Table S1: Consensus scoring matrix given by Peters *et al*. (2003). The matrix elements represent log (IC_{50}) values for TAP binding that add up to the log(IC_{50}) value of the peptide. A low matrix entry at a given position corresponds to an amino acid well suited for TAP binding

Amino Acid/ Position	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**
A	-1.56	-0.25	-0.10	0.24	-0.10	0.17	0.27	0.00	0.55
C	0.05	-0.01	-0.02	0.11	0.09	0.05	0.00	-0.13	0.00
D	1.37	1.42	1.83	-0.23	0.33	0.32	1.07	0.32	1.83
E	1.65	0.02	1.51	0.08	0.54	-0.13	0.64	0.44	1.58
F	1.03	-0.45	-1.05	-0.50	-0.26	0.08	-0.50	0.17	-2.52
G	0.28	1.14	1.70	0.45	0.66	0.12	1.41	-0.38	1.41
H	0.21	0.33	-0.23	-0.21	-0.11	-0.06	-0.19	0.39	0.55
I	-0.11	-0.49	-0.62	-0.09	-0.42	-0.75	-0.94	0.45	-0.52
K	-1.03	-0.41	0.09	-0.23	-0.08	-0.26	0.44	0.12	-0.45
L	-0.50	0.09	-0.11	0.11	-0.34	0.02	-0.73	0.01	-0.94
M	-0.38	-0.46	-0.58	-0.35	-0.26	0.30	-0.64	-0.11	-0.29
N	-1.43	0.69	1.01	0.38	0.49	-0.27	0.16	0.33	1.33
P	1.43	3.00	0.22	-0.04	-0.72	-0.13	-0.84	0.03	-0.09
Q	0.47	-0.97	0.39	0.15	0.15	-0.07	0.34	0.26	0.12
R	-1.34	-1.47	-0.42	-0.27	-0.32	-0.75	-0.09	-0.42	-1.47
S	-0.56	-0.34	0.11	0.27	0.45	0.31	0.87	-0.51	2.26
T	-0.12	-0.04	0.43	0.23	0.43	0.49	0.39	-0.46	0.72
V	-0.49	-0.50	-0.71	0.27	0.37	-0.02	-0.29	0.10	-0.30
W	0.54	-0.64	-1.65	-0.18	-0.78	0.31	-0.50	-0.63	-0.87
Y	0.50	-0.67	-1.80	-0.18	-0.13	0.28	-0.87	0.02	-2.91

Table S2: Additive scoring matrix given by Doytchinova *et al*. (2004). The matrix elements represent -log (IC_{50}) values for TAP binding that add up to the -log(IC_{50}) value of the peptide

Amino Acid/ Position	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**
A	0.400	-0.030	-0.240	0.094	-0.173	-0.140	-0.097	-0.178	-0.808
R	0.487	0.558	0.347	0.492	0.290	0.527	0.190	-0.016	0.198
N	0.444	-0.533	-0.367	0.140	-0.351	0.448	-0.010	0.109	-1.406
D	-1.240	-1.074	-1.145	0.191	-0.062	0.022	-0.634	0.109	-1.809
Q	-0.683	0.558	-0.237	0.316	0.151	0.381	-0.236	-0.174	-0.471
E	-1.349	0.035	-0.668	-0.082	-0.351	0.226	-0.053	-0.174	-1.114
G	-0.276	-0.791	-1.103	-0.268	-0.430	0.381	-0.685	0.711	-1.687
H	-0.522	-0.706	0.280	0.492	-0.038	0.184	0.093	-0.192	-0.950
I	-0.085	0.336	0.824	0.094	0.415	0.749	0.491	-0.091	-0.251
L	-0.351	0.637	0.347	0.094	0.591	0.022	0.424	0.146	-0.304
K	0.186	0.222	0.125	0.395	-0.086	0.381	-0.394	-0.259	-0.068
M	-0.027	0.491	0.824	0.316	0.415	-0.189	0.491	0.146	-0.439
F	-0.648	0.190	1.125	0.492	0.348	-0.029	0.491	-0.091	1.174
P	-1.094	-1.945	0.083	0.395	0.591	0.050	0.792	0.234	-0.633
S	-0.073	0.433	0.347	-0.272	-0.086	-0.189	-0.685	0.887	-2.352
T	-0.243	0.222	0.011	0.094	0.017	-0.172	-0.146	0.711	-1.292
W	-0.419	0.859	1.125	0.492	0.892	-0.136	0.269	0.586	0.308
Y	-0.546	0.433	1.125	0.395	0.494	-0.293	0.792	0.074	0.762
V	-0.012	0.558	0.824	0.249	-0.011	-0.117	0.366	0.146	-0.384
C	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

