

I EDB Analysis Resource

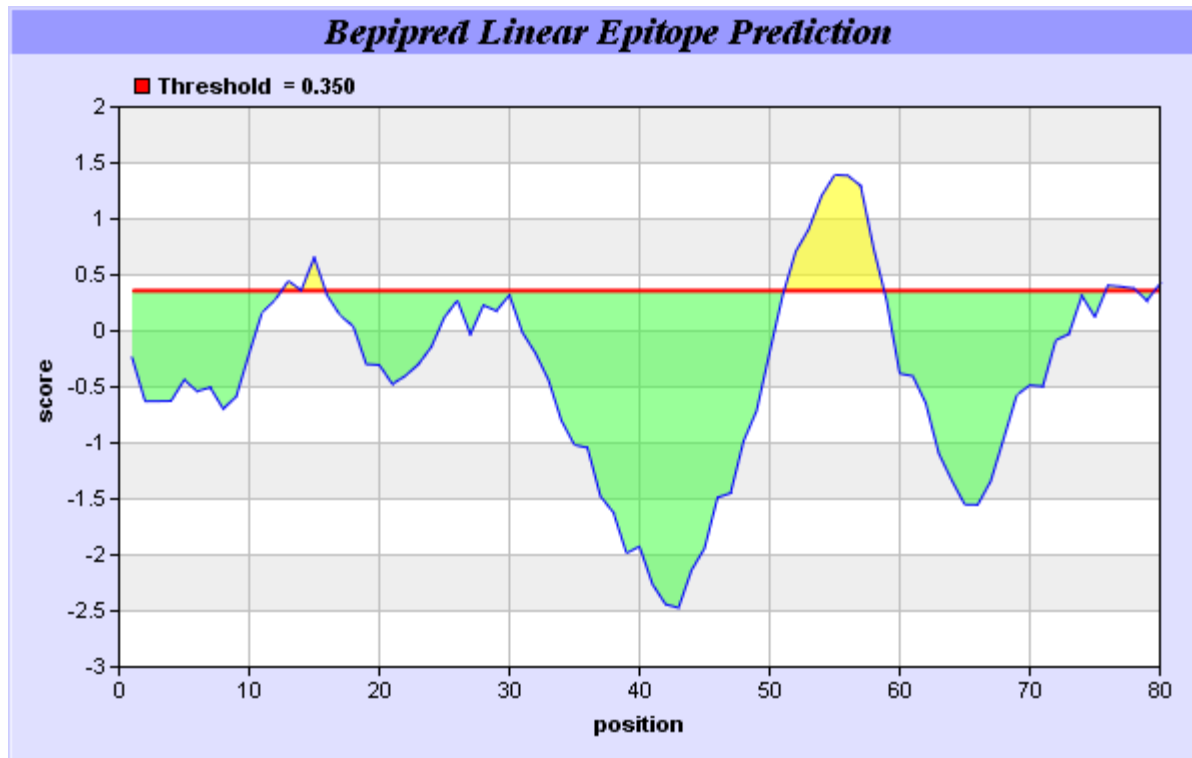
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Sequence:

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1 MTETILAAQI EVGEHHTATW LGMTVNTDTV LSTAIAGLIV IALAFYLRAK VTSTDVPGGV
61 QLFFEAITIQ MRNQVESAIG MRIAPFVLP LAVTIFVFIL ISNWLAVLPV QYTDKHGHTT
121 ELLKSAADI NYVLALALFV FVCYHTAGIW RRGIVGHPIK L LKGHVTLT APINLVEEVA
181 KPISLSLRLF GNIFAGGILV ALIALFPPYI MWAPNAIWKA FDLFVGAIQA FIFALLTILY
241 FS QAMELEE EHH

```



Average: -0.378 Minimum: -2.472 Maximum: 1.394 Threshold: 0.350

[Change](#)

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

Predicted epitopes:

No.	Start Position	End Position	Peptide	Peptide Length
1	13	15	GEH	3
2	52	58	TSTDVPG	7

3	76	78	ESA	3
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Reference: [Jens Erik Pontoppidan Larsen, Ole Lund and Morten Nielsen. Improved method for predicting linear B-cell epitopes. Immunome Res. 2006; 2: 2.](#)