

# IEDB Analysis Resource

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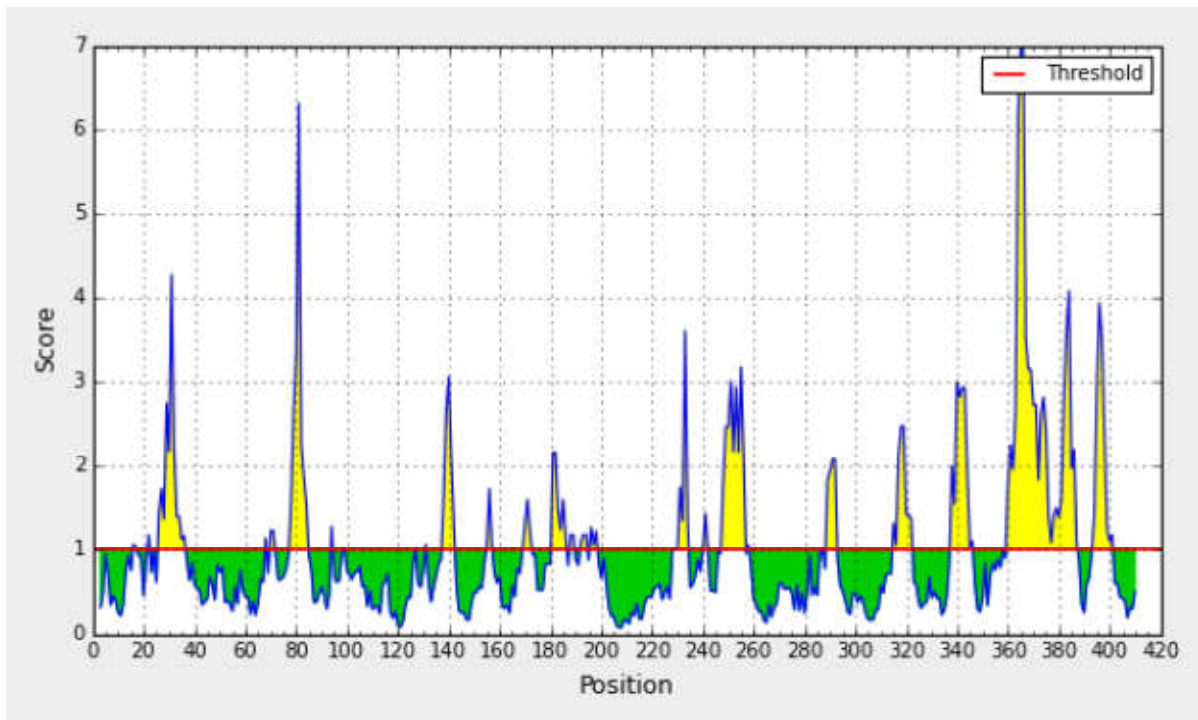
## Emini Surface Accessibility Prediction Prediction

### Input Sequences

```

1 MASPAAPRAV SFADNNDITN TNLSRGRGRN PKPRAAPNNT VSWYTGLTQH GKVPLTFPPG
61 QGVPLNANST PAQNAGYWRR QDRKINTGNG IKQLAPRWYF YYTGTGPEAA LPFRAVKDGI
121 VVWHEDGATD APSTFGTRNP NNSAIVTQF APGTKLPKNF HIEGTGGNSQ SSSRASSVSR
181 NSSRSSSQGS RSGNSTRGTS PGPSGIGAVG GDLLYLDLLN RLQALESGKV KQSQPKVITK
241 KDAAAAKNKM RHKRTSTKSF NMVQAFGLRG PGDLQGNFGD LQLNKLGTED PRWPQIAELA
301 PTASAFMGMS QFKLTHQNN DHDGNPVYFLR YSGAIKLDPK NPNYNKWLEL LEQNIDAYKT
361 FPKKEKKQKA PKEESTDQMS EPPKEQRVQG SITQRTRTRP SVQPGPMIDV NTD
  
```

Center position: 3 Window size: Threshold: 