Table S3: The weight matrix used for the prediction of constitutive proteasomal cleavage site

Amino acid/ Position	**P6**	**P5**	**P4**	**P3**	**P2**	**P1**	**P1'**	**P2'**	**P3'**	**P4'**	**P5'**	**P6'**
A	0.865	0.595	1.02	0.485	0.62	0.825	1.545	0.33	0.71	0.59	0.93	0.365
C	0	0	0	0	0.13	0	0	0	0	0	0	0
D	0.58	0.46	0.255	0.215	0.185	0.805	0.3	1.185	0.315	0.235	0.17	0.4
E	0.53	0.465	0.385	0.455	0.25	0.605	0.3	0.275	0.46	0.15	0.465	0.44
F	0.05	0.275	0.43	0.165	0.43	0.145	0.19	0.25	0.165	0.575	0.22	0.05
G	0.3	0.575	0.75	0.23	0.545	0.175	0.185	0.415	0.76	0.185	0.32	0.78
H	0.175	0.125	0.01	0.15	0.28	0.065	0.165	0.11	0.065	0.035	0.385	0.09
I	0.505	0.125	0.385	0.335	0.18	0.51	0.06	0.845	0.22	0.45	0.405	0.17
K	0.22	0.58	0.24	0.945	0.455	0.08	0.365	0.115	0.37	0.675	0.6	0.655
L	0.54	0.55	0.535	0.525	0.23	1.185	0.345	0.9	1.12	0.435	0.67	0.565
M	0.01	0	0.095	0.01	0.015	0.035	0.07	0.04	0.075	0.065	0.01	0.06
N	0.12	0.285	0.235	0.14	0.24	0.095	0.39	0.215	0.195	0.16	0.27	0.73
P	0.365	0.475	0.55	0.365	0.095	0.04	0.48	0.02	0.255	0.24	0.33	0.315
Q	0.045	0.26	0.025	0.02	0.34	0.06	0.075	0.06	0.155	0.305	0.035	0.075
R	0.125	0.045	0.045	0.425	0.29	0.275	0.595	0.095	0.155	0.145	0.08	0.06
S	0.575	0.365	0.38	0.09	0.535	0.395	0.5	0.215	0.17	0.53	0.49	0.555
T	0.735	0.46	0.14	0.365	0.365	0.14	0.15	0.43	0.14	0.36	0.25	0.105
V	0.27	0.38	0.365	0.92	0.84	0.45	0.275	0.41	0.695	0.705	0.355	0.695
W	0.04	0.015	0.035	0.03	0.02	0.03	0	0.05	0	0	0.05	0.01
X	0	0	0	0	0	0	0	0	0	0	0	0
Y	0.085	0.1	0.255	0.265	0.09	0.22	0.145	0.175	0.11	0.295	0.1	0.015

Threshold values for the prediction

Threshold (%)	1	2	3	4	5	6	7	8	9	10
Numerical value	7.16	6.815	6.59	6.42	6.265	6.13	5.99	5.83	5.635	4.835

Table S4: The weight matrix used for the prediction of immunoproteasomal cleavage site

