ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	486
Number of 16mers from the input sequence	471
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	GVPIWGDVELAWRLDA	90	0.93	
1	AWRLDAAGCYGPPRSW	100	0.93	
2	HWAPSLRPEAGAVLNI	173	0.92	
3	AVADGITYVDDSKATN	319	0.90	
3	TGQAVAAVLTRFGATP	19	0.90	
4	AGCYGPPRSWLVVTGT	106	0.89	
5	LGVRDAHLVDRAFSDD	249	0.88	
6	AGASFDQFTGYADRGE	460	0.86	
6	TGMPATVEVPVACVLD	407	0.86	
6	AVTSFRVGRHRAEVVA	304	0.86	
7	AVLIGRDRAAVAEALS	375	0.85	

7	HATMAEYTAAKARVLT	196	0.85	
7	RSWLVVTGTNGKTTTT	113	0.85	
8	TAAVAAARRMAQPGDT	439	0.83	
9	AVLNIAEDHLDWHATM	184	0.82	
9	HAMLIAGGRRAVLCGN	132	0.82	
10	ALSRHAPDVPVVQVVA	388	0.81	
11	VLVAGGRVTGQAVAAV	11	0.80	
12	DAVQQITGYALVVASP	59	0.79	
13	HAERGLPTVSSSDAVQ	47	0.78	
14	AGETVGAAVMTAAVAA	429	0.77	
14	PTVCDDDPVMLRPHAE	34	0.77	
14	VDDSKATNPHAARASV	327	0.77	
14	GVAVAGLDDSRAAALL	213	0.77	
15	AQPGDTVLLAPAGASF	449	0.76	
16	GSPAQVRVGFRLGEPA	230	0.74	
16	GSAVLDVLDEPAELLA	149	0.74	
17	EPAARELGVRDAHLVD	243	0.73	
18	VEVPVACVLDVAKDDK	413	0.72	
18	TRFGATPTVCDDDPVM	28	0.72	
19	DVAKDDKAGETVGAAV	422	0.71	
19	PLGPGAPVLVAGGRVT	4	0.71	
19	KARVLTGGVAVAGLDD	206	0.71	
20	EVAAMASRLVGAVLIG	364	0.70	
20	VVWIAGGLLKGASLHA	348	0.70	
20	ARSVGVPAGAIADAVT	291	0.70	
21	PGFSPATPLLAAAAAA	74	0.69	
21	RASVLAYPRVVWIAGG	339	0.69	
22	LPVASIPVPGPVGVLD	268	0.67	
22	GTNGKTTTTSMLHAML	120	0.67	
23	GYALVVASPGFSPATP	66	0.66	
23	DDSRAAALLDGSPAQV	220	0.66	
24	QFTGYADRGEAFATAV	466	0.65	
24	VVQVVAGEDTGMPATV	398	0.65	
25	DALAAAALARSVGVPA	283	0.64	

26	VGRHRAEVVAVADGIT	310	0.62	
27	DRAFSDDLTLLPVASI	258	0.60	
28	ELLAVELSSFQLHWAP	161	0.59	
29	GGRRAVLCGNIGSAVL	138	0.56	
30	GLLKGASLHAEVAAMA	354	0.54	

OVERLAP DISPLAY

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VLDPLGPGAPVLVAGGRVTGQAVAAVLTRFGATPTVCDDDPVMLRPHAERGLPTVSSSDAVQQITGYALVVASPGFSPATPLL
AAAAAAGVPIWGDVELAWRLDAAGCYGPPRSWLVVTGTNGKTTTTSMLHAMLIAGGRRAVLCGNIGSAVLDVLDEPAELLAVE
LSSFQLHWAPSLRPEAGAVLNIAEDHLDWHATMAEYTAAKARVLTGGVAVAGLDDSRAAALLDGSPAQVRVGFRLGEPAAREL
GVRDAHLVDRAFSDDLTLLPVASIPVPGPVGVLDALAAAALARSVGVPAGAIADAVTSFRVGRHRAEVVAVADGITYVDDSKA
TNPHAARASVLAYPRVVWIAGGLLKGASLHAEVAAMASRLVGAVLIGRDRAAVAEALSRHAPDVPVVQVVAGEDTGMPATVEV
PVACVLDVAKDDKAGETVGAAVMTAAVAAARRMAQPGDTVLLAPAGASFDQFTGYADRGEAFATAVRAVIR^486
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