

I EDB Analysis Resource

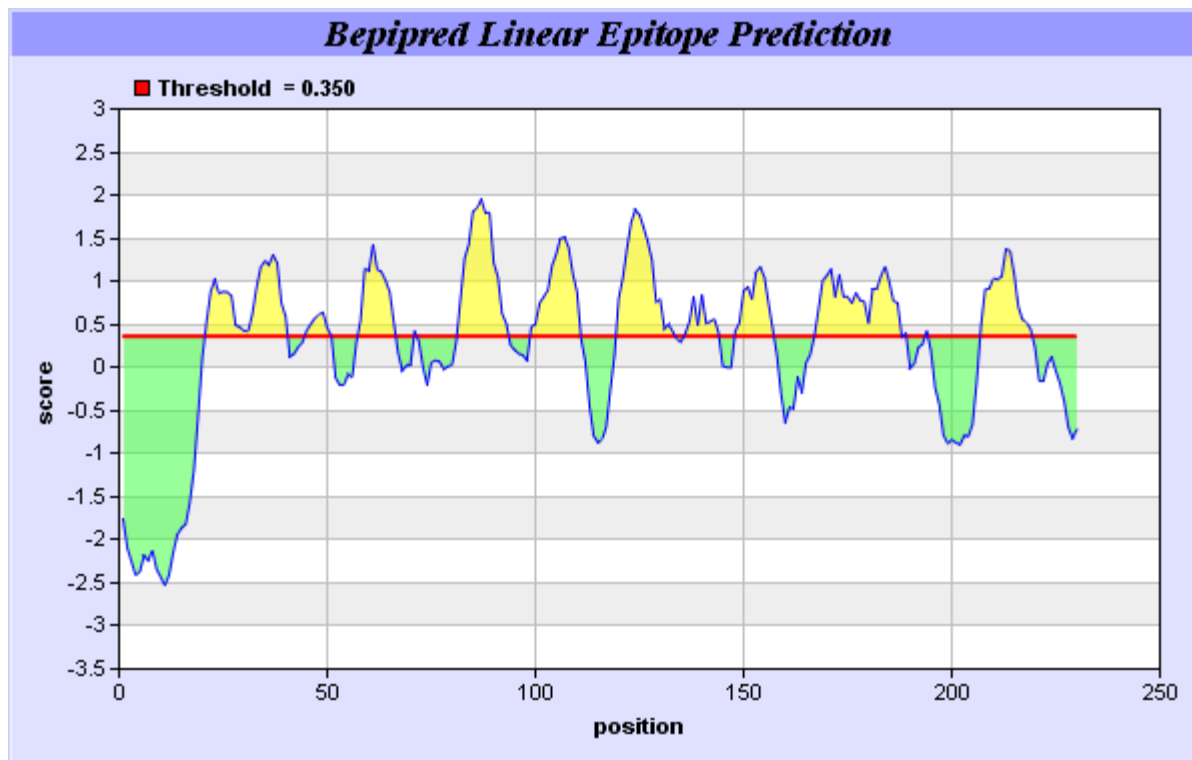
[Antibody Epitope Prediction](#)
[Example Sequences](#)
[Tutorial](#)
[External Links](#)
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[Reference](#)
[Contact](#)

Sequence:

```

1  VRIKIFMLVT  AVLLCCSGV  ATAAPKTYCE  ELKGTDTGQA  CQIQMSDPAY  NINISLPSYY
61  PDQKSLNYI  AQRDKFLSA  ATSSTPREAP  YELNITSATY  QSAIPPRGTQ  AVVLKVYQNA
121 GGTHTTTYK  AFDWDQAYRK  PITYDTLWQA  DTDPLPVVFP  IVQGELSKQT  GQQVSIAPNA
181 GLDPVNYQNF  AVTNDGVIFF  FNPGELLPEA  AGPTQVLVPR  SAIDSMLA

```



Average:0.3 Minimum:-2.532 Maximum:1.951 Threshold: 0.350

[Change](#)

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

Predicted epitopes:

No.	Start Position	End Position	Peptide	Peptide Length
1	21	40	ATAAPKTYCEELKGTDTGQA	20
2	45	51	MSDPAYN	7
3	58	66	SYYPDQKSL	9

4	71	71	A	1
5	82	93	TSSTPREAPYEL	12
6	99	110	TYQSAIPPRGTQ	12
7	120	133	AGGTHPTTTYKAFD	14
8	136	144	QAYRKPITY	9
9	148	157	WQADTDPLPV	10
10	167	189	SKQTGQQVSIAPNAGLDPVNYQN	23
11	194	194	N	1
12	207	219	LPEAAGPTQVLVP	13

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