Amino acid/ Position	**P6**	**P5**	**P4**	**P3**	**P2**	**P1**	**P1'**	**P2'**	**P3'**	**P4'**	**P5'**	**P6'**
A	0.68	0.615	0.94	0.42	0.59	0.745	1.44	0.665	0.56	0.775	0.48	0.81
C	0	0	0	0	0	0	0	0	0	0	0	0
D	0.725	0.36	0.19	0.225	0.16	0.15	0.335	1.21	0.255	0.325	0.22	0.375
E	0.3	0.37	0.515	0.87	0.58	0.155	0.255	0.32	0.41	0.27	0.4	0.515
F	0	0.495	0.28	0.105	0.665	0.55	0.05	0.1	0.12	0.26	0.19	0.25
G	0.5	0.55	0.485	0.18	0.36	0.17	0.88	0.475	0.97	0.265	0.465	0.675
H	0.3	0.03	0.08	0.285	0.205	0.13	0.14	0.04	0.05	0.04	0.34	0.285
I	0.44	0.345	0.29	0.47	0.145	0.585	0.02	0.8	0.295	0.42	0.73	0.395
K	0.09	0.475	0.4	1.065	0.62	0.175	0.45	0.275	0.29	0.405	0.59	0.83
L	0.56	0.975	0.45	0.235	0.16	2.305	0.065	0.37	1.025	0.41	0.105	0.51
M	0.02	0	0.215	0.01	0.08	0.05	0.295	0	0	0.1	0	0.05
N	0.245	0.285	0.29	0.165	0.205	0.095	0.52	0.29	0.56	0.575	0.19	0.29
P	0.325	0.37	0.255	0.38	0.035	0	0.375	0.175	0.305	0.18	0.44	0.08
Q	0.01	0.26	0.21	0.105	0.17	0.01	0.175	0.075	0.225	0.25	0.1	0.02
R	0.365	0.1	0.065	0.215	0.395	0.2	0.48	0	0.19	0.29	0.32	0.1
S	0.545	0.25	0.61	0.225	0.735	0.185	0.345	0.32	0.265	0.695	0.38	0.52
T	0.89	0.2	0.085	0.235	0.57	0.195	0.31	0.56	0.275	0.195	0.275	0.055
V	0.255	0.485	0.585	0.94	0.695	0.32	0.085	0.535	0.495	0.555	0.925	0.61
W	0.025	0.06	0	0.025	0	0.07	0	0	0	0.075	0	0
X	0	0	0	0	0	0	0	0	0	0	0	0
Y	0.095	0.14	0.425	0.215	0	0.28	0.15	0.16	0.08	0.285	0.22	0

Threshold values for the prediction

Threshold (%)	1	2	3	4	5	6	7	8	9	10
Numerical value	7.855	7.435	7.165	6.95	6.765	6.595	6.425	6.25	6.03	5.11

Table S5: Evaluation of position specific scoring matrices (PSSM) for 22 HLA class I alleles based on MHCIPREDS-IEDB dataset using binding affinity threshold (IC_{50}) ≤ 500 nM. PSSM selected as MHC class I predictors are shown in bold for respective alleles

S.No	**MHC class I allele**	**Weight on prior**	**Sequence weighting methods (PSSM)**					
			Henikoff & Henikoff 1/nr clustering		**Clustering at 62% identity**		**No clustering**	
			Aroc	**CC**	**Aroc**	**CC**	**Aroc**	**CC**
1	HLA-A*0201	50	0.89	0.65	0.89	0.63	0.89	0.63
		100	0.89	0.65	0.89	0.63	0.89	0.63
		150	0.89	0.64	0.90	0.64	0.89	0.63
		200	0.89	0.64	**0.90**	**0.64**	0.89	0.64
2	HLA-A*0203	50	0.93	0.71	0.93	0.70	0.93	0.70
		100	0.92	0.70	0.93	0.70	0.93	0.71
		150	0.92	0.70	0.93	0.71	0.93	0.71
		200	0.92	0.70	**0.93**	**0.71**	0.93	0.71
3	HLA-A*0206	50	0.89	0.65	0.89	0.65	0.89	0.64
		100	0.88	0.64	0.89	0.65	0.89	0.64
		150	0.88	0.64	0.89	0.65	0.89	0.65
		200	0.88	0.64	**0.89**	**0.65**	0.89	0.65
4	HLA-A*2902	50	0.66	0.19	0.65	0.14	0.65	0.14
		100	0.65	0.19	0.64	0.13	0.64	0.13
		150	0.66	0.19	0.64	0.13	0.64	0.13
		200	**0.66**	**0.19**	0.63	0.13	0.63	0.13
5	HLA-A*6801	50	0.70	0.36	0.64	0.25	0.64	0.25
		100	0.72	0.38	0.65	0.26	0.65	0.25

