ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	288
Number of 16mers from the input sequence	273
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	GTAWLDTGTFDSLLDA	217	0.93	
1	SGTRLYPITMGISKQL	10	0.93	
1	MRGIILAGGSGTRLYP	1	0.93	
2	GAEGMALSLEEKPVTP	148	0.92	
3	KPMIYYPLTTLMMAGI	31	0.88	
4	GGAIFAYWVANPSAYG	128	0.87	
5	KVSIPEEVAWRMGWID	246	0.84	
5	TMGISKQLLPVYDKPM	18	0.84	
6	GWIDDEQLVQRARALV	258	0.83	
6	LSLEEKPVTPKSNYAV	154	0.83	
7	YGVVEFGAEGMALSLE	142	0.82	

8	RGEYEITEVNQVYLNQ	191	0.81	
9	NISYATQDQPDGLAQA	74	0.79	
9	ITTPHDAPGFHRLLGD	52	0.79	
9	PGLGTSLKRFQSISGG	114	0.79	
10	ALVLGDNIFYGPGLGT	103	0.77	
11	DQPDGLAQAFVIGANH	81	0.76	
11	LTTLMMAGIRDIQLIT	38	0.76	
11	EVAWRMGWIDDEQLVQ	252	0.76	
12	AVEVLARGTAWLDTGT	210	0.73	
13	ANHIGADSVALVLGDN	94	0.72	
14	GFHRLLGDGAHLGVNI	60	0.71	
14	TEVNQVYLNQGRLAVE	197	0.71	
15	DVIEIARGLKKSARGE	178	0.69	
16	AGIRDIQLITTPHDAP	44	0.68	
16	PKSNYAVPGLYFYDND	163	0.68	
17	QAFVIGANHIGADSVA	88	0.67	
18	VQRARALVKSGYGNYL	266	0.62	
18	FVRTLERRQGLKVSIP	235	0.62	
19	PGLYFYDNDVIEIARG	170	0.60	

OVERLAP DISPLAY

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MRGIILAGGSGTRLYPITMGISKQLLPVYDKPMIYYPLTTLMMAGIRDIQLITTPHDAPGFHRLLGDGAHLGVNISYATQDQP
DGLAQAFVIGANHIGADSVALVLGDNIFYGPGLGTSLKRFQSISGGAIFAYWVANPSAYGVVEFGAEGMALSLEEKPVTPKSN
YAVPGLYFYDNDVIEIARGLKKSARGEYEITEVNQVYLNQGRLAVEVLARGTAWLDTGTFDSLLDAADFVRTLERRQGLKVSI
PEEVAWRMGWIDDEQLVQRARALVKSGYGNYLLELLERN288
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GTAWLDTGTFDSLLDA--------------------------------------------------------
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SGTRLYPITMGISKQL-------------------------------------------------------------------
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MRGIILAGGSGTRLYP-------------------------------------------------------------------
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GAEGMALSLEEKPVTP--------------------------------------------------------------------
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KPMIYYPLTTLMMAGI--------------------------------------------------------------------
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GGAIFAYWVANPSAYG--------------------------------------------------------------------
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KVSIPEEVAWRMGWID---------------------------
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TMGISKQLLPVYDKPM--------------------------------------------------------------------
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--------GWIDDEQLVQRARALV---------------
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LSLEEKPVTPKSNYAV--------------------------------------------------------------------
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YGVVEFGAEGMALSLE--------------------------------------------------------------------
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RGEYEITEVNQVYLNQ--------------------------------------------------------------------
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NISYATQDQPDGLAQA--------------------------------------------------------------------
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ITTPHDAPGFHRLLGD--------------------------------------------------------------------
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PGLGTSLKRFQSISGG--------------------------------------------------------------------
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ALVLGDNIFYGPGLGT--------------------------------------------------------------------
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DQPDGLAQAFVIGANH-------------------------------------------------------------------
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LTTLMMAGIRDIQLIT-------------------------------------------------------------------
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--EVAWRMGWIDDEQLVQ---------------------
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AVEVLARGTAWLDTGT---------------------------------------------------------------
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ANHIGADSVALVLGDN-------------------------------------------------------------------
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GFHRLLGDGAHLGVNI-------------------------------------------------------------------
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TEVNQVYLNQGRLAVE-------------------------------------------------------------------
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DVIEIARGLKKSARGE-------------------------------------------------------------------
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AGIRDIQLITTPHDAP-------------------------------------------------------------------
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PKSNYAVPGLYFYDND-------------------------------------------------------------------
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QAFVIGANHIGADSVA-------------------------------------------------------------------
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----------------VQRARALVKSGYGNYL-------
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FVRTLERRQGLKVSIP--------------------------------------
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PGLYFYDNDVIEIARG-------------------------------------------------------------------
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