Average: 1.000 Minimum: 0.074 Maximum: 6.971

### Predicted residue scores:

Position	Residue	Start	End	Peptide	Score
3	S	1	6	MASPAA	0.307
4	P	2	7	ASPAAP	0.48
5	A	3	8	SPAAPR	0.931
6	A	4	9	PAAPRA	0.702
7	P	5	10	AAPRAV	0.337
8	R	6	11	APRAVS	0.447
9	A	7	12	PRAVSF	0.383
10	V	8	13	RAVSFA	0.25

Position	Residue	Start	End	Peptide	Score
11	S	9	14	AVSFAD	0.213
12	F	10	15	VSFADN	0.34
13	A	11	16	SFADNN	0.736
14	D	12	17	FADNND	0.917
15	N	13	18	ADNNDI	0.742
16	N	14	19	DNNDIT	1.06
17	D	15	20	NNDITN	1.021
18	I	16	21	NDITNT	0.916
19	T	17	22	DITNTN	0.916
20	N	18	23	ITNTNL	0.452
21	T	19	24	TNTNLS	0.865
22	N	20	25	NTNLSR	1.174
23	L	21	26	TNLSRG	0.722
24	S	22	27	NLSRGR	0.98
25	R	23	28	LSRGRG	0.603
26	G	24	29	SRGRGR	1.433
27	R	25	30	RGRGRN	1.72
28	G	26	31	GRGRNP	1.358
29	R	27	32	RGRNPK	2.743
30	N	28	33	GRNPKP	2.166
31	P	29	34	RNPKPR	4.286
32	K	30	35	NPKPRA	2.211
33	P	31	36	PKPRAA	1.389
34	R	32	37	KPRAAP	1.389
35	A	33	38	PRAAPN	1.117
36	A	34	39	RAAPNN	1.162
37	P	35	40	AAPNNT	0.856
38	N	36	41	APNNTV	0.629
39	N	37	42	PNNTVS	0.834
40	T	38	43	NNTVSW	0.567
41	V	39	44	NTVSWY	0.553
42	S	40	45	TVSWYT	0.496
43	W	41	46	VSWYTG	0.34
44	Y	42	47	SWYTGL	0.378
45	T	43	48	WYTGLT	0.407
46	G	44	49	YTGLTQ	0.67
47	L	45	50	TGLTQH	0.582
48	T	46	51	GLTQHG	0.399
49	Q	47	52	LTQHGK	0.807
50	H	48	53	TQHGKV	0.726
51	G	49	54	QHGKVP	0.778

Position	Residue	Start	End	Peptide	Score
52	K	50	55	HGKVPL	0.37
53	V	51	56	GKVPLT	0.393
54	P	52	57	KVPLTF	0.344
55	L	53	58	VPLTFP	0.266
56	T	54	59	PLTFPP	0.554
57	F	55	60	LTFPPG	0.354
58	P	56	61	TFPPGQ	0.744
59	P	57	62	FPPGQG	0.51
60	G	58	63	PPGQGV	0.437
61	Q	59	64	PGQGVV	0.437
62	G	60	65	GQGVPL	0.233
63	V	61	66	QGVPLN	0.379
64	P	62	67	GVPLNA	0.221
65	L	63	68	VPLNAN	0.359
66	N	64	69	PLNANS	0.649
67	A	65	70	LNANST	0.606
68	N	66	71	NANSTP	1.135
69	S	67	72	ANSTPA	0.713
70	T	68	73	NSTPAQ	1.223
71	P	69	74	STPAQN	1.223
72	A	70	75	TPAQNA	0.922
73	Q	71	76	PAQNAG	0.632
74	N	72	77	AQNAGY	0.64
75	A	73	78	QNAGYW	0.667
76	G	74	79	NAGYWR	0.754
77	Y	75	80	AGYWRR	0.918
78	W	76	81	GYWRRQ	1.574
79	R	77	82	YWRRQD	2.656
80	R	78	83	WRRQDR	3.32
81	Q	79	84	RRQDRK	6.315
82	D	80	85	RQDRKI	2.26
83	R	81	86	QDRKIN	1.856
84	K	82	87	DRKINT	1.546
85	I	83	88	RKINTG	0.916
86	N	84	89	KINTGN	0.752
87	T	85	90	INTGNG	0.372
88	G	86	91	NTGNGI	0.372
89	N	87	92	TGNGIK	0.463
90	G	88	93	GNGIKQ	0.556
91	I	89	94	NGIKQL	0.463
92	K	90	95	GIKQLA	0.291
93	Q	91	96	IKQLAP	0.454