		150	0.72	0.38	0.65	0.26	0.65	0.26
		200	**0.72**	**0.39**	0.66	0.27	0.65	0.27
6	HLA-A*6802	50	0.77	0.47	**0.78**	**0.48**	0.78	0.48
		100	0.76	0.46	0.76	0.48	0.78	0.48
		150	0.76	0.45	0.77	0.48	0.77	0.48
		200	0.75	0.44	0.77	0.48	0.77	0.48
7	HLA-A*3301	50	0.79	0.45	0.78	0.45	0.78	0.45
		100	0.79	0.45	0.78	0.46	0.78	0.46
		150	0.79	0.45	0.79	0.46	0.79	0.46
		200	0.79	0.45	**0.79**	**0.46**	0.79	0.46
8	HLA-A*0101	50	0.85	0.56	0.80	0.51	0.81	0.51
		100	0.85	0.56	0.81	0.51	0.82	0.52
		150	0.85	0.56	0.82	0.51	0.83	0.52
		200	**0.86**	**0.55**	0.82	0.52	0.83	0.52
9	HLA-A*0202	50	**0.91**	**0.69**	0.89	0.66	0.89	0.67
		100	0.90	0.69	0.89	0.66	0.89	0.67
		150	0.90	0.68	0.89	0.66	0.89	0.67
		200	0.90	0.68	0.89	0.67	0.89	0.68
10	HLA-A*3002	50	**0.70**	**0.39**	0.68	0.36	0.68	0.36
		100	0.69	0.39	0.69	0.37	0.69	0.37
		150	0.68	0.39	0.68	0.37	0.68	0.37
		200	0.68	0.38	0.68	0.38	0.68	0.38
11	HLA-A*3101	50	0.79	0.45	0.77	0.42	0.77	0.42
		100	0.79	0.46	0.77	0.43	0.77	0.43

		150	0.79	0.47	0.77	0.44	0.78	0.44
		200	**0.79**	**0.47**	0.78	0.44	0.78	0.44
12	HLA-A*0301	50	**0.79**	**0.48**	0.76	0.44	0.76	0.44
		100	0.79	0.48	0.77	0.45	0.76	0.44
		150	0.79	0.48	0.77	0.45	0.77	0.45
		200	0.79	0.47	0.77	0.45	0.77	0.45
13	HLA-A*1101	50	**0.85**	**0.57**	0.83	0.51	0.83	0.51
		100	0.85	0.56	0.83	0.52	0.83	0.52
		150	0.85	0.56	0.83	0.52	0.83	0.52
		200	0.85	0.56	0.84	0.53	0.84	0.53
14	HLA-A*2402	50	0.67	0.32	0.66	0.26	0.66	0.26
		100	0.67	0.32	0.66	0.27	0.66	0.27
		150	0.67	0.32	0.67	0.27	0.66	0.27
		200	**0.67**	**0.32**	0.67	0.27	0.67	0.28
15	HLA-B*0702	50	0.79	0.52	0.75	0.46	0.75	0.46
		100	0.80	0.53	0.76	0.47	0.76	0.47
		150	0.80	0.53	0.76	0.48	0.76	0.48
		200	**0.80**	**0.53**	0.76	0.48	0.76	0.48
16	HLA-B*1501	50	0.78	0.53	0.78	0.52	0.78	0.52
		100	0.77	0.52	0.78	0.54	**0.78**	**0.54**
		150	0.77	0.52	0.77	0.54	0.77	0.54
		200	0.77	0.52	0.77	0.54	0.77	0.54
17	HLA-B*3501	50	0.82	0.58	0.79	0.52	0.79	0.51
		100	0.82	0.59	0.80	0.54	0.79	0.53

