

I EDB Analysis Resource

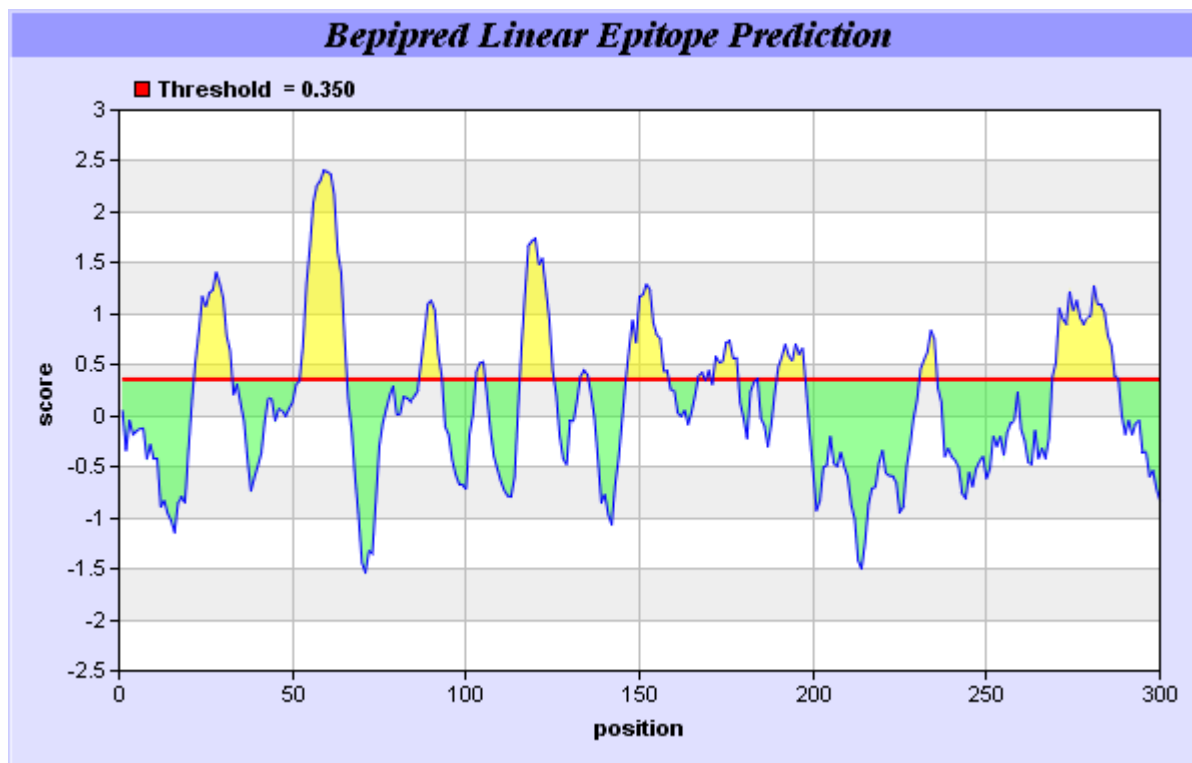
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Sequence:

```

1 VTTVGFDVAA RLGTLTAMV TPFSGDGSLD TATAARLANH LVDQGC DGLV VSGTTGESPT
61 TTDGEKIELL RAVLEAVGDR ARVIAGAGTY DTAHSIRLAK ACAAEGAHGL LVVTPYYSKP
121 PQRGLQAHFT AVADATELPM LLYDIPGRSA VPIEPDTIRA LASHPNIVGV KDAKADLHSG
181 AQIMADTGLA YYSGDDALNL PWLAMGATGF ISVIAHLAAG QLRELLSAFG SGDIATARKI
241 NIAVAPLCNA MSRLGGVTL S KAGLRLQID VGDPRLPQVA ATPEQIDALA ADMRAASVLR

```



Average:0.113 Minimum:-1.539 Maximum:2.407 Threshold:

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

Predicted epitopes:

No.	Start Position	End Position	Peptide	Peptide Length
1	22	32	PFSGDGSLDTA	11
2	53	65	GTTGESPTTTDGE	13
3	87	93	AGTYDTA	7
4	103	105	AAE	3
5	116	125	YYSKPPQRGL	10
6	133	135	ADA	3
7	147	158	GRSAVPIEPDTI	12
8	167	168	IV	2
9	170	170	V	1
10	172	178	DAKADLH	7
11	184	184	M	1
12	190	197	AYYSGDDA	8
13	231	235	SGDIA	5
14	269	288	IDVGDPRLPQVAATPEQIDA	20

Reference: [Jens Erik Pontoppidan Larsen, Ole Lund and Morten Nielsen. Improved method for predicting lir](#)