ABCpred Prediction Server

`INPUT INFORMATION`

Sequence name	
Length of the sequence	575
Number of 16mers from the input sequence	560
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	FSAGGYPLEFGTISVS	80	0.90	
1	TPPDPDGKVLRALANP	376	0.90	
1	DVTIIDAFEAVGACSR	177	0.90	
2	FSRIGSGVPHLADVKP	313	0.89	
2	ICPGEGACGGMYTANT	207	0.89	
3	YEGPKGGPGMREMLAI	454	0.87	
3	DHIGGVPVVMKALLDA	338	0.87	
4	DGISMGHEGMHFSLVS	96	0.86	
4	RFSGGTTGLCVGHIAP	489	0.86	
4	EMLAITGAIKGAGLGK	465	0.86	
4	HPSGGITILHGSLAPE	393	0.86	

4	TVTGHTMAENLAAITP	362	0.86	
5	GRHVMSDVDHIGGVPV	330	0.85	
5	VGACSRGLMSRADVDA	187	0.85	
6	PHLADVKPFGRHVMSD	321	0.84	
6	CGGMYTANTMASAAEA	214	0.84	
7	ASRQQDFSPPPPRYTT	540	0.83	
7	LDVLADPAEFASRQQD	530	0.83	
7	KALLDAGLLHGDCLTV	348	0.83	
7	TDRRRDGFARRSGQAV	243	0.83	
7	SVSTVADIKPRSRDVT	10	0.83	
8	IRLDVAGRVLDVLADP	521	0.82	
8	DVFEGTARVFDGERAA	420	0.82	
8	GITARDILTKEAFENA	265	0.82	
8	SREVIADSVEVVMQAE	111	0.82	
9	TITVGDAVVIRYEGPK	443	0.81	
10	ASSWNEITPCNLSLDR	55	0.80	
10	GHIAPEAVDGGPIALL	500	0.80	
10	AVVKTAGFDSDVFEGT	410	0.80	
10	VDAIERAICPGEGACG	200	0.80	
11	RAVGMDDEDFAKPQIG	38	0.79	
11	HLLAIAHEANVALSLQ	296	0.79	
11	SRDVTDGLEKAAARGM	21	0.79	
11	GLMSRADVDAIERAIC	193	0.79	
12	PGRAKLSDGSERDVTI	165	0.78	
13	FLYAGSILPGRAKLSD	157	0.77	
14	LRALANPIHPSGGITI	385	0.74	
15	GGPIALLRNGDRIRLD	509	0.73	
15	PGMLMAAARLDLAAVF	142	0.73	
16	DVLLLTDGRFSGGTTG	481	0.71	
16	AKPQIGVASSWNEITP	48	0.71	
16	VVMAFGGSTNAVLHLL	283	0.71	
16	EGMHFSLVSREVIADS	103	0.71	
17	PPPRYTTGVLSKYVKL	549	0.69	
18	AEALGMSLPGSAAPPA	227	0.67	

19	SVEVVMQAERLDGSVL	118	0.66	
20	ITPCNLSLDRLANAVK	61	0.65	
20	TGVLSKYVKLVSSAAV	555	0.65	
21	QAERLDGSVLLAGCDK	124	0.64	
22	AFENAIAVVMAFGGST	276	0.63	
23	LLAGCDKSLPGMLMAA	133	0.62	
24	LANAVKEGVFSAGGYP	71	0.61	
25	GAIKGAGLGKDVLLLT	471	0.60	
26	TTDEAASVSTVADIKP	4	0.59	

OVERLAP DISPLAY

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MPQTTDEAASVSTVADIKPRSRDVTDGLEKAAARGMLRAVGMDDEDFAKPQIGVASSWNEITPCNLSLDRLANAVKEGVFSAG
GYPLEFGTISVSDGISMGHEGMHFSLVSREVIADSVEVVMQAERLDGSVLLAGCDKSLPGMLMAAARLDLAAVFLYAGSILPG
RAKLSDGSERDVTIIDAFEAVGACSRGLMSRADVDAIERAICPGEGACGGMYTANTMASAAEALGMSLPGSAAPPATDRRRDG
FARRSGQAVVELLRRGITARDILTKEAFENAIAVVMAFGGSTNAVLHLLAIAHEANVALSLQDFSRIGSGVPHLADVKPFGRH
VMSDVDHIGGVPVVMKALLDAGLLHGDCLTVTGHTMAENLAAITPPDPDGKVLRALANPIHPSGGITILHGSLAPEGAVVKTA
GFDSDVFEGTARVFDGERAALDALEDGTITVGDAVVIRYEGPKGGPGMREMLAITGAIKGAGLGKDVLLLTDGRFSGGTTGLC
VGHIAPEAVDGGPIALLRNGDRIRLDVAGRVLDVLADPAEFASRQQDFSPPPPRYTTGVLSKYVKLVSSAAVGAVCG575
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