		150	0.82	0.59	0.80	0.55	0.80	0.53
		200	**0.83**	**0.59**	0.81	0.55	0.80	0.54
18	HLA-B*4002	50	0.59	0.02	0.61	0.13	0.56	-0.07
		100	0.60	0.03	0.61	0.15	0.56	-0.07
		150	0.61	0.04	0.61	0.16	0.56	-0.07
		200	0.61	0.04	**0.62**	**0.17**	0.56	-0.07
19	HLA-B*4501	50	0.42	-0.26	**0.49**	**-0.07**	0.46	-0.26
		100	0.40	-0.27	0.46	-0.09	0.44	-0.28
		150	0.40	-0.28	0.47	-0.10	0.44	-0.29
		200	0.40	-0.28	0.47	-0.10	0.44	-0.29
20	HLA-B*5101	50	0.71	0.38	0.61	0.23	0.61	0.21
		100	0.72	0.41	0.64	0.29	0.63	0.26
		150	0.72	0.42	0.65	0.31	0.64	0.29
		200	**0.73**	**0.43**	0.67	0.34	0.65	0.31
21	HLA-B*5301	50	0.81	0.53	0.81	0.53	0.81	0.50
		100	0.81	0.53	0.82	0.54	0.80	0.52
		150	0.81	0.53	**0.83**	**0.55**	0.81	0.52
		200	0.81	0.53	0.83	0.55	0.81	0.53
22		50	0.72	0.36	0.71	0.34	0.70	0.33

	HLA-B*5401	100	0.72	0.37	0.72	0.36	0.72	0.35
		150	0.72	0.37	0.74	0.37	0.73	0.36
		200	0.72	0.37	**0.74**	**0.38**	0.73	0.36

Table S6: Evaluation of ANN weights for 22 HLA class I alleles based on MHCIPREDS-IEDB dataset for binding affinity threshold (IC_{50}) ≤ 500 nM. ANN weight selected as MHC class I predictors are shown in bold for respective alleles

S. No	**MHC class I allele**	**No. of hidden layer neuron**			
		1		**2**	
		Aroc	**CC**	**Aroc**	**CC**
1	HLA-A*0201	**0.91**	**0.71**	0.91	0.70
2	HLA-A*0203	**0.97**	**0.78**	0.97	0.77
3	HLA-A*0206	**0.96**	**0.78**	0.95	0.77
4	HLA-A*2902	**0.56**	**0.03**	0.66	0.10
5	HLA-A*6801	**0.94**	**0.74**	0.94	0.75
6	HLA-A*6802	**0.92**	**0.73**	0.92	0.73
7	HLA-A*3301	**0.75**	**0.44**	0.74	0.43
8	HLA-A*0101	**0.76**	**0.46**	0.84	0.55
9	HLA-A*0202	**0.97**	**0.79**	0.97	0.79
10	HLA-A*3002	**0.73**	**0.47**	0.78	0.47
11	HLA-A*3101	**0.91**	**0.72**	0.92	0.73
12	HLA-A*0301	**0.82**	**0.56**	0.83	0.56
13	HLA-A*1101	**0.92**	**0.69**	0.92	0.69
14	HLA-A*2402	**0.76**	**0.47**	0.75	0.46
15	HLA-B*0702	**0.79**	**0.50**	0.77	0.47

16	HLA-B*1501	**0.64**	**0.22**	0.62	0.15
17	HLA-B*3501	**0.70**	**0.34**	0.71	0.35
18	HLA-B*4002	**0.77**	**0.42**	0.88	0.60
19	HLA-B*4501	**0.76**	**0.51**	0.76	0.50
20	HLA-B*5101	**0.70**	**0.31**	0.71	0.36
21	HLA-B*5301	**0.86**	**0.61**	0.86	0.61
22	HLA-B*5401	**0.77**	**0.45**	0.73	0.40

