

I EDB Analysis Resource

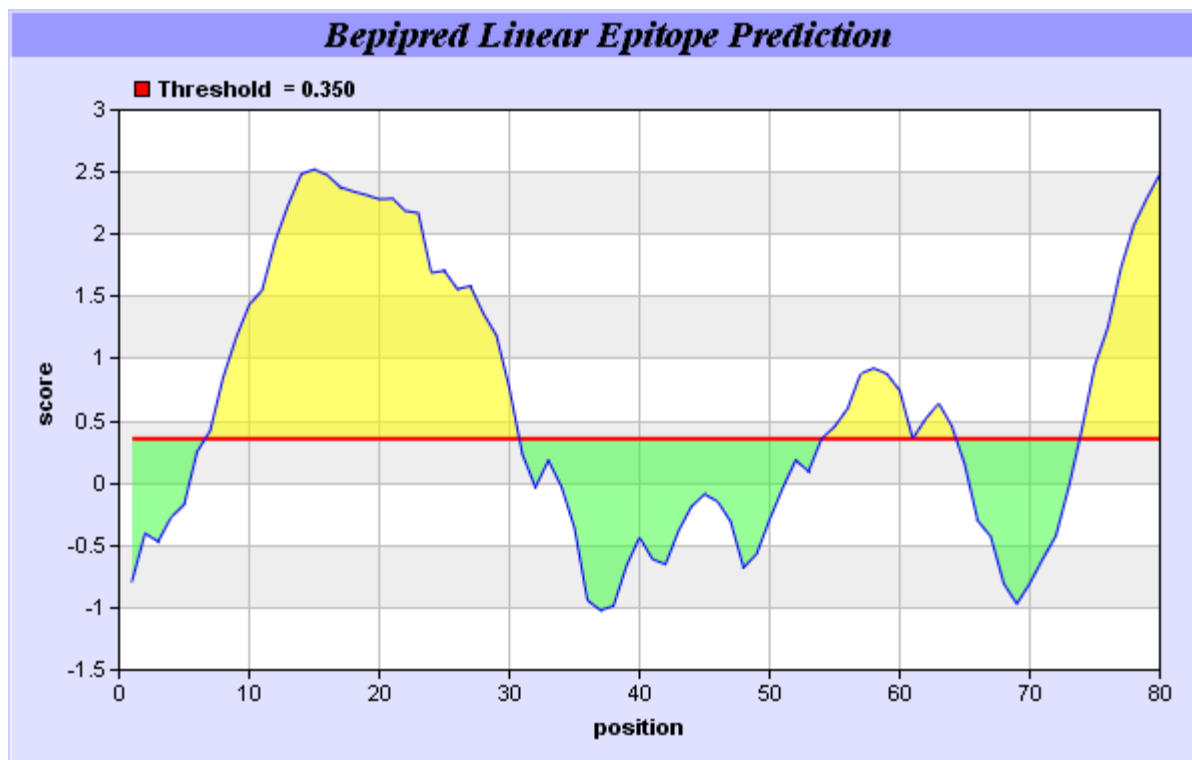
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Sequence:

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1 MAVVDDLAPG MDSSPPSEDY GRQPPQDLAA EQSVLGGMLL SKDAIADVLE RLRPGDFYRP
61 AHQNVYDAIL DLYGRGEPAD AVTVAAELD RRGLLRRIGG APYLHTLIST VPTAANAGYY
121 ASIVA EKALL RRLVEAGTRV VQYG YAGAEG ADVAEVVDRA Q AEIYDVAD RRLSEDFVAL
181 EDLLQPTMDE IDAIASSGGL ARGVATGFTE LDEV TNLHP GQMVI VAARP GVGKSTLGLD
241 FM RSCSIRH RMASVIFSLE MSKSEIVMRL LSAEAKIKLS DMRSGRMSDD DWTRLARMS
301 EISEAPLFID DSPNLTMMEI RAK ARRLRQ KANLKLIVVD YLQLMTSGKK YESRQVEVSE
361 FSRHLKLLAK ELEVPVVAIS QLNRGPEQRT DKKPMLADLR ESGC LTAST RILRADTGAE
421 VAFGELMRSG ERPMVWSLDE RLRMVARPMI NVFPSGRKEV FRLRLASGRE VEATGSHPFM
481 KFEGW TPLA QLKVGDR IAA PRRVPEPIDT QRMPESELIS LARMIGDGSC LKNQPIRYEP
541 VDEANLAAVT VSAAHSDRAA IRDDYL AAR VPSLRPARQR LPRGRCTPIA AWLAGLGLFT
601 KRSHEKCVPE AVFRAPNDQV ALFLRHLWSA GGSVRWDPTN GQGRVYY GS TSRRLIDDVA
661 QLLLRVGFIS WITHAPKLG G HDSWRLHIHG AKDQVRFLRH VGVHGAEAVA AQEMLRQLKG
721 PVRNPNLD S APKKVWAQVR NRLSAKQMMD IQLHEPTMWK HSPSRSRPHR AEARIEDRAI
781 HELARGDAYW DTVVEITSIG DQHVFDGTV SGTHNFVANG ISLHNSLEQD ADVVILLHRP
841 DAFDRDDPRG GEADFILAKH RNGPTKTVTV AHQLHLSRFA NMAR

```



Average:0.6 Minimum:-1.02 Maximum:2.522 Threshold: 0.350

[Change](#)

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

Predicted epitopes:

No.	Start Position	End Position	Peptide	Peptide Length
1	7	30	LAPGMDSSPPSEDYGRQPPQDLAA	24
2	54	64	PGDFYRPAHQN	11

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