

I EDB Analysis Resource

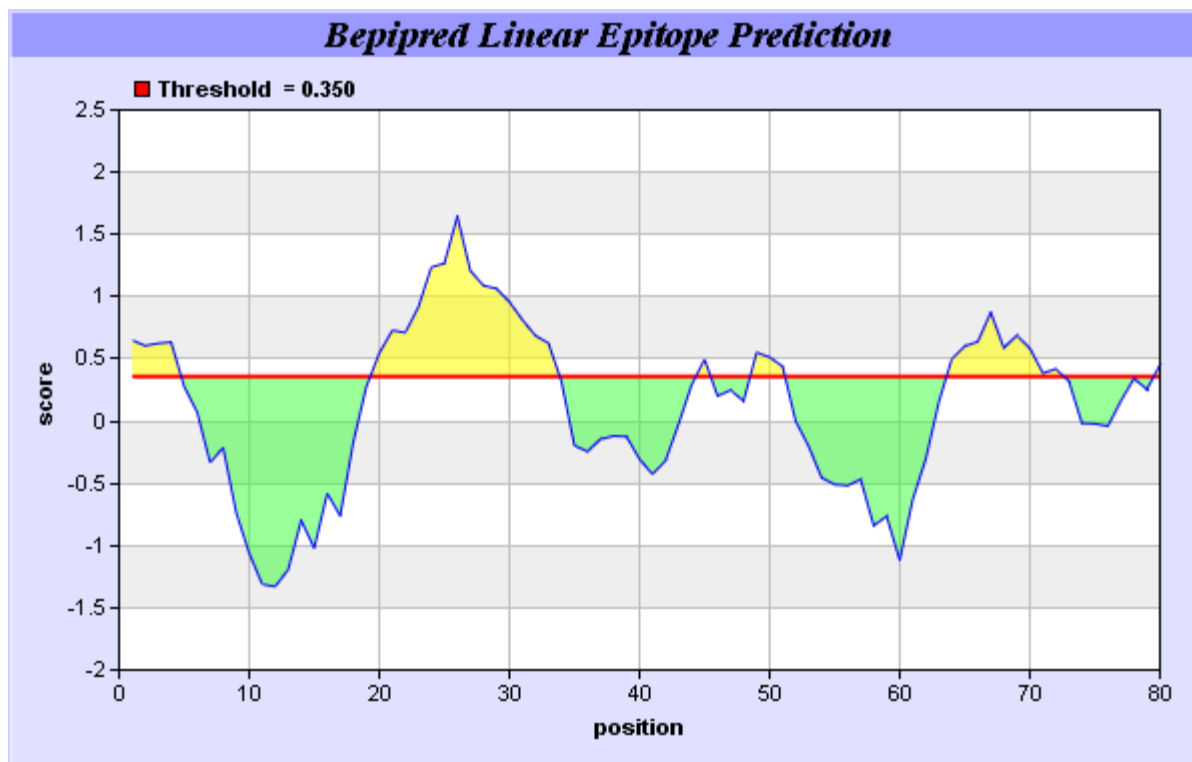
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Sequence:

```

1  DPFRAAKTLN  INFFVHDPFT  LEPYSRDP RN  IARKAENYLI  STGIADTAYF  GAEAEFYIFD
61  SVSFDSRANG  SFYEVDAISG  WWNTGAATE  ADGSPNRGYK  VRHKGGYFPV  APNDQYVDLR
121 DKMLTNLINS  GFILEKGHHE  VGSGGQAEIN  YQFNSLLHAA  D  DMQLYKYI  IKNTAWQNGK
181 TVTFMPKPLF  GDN GSGMHCH  QSLWKDGAPL  MYDETYAGL  SDTARHYIGG  LLHHAPSLLA
241 FT  NPTVNSY  KRLVPGYEAP  INLVYSQRNR  SACVRIPITG  SNPKAKRLEF  RSPDSSGNPY
301 LAFSAML MAG  LDGIKNKIEP  QAP  VDKDLY  ELPPEEAASI  PQTPTQLSDV  IDRLEADHEY
361 LTEGGVFTND  LIETWISFKR  ENEIEPVNIR  PHPYEFALYY  DV

```



Average:0.111 Minimum:-1.33 Maximum:1.643 Threshold: 0.350

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

Predicted epitopes:

No.	Start Position	End Position	Peptide	Peptide Length
1	1	4	DPFR	4

2	20	33	TLEPYSRDPRNIAR	14
3	45	45	A	1
4	49	51	YFG	3
5	64	72	FDSRANGSF	9

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