Table S7: Relative rank (%) of epitopes binding to 7 HLA class I molecules in their source antigen predicted by EasyPred predictors (PSSM/ANN) and NetMHCpan4.0 (E/BA) methods

HLA-A*01:01													
S.No.	**Protein accession number**	**Epitope sequence**	**Total no. of peptides**	**MHC binding score**		**TAP binding score**		**C-terminal cleavage score**		**Average relative rank of epitopes in their source antigen (%)**			
				PSSM	**ANN**	**TAP-2003**	**TAP-2004**	**Constitutive proteasome**	**Immuno-proteasome**	**PSSM**	**ANN**	**NetMHCpan4.0 (E)**	**NetMHCpan4.0 (BA)**
1	O43707	AIDQLHLEY	903	8.916	0.430	3.67	1.694	5.25	5.40	0.22	2.77	0.1107	0.1107
2	Q53EP0	ATDYHVRVY	1196	10.036	0.482	2.98	0.815	5.10	4.985	0.08	0.42	0.0836	0.0836
3	Q969N2	DTDHYFLRY	570	13.688	0.511	1.160	-0.036	5.575	5.645	0.18	0.18	0.1754	0.1754
4	Q15149	ELEDSTLRY	4676	7.601	0.449	0.100	-0.277	4.310	3.69	0.47	1.18	0.0213	0.0213
5	P26232	FIDASRLVY	945	9.058	0.437	1.23	0.410	4.775	4.415	0.42	1.38	0.1058	0.1058

6	Q9Y4W2	GTDELRLLY	726	11.266	0.466	2.57	1.169	3.885	4.890	0.14	0.96	0.1377	0.1377
7	Q9H3H5	HLDLGILYY	400	8.920	0.452	1.47	0.643	4.280	3.04	0.25	0.75	0.25	0.25
8	O15294	LAELAHREY	1308	9.173	0.451	1.85	-0.166	4.10	5.17	0.15	1.30	0.6116	0.7645
9	Q96AY3	LEDVVIERY	574	7.374	0.450	1.45	0.219	4.340	4.59	1.57	1.74	1.7421	1.7421
10	Q9H7Z6	LSDLGKLSY	450	11.236	0.504	2.65	1.055	4.055	4.095	0.22	0.22	0.2222	0.2222
11	P35611	LTDRELEEY	729	11.786	0.462	0.250	-0.576	4.430	4.86	0.14	0.69	0.1371	0.1371
12	Q14653	LTDRGVMSY	419	10.808	0.474	2.40	0.811	4.195	3.84	0.48	0.48	0.2386	0.2386
13	Q9Y4K1	PTDPKVVVY	1715	10.014	0.475	-0.020	-0.551	5.195	5.10	0.12	0.06	0.0583	0.0583
14	Q6ICG6	RADGNFLLY	396	9.562	0.491	2.37	-0.004	5.920	5.27	0.25	0.25	0.2525	0.2525
15	Q07837	SIDRTVMYY	677	9.680	0.401	2.61	0.837	3.665	4.005	0.59	17.13	0.1477	0.1477
16	Q16625	TSDQQRQLY	514	12.706	0.485	1.64	0.711	2.325	2.425	0.39	0.58	0.1945	0.1945
17	O15533	TTEQHGARY	440	10.068	0.460	1.55	0.619	4.540	4.295	0.23	0.23	0.2272	0.2272