Position	Residue	Start	End	Peptide	Score
94	L	92	97	KQLAPR	1.27
95	A	93	98	QLAPRW	0.668
96	P	94	99	LAPRWY	0.604
97	R	95	100	APRWYF	0.634
98	W	96	101	PRWYFY	0.984
99	Y	97	102	RWYFYY	0.997
100	F	98	103	WYFYIT	0.735
101	Y	99	104	YFYITG	0.691
102	Y	100	105	FYITGT	0.637
103	T	101	106	YITGTG	0.728
104	G	102	107	YITGTP	0.718
105	T	103	108	TITGPE	0.794
106	G	104	109	GTGPEA	0.556
107	P	105	110	TGPEAA	0.567
108	E	106	111	GPEAAL	0.324
109	A	107	112	PEAALP	0.506
110	A	108	113	EAAALP	0.284
111	L	109	114	AALPFR	0.321
112	P	110	115	ALPFRA	0.321
113	F	111	116	LPFRAV	0.236
114	R	112	117	PFRAVK	0.571
115	A	113	118	FRAVKD	0.617
116	V	114	119	RAVKDG	0.705
117	K	115	120	AVKDG I	0.252
118	D	116	121	VKDGIV	0.185
119	G	117	122	KDGIVW	0.263
120	I	118	123	DGIVWV	0.098
121	V	119	124	GIVWVH	0.079
122	W	120	125	IVWVHE	0.139
123	V	121	126	VWVHED	0.331
124	H	122	127	WVHEDG	0.442
125	E	123	128	VHEDGA	0.424
126	D	124	129	HEDGAT	0.825
127	G	125	130	EDGATD	1.013
128	A	126	131	DGATDA	0.591
129	T	127	132	GATDAP	0.547
130	D	128	133	ATDAPS	0.741
131	A	129	134	TDAPST	1.058
132	P	130	135	DAPSTF	0.635
133	S	131	136	APSTFG	0.376
134	T	132	137	PSTFGT	0.537

Position	Residue	Start	End	Peptide	Score
135	F	133	138	STFGTR	0.681
136	G	134	139	TFGTRN	0.817
137	T	135	140	FGTRNP	0.875
138	R	136	141	GTRNPN	1.625
139	N	137	142	TRNPNN	2.641
140	P	138	143	RNPNND	3.056
141	N	139	144	NPNNDS	2.091
142	N	140	145	PNNDSA	1.314
143	D	141	146	NNNSAI	0.596
144	S	142	147	NNSAIV	0.275
145	A	143	148	NSAIVT	0.247
146	I	144	149	SAIVTQ	0.256
147	V	145	150	AIVTQF	0.165
148	T	146	151	IVTQFA	0.165
149	Q	147	152	VTQFAP	0.365
150	F	148	153	TQFAPG	0.486
151	A	149	154	QFAPGT	0.486
152	P	150	155	FAPGTK	0.561
153	G	151	156	APGTKL	0.535
154	T	152	157	PGTKLP	0.818
155	K	153	158	GTKLPK	1.058
156	L	154	159	TKLPKN	1.72
157	P	155	160	KLPKNF	1.032
158	K	156	161	LPKNFH	0.702
159	N	157	162	PKNFHI	0.597
160	F	158	163	KNFHIE	0.668
161	H	159	164	NFHIEG	0.331
162	I	160	165	FHIEGT	0.297
163	E	161	166	HIEGTG	0.339
164	G	162	167	IEGTGG	0.247
165	T	163	168	EGTGGN	0.566
166	G	164	169	GTGGNS	0.438
167	G	165	170	TGGNSQ	0.767
168	N	166	171	GGNSQS	0.712
169	S	167	172	GNSQSS	0.964
170	Q	168	173	NSQSSS	1.305
171	S	169	174	SQSSSR	1.59
172	S	170	175	QSSSRA	1.198
173	S	171	176	SSSRAS	0.927
174	R	172	177	SSRASS	0.927
175	A	173	178	SRASSV	0.514
176	S	174	179	RASSVS	0.514

