

I EDB Analysis Resource

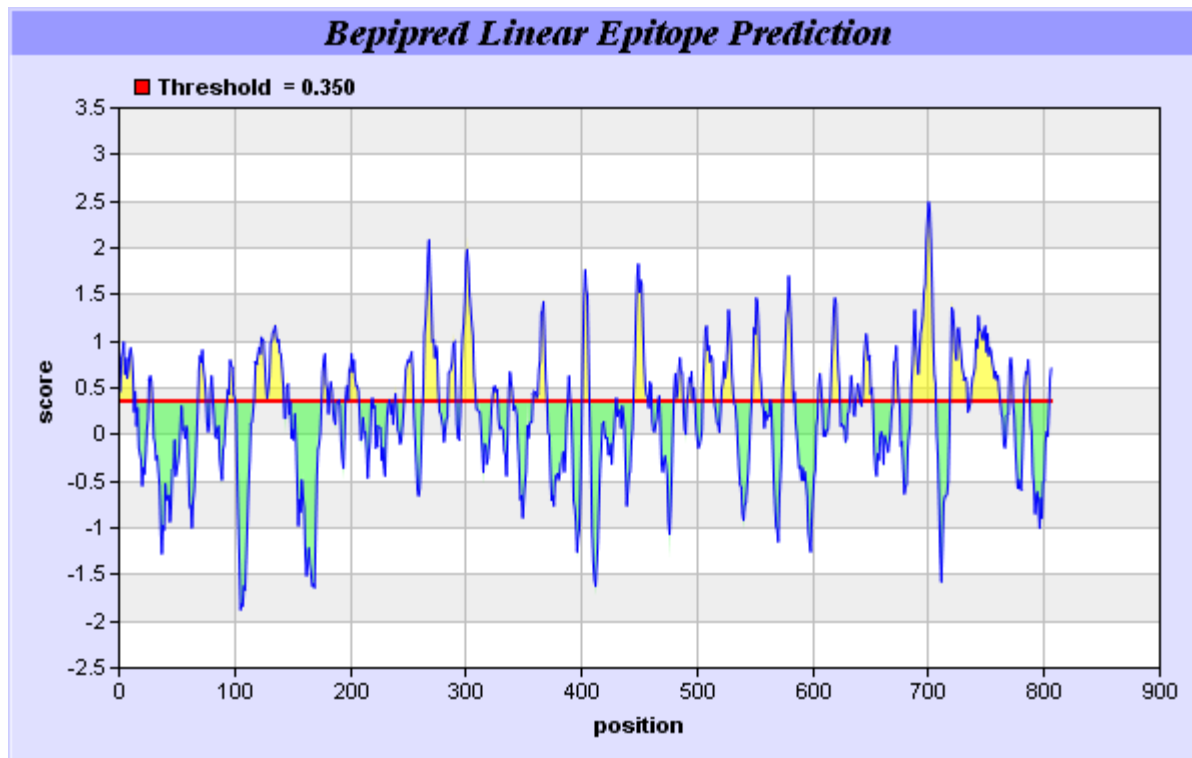
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Sequence: P95175

```

1  MTQAADTDIR  VGQPEMVTLT  IDGVEISVPK  GTLVIRAAEL  MGIQIPRFCD  HPLLEPVGAC
61  RQCLVEVEGQ  RKPLASCTTV  ATDDMVVRTQ  LTSEIADKAQ  HGVMELLIN  HPLDCPMCDK
121  GGECPLQNGA  MSNGRTDSRF  TEAKRTFAKP  INISAQVLLD  RERCILCARC  TRFSDQIAGD
181  PFIDMQERGA  LQQVGIYADE  PFESYFSGNT  VQICPVGALT  GTAYRFRARP  FDLVSSPSVC
241  EHCASGCAQR  TDHRRGKVLK  RLAGDDPEVN  EEWNCDKGRW  AFTYATQPDV  ITTPLIRDGG
301  DPKGALVPTS  WSHAMAVAAQ  GLAAARGRTG  VLVGGRVTWE  DAYAYAKFAR  ITLTNDIDF
361  RARPHSAEEA  DFLAARIAGR  HMAVSADLE  SAPVLLVGF  EPEDESPIVF  LRLRKAARRH
421  RVPVYTIAPF  ATGGLHKMSG  RLIKTVPGGE  PAALDDLATG  AVGDLLATPG  AVIIVGERLA
481  TVPGGLSAAA  RLADTTGARL  AWPVRRAGER  GALEAGALPT  LLPGGRPLAD  EVARAQVCAA
541  WHIAELPAAA  GRDADGILAA  AADETLAALL  VGGIEPADFA  DPDAVLAALD  ATGFVVSLEL
601  RHSTVTERAD  VVFPVAPTQ  KAGAFVNWEG  RYRTFEPALR  GSTLQAGQSD  HRVLDALADD
661  MGVHLGVPTV  EAAREELAAL  GIWDGKHAAG  PHIAATGPTQ  PEAGEAILTG  WRMLLDEGRL
721  QDGEPYLAGT  ARTPVRLSP  DTAAEIGAAD  GEAVTVSTSR  GSITLPCSVT  DMPDRVVWLP
781  LNSAGSTVHR  QLRVTIGSIV  KIGAGS

```



Average:0.209 Minimum:-1.889 Maximum:2.492 Threshold: 0.350

[Change](#)

[Click here to view plotted values in table format](#)

Predicted epitopes:

No.	Start Position	End Position	Peptide	Peptide Length
1	1	12	MTQAADTDIRVG	12
2	14	14	P	1
3	26	29	ISVP	4
4	69	75	GQRKPLA	7
5	79	81	TVA	3
6	94	100	EIADKAQ	7
7	117	142	MCDKGGECPLQNQAMSNGR TDSRFTE	26
8	145	146	RT	2
9	176	180	QIAGD	5
10	182	184	FID	3
11	190	190	A	1
12	196	207	IYADEPFESYFS	12
13	219	219	L	1
14	234	234	V	1
15	239	239	V	1
16	247	254	CAQRTDHR	8
17	263	276	AGDDPEVNEEW NCD	14
18	285	291	ATQPDVI	7
19	296	308	IRDGGDPKGALVP	13
20	323	327	AAARG	5
21	337	340	VTWE	4
22	358	370	IDFRARPHSAEEA	13
23	388	390	DLE	3
24	401	406	EPEDES	6
25	430	430	F	1
26	445	457	TVPGGEP AALDDL	13
27	459	460	TG	2
28	467	467	A	1
29	480	487	ATVPGGLS	8
30	491	497	RLADTTG	7
31	505	514	RRAGERGALE	10
32	521	531	LLPGGRPLADE	11
33	547	555	PAAAGR DAD	9
34	563	563	D	1
35	574	584	IEPADFADPDA	11

36	605	607	VTE	3
37	615	623	VAPTTQKAG	9
38	632	634	YRT	3
39	638	640	ALR	3
40	643	651	TLQAGQSDH	9
41	670	674	VEAAR	5
42	685	706	GKHAAGPHIAATGPTQPEAGEA	22
43	719	733	RLQDGEPYLAGTART	15
44	737	762	RLSPDTAAEIGAADGEAVTVSTSRGS	26
45	770	772	TDM	3
46	783	787	SAGST	5

Reference: [Jens Erik Pontoppidan Larsen, Ole Lund and Morten Nielsen. Improved method for predicting linear B-cell epitopes. Immunome Res. 2006; 2: 2.](#)