----------------------------------------------------
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ATHLELTMVHEAMVLE----------------------------------------------------------------
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AVFALSIPAGSANLGA----------------------------------------------------------------
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-----LLANLFLPWGIAGAAP-----------------------------------------------------------
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AGPRLALVEWAAGMRL----------------------------------------------------------------
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GRLPVDNPATHLELTM----------------------------------------------------------------
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PVIVAGTTLLIAAIAP----------------------------------------------------------------
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-----------------------------AVAAKVAILAVLLATF-----------------------------------
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GVLAFVALVIVIVAET----------------------------------------------------------------
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-----------------------------------AVLLATFEVFLAKLRL----------------------------
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LGTVALTLAGIDTGTS------------------------------------------------------------------------------
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PLDPSADLFAVVGLLF------------------------------------------------------------------------------
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