Position	Residue	Start	End	Peptide	Score
177	S	175	180	ASSVSR	0.514
178	V	176	181	SSVSRN	0.818
179	S	177	182	SVSRNS	0.818
180	R	178	183	VSRNSS	0.818
181	N	179	184	SRNSSR	2.157
182	S	180	185	RNSSRS	2.157
183	S	181	186	NSSRSS	1.476
184	R	182	187	SSRSSS	1.23
185	S	183	188	SRSSSQ	1.59
186	S	184	189	RSSSQG	1.174
187	S	185	190	SSSQGS	0.803
188	Q	186	191	SSQGSR	1.174
189	G	187	192	SQGSRG	1.174
190	S	188	193	QGSRSG	0.867
191	R	189	194	GSRSGN	0.805
192	S	190	195	SRSGNS	1.09
193	G	191	196	RSGNST	1.174
194	N	192	197	SGNSTR	1.174
195	S	193	198	GNSTRG	0.867
196	T	194	199	NSTRGT	1.264
197	R	195	200	STRGTS	1.054
198	G	196	201	TRGTSP	1.216
199	T	197	202	RGTSPG	0.834
200	S	198	203	GTSPGP	0.658
201	P	199	204	TSPGPS	0.891
202	G	200	205	SPGPSG	0.611
203	P	201	206	PGPSGI	0.32
204	S	202	207	GPSGIG	0.205
205	G	203	208	PSGIGA	0.209
206	I	204	209	SGIGAV	0.1
207	G	205	210	GIGAVG	0.074
208	A	206	211	IGAVGG	0.074
209	V	207	212	GAVGGD	0.176
210	G	208	213	AVGGDL	0.147
211	G	209	214	VGGDLL	0.12
212	D	210	215	GGDLLY	0.253
213	L	211	216	GDLLYL	0.211
214	L	212	217	DLLYLD	0.356
215	Y	213	218	LLYLDL	0.176
216	L	214	219	LYLDLL	0.176
217	D	215	220	YLDLLN	0.343

Position	Residue	Start	End	Peptide	Score
218	L	216	221	LDLLNR	0.429
219	L	217	222	DLLNRL	0.429
220	N	218	223	LLNRLQ	0.445
221	R	219	224	LNRLQA	0.545
222	L	220	225	NRLQAL	0.545
223	Q	221	226	RLQALE	0.586
224	A	222	227	LQALES	0.401
225	L	223	228	QALESG	0.482
226	E	224	229	ALESGK	0.556
227	S	225	230	LESGKV	0.409
228	G	226	231	ESGKVK	0.991
229	K	227	232	SGKVKQ	0.991
230	V	228	233	GKVKQS	0.991
231	K	229	234	KVKQSQ	1.734
232	Q	230	235	VKQSQP	1.34
233	S	231	236	KQSQPK	3.612
234	Q	232	237	QSQPKV	1.34
235	P	233	238	SQPKVI	0.543
236	K	234	239	QPKVIT	0.584
237	V	235	240	PKVITK	0.675
238	I	236	241	KVITKK	0.873
239	T	237	242	VITKKD	0.729
240	K	238	243	ITKKDA	0.992
241	K	239	244	TKKDAA	1.429
242	D	240	245	KKDAAA	1.001
243	A	241	246	KDAAAA	0.505
244	A	242	247	DAAAAK	0.505
245	A	243	248	AAAAKN	0.487
246	A	244	249	AAAKNK	0.964
247	K	245	250	AAKNKM	0.944
248	N	246	251	AKNKMR	1.83
249	K	247	252	KNKMRH	2.465
250	M	248	253	NKMRHK	2.465
251	R	249	254	KMRHKK	3.002
252	H	250	255	MRHKRT	2.167
253	K	251	256	RHKRTS	2.934
254	R	252	257	HKRTST	2.162
255	T	253	258	KRTSTK	3.177
256	S	254	259	RTSTKS	2.129
257	T	255	260	TSTKSF	0.941
258	K	256	261	STKSFN	1.049
259	S	257	262	TKSFNM	0.775