18	Q9Y282	TTEVHPELY	375	10.458	0.472	0.88	0.427	4.540	5.125	0.27	0.27	0.2666	0.2666
19	P00450	TVDQVKDLY	1057	9.589	0.457	0.36	0.130	4.450	4.37	0.66	1.89	0.0946	0.0946
20	Q16531	VAVGRALYY	1132	6.775	0.467	4.77	1.924	3.265	2.99	0.88	0.35	1.1484	1.1484
21	Q9Y2R5	VLDPYLLKY	122	12.529	0.467	2.24	1.318	3.825	3.615	0.82	0.82	0.8196	0.8196
22	O00429	VTDSIRDEY	728	11.503	0.425	1.00	-0.311	5.905	6.275	0.14	2.88	0.1373	0.1373
23	P21333	VTEIDQDKY	2639	10.794	0.480	0.570	-0.176	5.285	5.370	0.08	0.27	0.0378	0.0378
24	Q6GYQ0	VTEIFRQAF	2028	8.242	0.402	2.30	1.271	4.00	3.920	0.59	13.51	0.9368	1.5779
25	Q15019	YIDEQFERY	353	10.619	0.472	0.54	-0.622	4.375	4.07	0.28	0.85	0.2832	0.2832
26	P04899	YSEEECRQY	347	11.230	0.503	-0.400	-0.436	4.960	4.27	0.29	0.29	0.5763	0.5763
27	P35749	YSEKIVDMY	1964	10.933	0.490	0.95	0.186	3.155	3.83	0.05	0.10	0.0509	0.0509
28	Q16647	YTDPEVFKY	492	13.957	0.453	0.52	-0.548	3.705	3.605	0.20	1.62	0.2032	0.2032
29	O43164	YVDPQFLTY	700	12.286	0.477	2.08	1.281	4.360	4.705	0.14	0.14	0.1428	0.1428

HLA-A*02:01													
S.No.	Protein accession number	Epitope sequence	Total no. of peptides	MHC binding score		TAP binding score		C-terminal cleavage score		Average relative rank of epitopes in their source antigen (%)			
				PSSM	ANN	TAP-2003	TAP-2004	Constitutive proteasome	Immuno-proteasome	PSSM	ANN	NetMHCpan4.0 (E)	NetMHCpan4.0 (BA)
1	Q9NYL9	AAILGMHNL	344	1.513	0.234	2.16	0.567	4.480	6.295	8.72	12.50	5.523	6.1046
2	P63208	AILKKVIQW	155	-2.891	0.15	4.040	1.900	3.40	3.475	14.84	23.87	11.612	21.2903
3	O14791	ALADGVQKV	390	8.244	0.778	1.00	-0.438	4.265	5.155	1.79	0.77	0.256	0.5405
4	Q9Y646	ALASLIRSV	464	8.855	0.728	3.290	2.558	5.795	6.385	1.07	1.08	0.6465	1.0775
5	Q9UBW8	ALATLIHQV	267	10.726	0.801	2.66	1.766	5.195	5.130	0.37	0.37	0.374	0.3745
6	Q8V2N2	ALDEKLFLI	374	10.903	0.799	6.30	0.132	4.250	4.260	1.34	0.53	0.534	0.8021

7	Q58A63	ALFDGDPHL	2716	7.764	0.713	3.16	2.241	5.486	7.495	0.66	0.22	0.0368	0.1104
8	Q04609	ALFDIESKV	742	8.814	0.748	2.61	1.666	4.19	4.41	0.80	0.54	0.134	0.5390
9	P55058	ALFGALFLA	485	12.007	0.814	2.09	1.572	5.810	4.60	0.21	0.21	0.206	0.2061
10	O60832	ALFQRPPLI	506	8.17	0.682	4.17	3.505	5.145	4.835	0.59	0.59	0.395	0.9881
11	P35503	ALGKIPQTV	526	7.094	0.656	9.70	0.885	3.605	3.175	2.28	1.33	0.760	2.6615
12	O75444	ALISNSHQL	365	9.443	0.631	1.89	0.664	5.69	6.975	0.55	0.55	0.273	0.2739
13	O95864	ALLDIIRSL	436	9.114	0.729	4.52	3.512	5.235	6.970	0.92	0.69	0.229	0.6880
14	Q9NV31	ALLDKLYAL	176	10.932	0.791	3.68	1.821	6.095	7.06	1.13	1.170	0.568	0.5681
15	Q9UNW1	ALLSSLARC	479	3.988	0.394	0.99	0.935	5.310	4.610	3.96	6.05	2.087	2.9227
16	Q9GZT8	ALLSSLNDF	369	0.358	0.151	2.88	2.321	5.94	6.60	11.11	26.29	7.046	8.6720
17	O75691	ALMELFPKL	2777	11.049	0.786	3.89	2.570	5.16	7.115	0.40	0.32	0.0720	0.1080
18	Q5RKV6	ALMPVLNQV	264	11.484	0.754	1.58	1.699	6.60	6.25	0.38	0.76	0.378	0.378

