

IEDB Analysis Resource

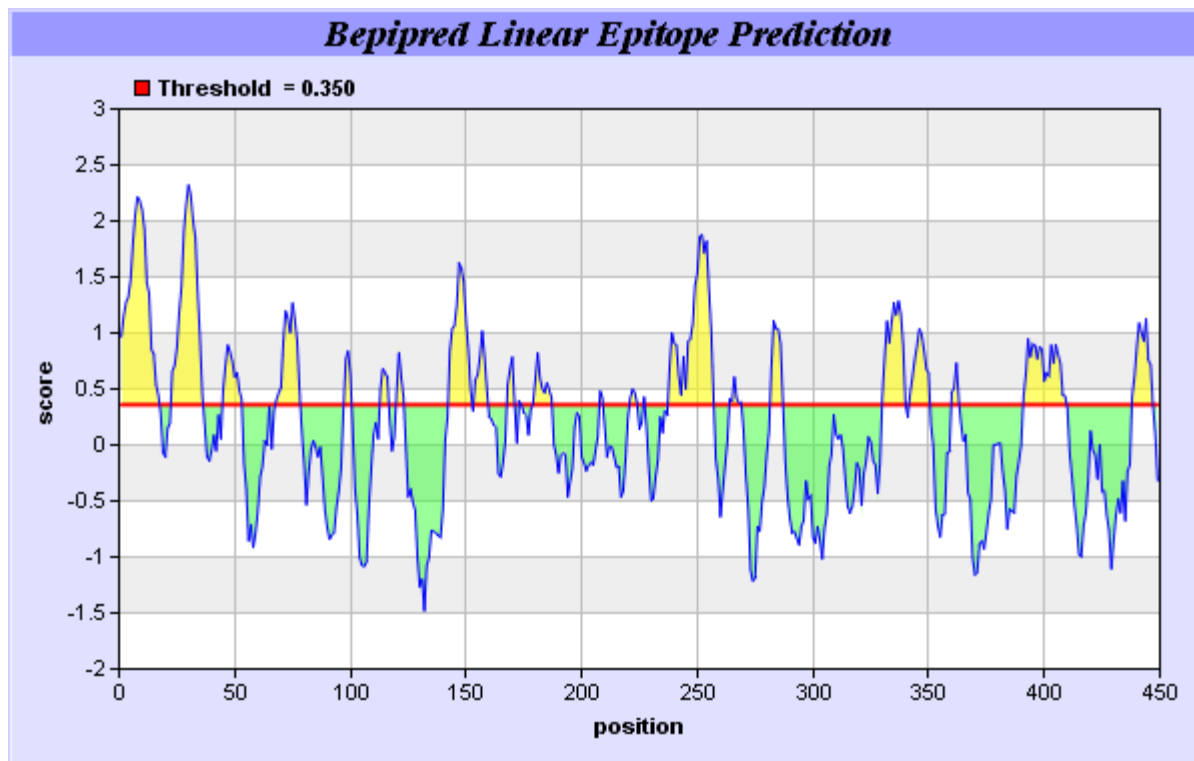
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Sequence: O53390

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1 MSADSNSTDA DPTAHWSFET KQIHAGQHPD PTTNARALPI YATTSYTFDD TAHAAALFGL
61 EIPGNIYTRI GNPTDVVEQ RIAALEGGVA ALFLSSGQAA ETFAILNLAG AGDHIVSSPR
121 LYGGTYNLFH YSLAKLGIEV SFVDDPDDL TWQAAVRPNT KAFFAETISN PQIDLLDTPA
181 VSEVAHRNGV PLIVDNTIAT PYLIQPLAQQ ADIVVHSATK YLGGHGAAIA GVIVDGGNFD
241 WTQGRFPGFT TPDPsyHGvV FAELGPPAFA LKARVQLLRD YGSAASPFNA FLVAQGLETl
301 SLRIERHVAN AQRVAEFLAA RDDVLSVNYA GLPSSPWHER AKRLAPKGTG AVLSFELAGG
361 IEAGKAFVNA LKLHSHVANI GDVRSLVlHP ASTTHAQLSP AEQLATGVSP GLVRLAVGIE
421 GIDDILADLE LGFAAARRFS ADPQSVAAF

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Average:0.178 Minimum:-1.486 Maximum:2.32 Threshold: 0.350

Predicted epitopes:

No.	Start Position	End Position	Peptide	Peptide Length
1	1	17	MSADSNSTDADPTAHWS	17

2	23	36	IHAGQHPDPTTNAR	14
3	45	53	SYTFDDTAH	9
4	68	78	TRIGNPTTDVV	11
5	98	100	QAA	3
6	113	116	DHIV	4
7	120	123	RLYG	4
8	143	152	VDDPDDLDTW	10
9	154	159	AAVRPN	6
10	168	171	ISNP	4
11	173	174	ID	2
12	179	187	PAVSEVAHR	9
13	208	209	AQ	2
14	221	224	YLGG	4
15	227	227	A	1
16	238	257	NFDWTQGRFPGFTTPDPSYH	20
17	264	269	LGPPAF	6
18	282	287	GSAASP	6
19	330	340	AGLPSSPWHHER	11
20	342	350	KRLAPKGTG	9
21	360	363	GIEA	4
22	391	409	ASTTHAQLSPAQLATGVS	19
23	438	446	RFSADPOSV	9

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