Position	Residue	Start	End	Peptide	Score
260	F	258	263	KSFNMV	0.398
261	N	259	264	SFNMVQ	0.345
262	M	260	265	FNMVQA	0.26
263	V	261	266	NMVQAF	0.26
264	Q	262	267	MVQAFG	0.16
265	A	263	268	VQAFGL	0.133
266	F	264	269	QAFGLR	0.352
267	G	265	270	AFGLRG	0.201
268	L	266	271	FGLRGP	0.308
269	R	267	272	GLRGPG	0.352
270	G	268	273	LRGPGD	0.594
271	P	269	274	RGPGDL	0.594
272	G	270	275	GPGDLQ	0.525
273	D	271	276	PGDLQG	0.525
274	L	272	277	GDLQGN	0.546
275	Q	273	278	DLQGNF	0.478
276	G	274	279	LQGNFG	0.283
277	N	275	280	QGNFGD	0.573
278	F	276	281	GNFGDL	0.273
279	G	277	282	NFGDLQ	0.478
280	D	278	283	FGDLQL	0.245
281	L	279	284	GDLQLN	0.455
282	Q	280	285	DLQLNK	0.919
283	L	281	286	LQLNKL	0.454
284	N	282	287	QLNKLG	0.545
285	K	283	288	LNKLGT	0.454
286	L	284	289	NKLGTE	0.953
287	G	285	290	KLGTED	0.99
288	T	286	291	LGTEDP	0.765
289	E	287	292	GTEDPR	1.818
290	D	288	293	TEDPRW	1.931
291	P	289	294	EDPRWP	2.069
292	R	290	295	DPRWPQ	2.069
293	W	291	296	PRWPQI	0.869
294	P	292	297	RWPQIA	0.568
295	Q	293	298	WPQIAE	0.502
296	I	294	299	PQIAEL	0.394
297	A	295	300	QIAELA	0.257
298	E	296	301	IAELAP	0.23
299	L	297	302	AELAPT	0.473
300	A	298	303	ELAPTA	0.473



Position	Residue	Start	End	Peptide	Score
301	P	299	304	LAPTAS	0.366
302	T	300	305	APTASA	0.448
303	A	301	306	PTASAF	0.384
304	S	302	307	TASAFM	0.246
305	A	303	308	ASAFMG	0.169
306	F	304	309	SAFMGM	0.165
307	M	305	310	AFMGMS	0.165
308	G	306	311	FMGMSQ	0.283
309	M	307	312	MGMSQF	0.283
310	S	308	313	GMSQFK	0.572
311	Q	309	314	MSQFKL	0.477
312	F	310	315	SQFKLT	0.695
313	K	311	316	QFKLTH	0.706
314	L	312	317	FKLTHQ	0.706
315	T	313	318	KLTHQN	1.311
316	H	314	319	LTHQNN	1.054
317	Q	315	320	THQNNQ	2.134
318	N	316	321	HQNNDD	2.47
319	N	317	322	QNNDDH	2.47
320	D	318	323	NNDDHG	1.411
321	D	319	324	NDDHGN	1.411
322	H	320	325	DDHGND	1.357
323	G	321	326	DHGNDV	0.603
324	N	322	327	HGNPDV	0.566
325	P	323	328	GNPDVF	0.36
326	V	324	329	NPVDFL	0.3
327	Y	325	330	PVDFLR	0.365
328	F	326	331	VDFLRY	0.37
329	L	327	332	YDFLRY	0.669
330	R	328	333	FLRYSG	0.422
331	Y	329	334	LRYSGL	0.493
332	S	330	335	RYSGAL	0.419
333	G	331	336	YSGALK	0.428
334	A	332	337	SGALKL	0.225
335	I	333	338	GALKLD	0.28
336	K	334	339	AIKLDP	0.438
337	L	335	340	IKLDPK	0.868
338	D	336	341	KLDPKN	1.99
339	P	337	342	LDPKNP	1.539
340	K	338	343	DPKNPN	3.001
341	N	339	344	PKNPNY	2.815
342	P	340	345	KNPNYN	2.928

