ABCpred Prediction Server

INPUT INFORMATION

Sequence name	
Length of the sequence	679
Number of 16mers from the input sequence	664
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	PGSIQMGGVTVHDAWE	411	0.95	
2	VGGIDWDGHGLLGLED	255	0.93	
3	GVVIPGSYRNRHKAVH	291	0.92	
4	PGAQEVGQRKRPGKTQ	25	0.91	
4	SQSQSTRPARGLRRPP	10	0.91	
5	PRIIKATVAPDGSRTE	526	0.90	
5	DGSVTYDRGSDGVVIP	280	0.90	
6	PGYQMAGKTGTAQQIN	585	0.89	
6	DGSRTEEPRPDDIRVV	536	0.89	
6	TGMYQAIANDGVRVPP	511	0.89	
6	MTLLQMTGMYQAIAND	505	0.89	

6	HGVMPYTTTGVFGKSS	427	0.89
7	GVTVHDAWEHGVMPYT	418	0.88
8	AVVQRDPMGYQQGTGP	565	0.87
9	SDVAPAGRSTRARRTR	57	0.86
9	DPSQDIGRQGDKQLGN	360	0.86
9	AICAKYPEVGAERQDL	227	0.86
10	YQQGTGPTAGVPGYQM	574	0.85
10	VSSPFEPGSVNKIVAA	378	0.85
11	VGTRGASFVFRHRTGN	77	0.84
11	DGVRVPPRIIKATVAP	520	0.84
11	QRTGVGLPGESAGLVP	469	0.84
12	PGHSAAPLFHNIAGWL	643	0.83
12	QQVQQAKNLSGAHNVS	324	0.83
12	PKRIRRQLEEARKKTS	159	0.83
13	MQRENVPLSPDPGPPL	659	0.82
13	RYVIGIMLDNPARNSD	625	0.82
13	ERYYDMLRKFGLGQRT	456	0.82
13	AERQDLRQYPGGSLAA	237	0.82
14	VVSAQTAQTVRQMLRA	550	0.81
14	GRQGDKQLGNPAVSSP	366	0.81
15	CGCYFDDVYWITFAGI	603	0.80
15	GQRKRPGKTQKARQAQ	31	0.80
16	LFHNIAGWLMQRENVP	650	0.79
16	AQTVRQMLRAVVQRDP	556	0.79
16	RGSIVDRNNDRLAFTI	135	0.79
16	TDVQPAARGSIVDRNN	128	0.79
17	GAHNVSAVVLDAKTGE	334	0.78
17	PGGSLAANVVGGIDWD	246	0.78
17	TSAAPDPQQRLRDIAQ	173	0.78
18	RRTRQVVDVGTRGASF	69	0.77
18	QEATKSRPATRSDVAP	46	0.77
18	RHKAVHGSTVVLTLDN	301	0.77
18	RGLRRPPGAQEVGQRK	19	0.77
19	GRSTRARRTRQVVDVG	63	0.76

19	LDAKTGEVLAMANDNT	343	0.76
19	LRDIAQEVAGKLNNKP	183	0.76
20	AGIATADNPRYVIGIM	616	0.75
21	ASAVIEHGLSSPDEVL	393	0.74
21	EVAGKLNNKPDAAAVL	189	0.74
22	VPPIDQWSGSTFANLP	483	0.73
22	VLAMANDNTFDPSQDI	350	0.73
23	GVFGKSSNVGTLMLSQ	436	0.72
23	LRAQAAGQLKVTDVQP	117	0.72
24	TQKARQAQEATKSRPA	39	0.71
24	DGHGLLGLEDSLDAVL	261	0.71
25	SGSTFANLPIGQGLSM	490	0.69
25	VGTLMLSQRVGPERYY	444	0.69
25	LARAVDPAVASAICAK	216	0.69
26	LPGESAGLVPPIDQWS	475	0.68
26	KLQSDETFVYLARAVD	206	0.68
27	DRLAFTIEARALTFQP	144	0.67
28	DVYWITFAGIATADNP	609	0.66
29	GSTVVLTLDNDIQFYV	307	0.65
30	PRPDDIRVVSAQTAQT	543	0.63
30	DEVLQVPGSIQMGGVT	405	0.63
31	DNDIQFYVQQQVQQAK	315	0.60
32	EARALTFQPKRIRRQL	151	0.59
33	NNKPDAAAVLKKLQSD	195	0.51

OVERLAP DISPLAY

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VSRAAPRRASQSQSTRPARGLRRPPGAQEVGQRKRPGKTQKARQAQEATKSRPATRSDVAPAGRSTRARRTRQVVDVGTRGAS
FVFRHRTGNAVILVLMLVAATQLFFLQVSHAAGLRAQAAGQLKVTDVQPAARGSIVDRNNDRLAFTIEARALTFQPKRIRRQL
EEARKKTSAAPDPQQRLRDIAQEVAGKLNNKPDAAAVLKKLQSDETFVYLARAVDPAVASAICAKYPEVGAERQDLRQYPGGS
LAANVVGGIDWDGHGLLGLEDSLDAVLAGTDGSVTYDRGSDGVVIPGSYRNRHKAVHGSTVVLTLDNDIQFYVQQQVQQAKNL
SGAHNVSAVVLDAKTGEVLAMANDNTFDPSQDIGRQGDKQLGNPAVSSPFEPGSVNKIVAASAVIEHGLSSPDEVLQVPGSIQ
MGGVTVHDAWEHGVMPYTTTGVFGKSSNVGTLMLSQRVGPERYYDMLRKFGLGQRTGVGLPGESAGLVPPIDQWSGSTFANLP
IGQGLSMTLLQMTGMYQAIANDGVRVPPRIIKATVAPDGSRTEEPRPDDIRVVSAQTAQTVRQMLRAVVQRDPMGYQQGTGPT
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AGVPGYQMAGKTGTAQQINPGCGCYFDDVYWITFAGIATADNPRYVIGIMLDNPARNSDGAPGHSAAPLFHNIAGWLMQRENV
PLSPDPGPPLVLQAT^{679}

PGSIQMGGVTVHDAWE---

VGGIDWDGHGLLGLED---

GVVIPGSYRNRHKAVH---

PGAQEVGQRKRPGKTQ---

SQSQSTRPARGLRRPP---

PRIIKATVAPDGSRTE---


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