Position	Residue	Start	End	Peptide	Score
343	N	341	346	NPNYNK	2.928
344	Y	342	347	PNYNKW	1.915
345	N	343	348	NYNKWL	1.021
346	K	344	349	YNKWLE	1.1
347	W	345	350	NKWLEL	0.579
348	L	346	351	KWLELL	0.297
349	E	347	352	WLELLE	0.257
350	L	348	353	LELLEQ	0.423
351	L	349	354	ELLEQN	0.825
352	E	350	355	LLEQNI	0.334
353	Q	351	356	LEQNID	0.677
354	N	352	357	EQNIDA	0.829
355	I	353	358	QNIDAY	0.75
356	D	354	359	NIDAYK	0.866
357	A	355	360	IDAYKT	0.777
358	Y	356	361	DAYKTF	0.96
359	K	357	362	AYKTFP	0.889
360	T	358	363	YKTFPK	1.76
361	F	359	364	KTFPKK	2.246
362	P	360	365	TFPKKE	1.945
363	K	361	366	FPKKEK	2.695
364	K	362	367	PKKEKK	6.224
365	E	363	368	KKEKKQ	6.971
366	K	364	369	KEKKQK	6.971
367	K	365	370	EKKQKA	3.522
368	Q	366	371	KKQKAP	3.144
369	K	367	372	KQKAPK	3.144
370	A	368	373	QKAPKE	2.723
371	P	369	374	KAPKEE	2.723
372	K	370	375	APKEES	1.825
373	E	371	376	PKEEST	2.607
374	E	372	377	KEESTD	2.815
375	S	373	378	EESTDQ	2.438
376	T	374	379	ESTDQM	1.393
377	D	375	380	STDQMS	1.078
378	Q	376	381	TDQMSE	1.393
379	M	377	382	DQMSEP	1.493
380	S	378	383	QMSEPP	1.382
381	E	379	384	MSEPPK	1.596
382	P	380	385	SEPPKE	2.793
383	P	381	386	EPPKEQ	3.609

Position	Residue	Start	End	Peptide	Score
384	K	382	387	PPKEQR	4.082
385	E	383	388	PKEQRV	1.959
386	Q	384	389	KEQRVQ	2.194
387	R	385	390	EQRVQG	1.086
388	V	386	391	QRVQGS	0.84
389	Q	387	392	RVQGSI	0.34
390	G	388	393	VQGSIT	0.251
391	S	389	394	QGSITQ	0.585
392	I	390	395	GSITQR	0.661
393	T	391	396	SITQRT	0.964
394	Q	392	397	ITQRTR	1.409
395	R	393	398	TQRTRT	2.902
396	T	394	399	QRTRTR	3.938
397	R	395	400	RTRTRP	3.516
398	T	396	401	TRTRPS	2.406
399	R	397	402	RTRPSV	1.237
400	P	398	403	TRPSVQ	1.094
401	S	399	404	RPSVQP	1.172
402	V	400	405	PSVQPG	0.592
403	Q	401	406	SVQPGP	0.592
404	P	402	407	VQPGPM	0.437
405	G	403	408	QPGPMI	0.413
406	P	404	409	PGPMID	0.398
407	M	405	410	GPMIDV	0.191
408	I	406	411	PMIDVN	0.311
409	D	407	412	MIDVNT	0.29
410	V	408	413	IDVNTD	0.489

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