19	Q14511	ALQEMVHQV	826	10.394	0.775	1.51	0.551	5.63	5.510	0.48	0.36	0.121	03631
20	P04075	ALSDHHIYL	356	9.047	0.747	3.62	1.982	4.94	5.96	0.28	0.28	0.280	0.2808
21	Q86UX7	ALSNLEVKL	659	3.880	0.421	2.560	2.144	5.525	7.865	3.49	3.34	0.455	0.9104
22	P33059	ALWDSKFFT	317	9.148	0.730	2.77	1.756	4.995	5.370	2.52	1.58	1.261	1.8927
23	P30499	AVLGAVVAV	358	6.862	0.611	2.43	0.551	4.445	5.075	1.40	1.40	0.3279	0.5586
24	P17181	CIALFALPF	549	-4.652	0.136	3.74	2.230	6.005	5.865	28.60	31.69	45.253	18.3970
25	P13639	ETAKLIEKL	850	-2.14	0.170	-0.010	-0.248	5.925	7.725	17.53	20.47	17.529	23.8823
26	P49588	ETYPDPVRV	960	1.104	0.240	1.040	0.347	4.60	4.565	7.29	11.04	2.916	8.2291
27	Q96EA4	FANERCLQL	597	3.94	0.418	-0.19	-0.891	4.050	4.55	5.03	3.69	6.532	4.8576
28	Q8N6L1	FASGLIHRV	154	5.091	0.575	0.66	0.434	3.085	4.02	8.44	9.09	5.194	6.4935
29	Q9NP61	FASHVSPEV	508	5.136	0.558	-0.66	0.195	4.830	6.09	1.97	1.38	0.787	0.5905
30	O94833	FIWENIHTL	5163	12.060	0.793	2.88	1.629	4.885	6.350	0.10	0.12	72.147	0.0387

31	O00299	FLDGNELTL	233	8.320	0.649	-1.63	-0.178	7.17	8.25	1.29	2.15	0.429	0.4291
32	Q9Y696	FLDGNEMTL	245	7.85	0.664	-1.72	-0.651	6.55	8.025	2.04	2.45	0.4089	0.8163
33	Q96JB1	FLDILNTLI	4482	10.613	0.733	-2.13	-0.274	4.24	4.29	0.40	0.71	0.401	0.2900
34	Q8IZF2	FLDPIKAYL	1338	9.702	0.775	-1.58	-0.292	5.28	6.625	1.12	0.30	0.074	0.2242
35	Q16678	FLDPRPLTV	535	10.253	0.765	-0.970	0.330	5.155	4.625	1.12	0.93	0.186	0.1869
36	P30533	FLGPWPAAS	349	2.543	0.365	-4.40	-2.404	5.10	4.565	6.02	5.44	2.292	1.713
37	P11274	FLLDHLKRV	1263	9.582	0.803	-0.410	-0.283	6.890	6.395	0.55	0.16	0.079	0.0791
38	O00270	FLLDLSRSV	311	10.788	0.784	0.150	1.622	5.465	6.195	1.93	1.93	0.321	1.2861
39	O60547	FLLEKGYEV	364	11.661	0.830	-0.400	0.783	4.470	4.260	0.55	0.27	0.274	0.2747
40	Q9NVG8	FLLPDVIRI	267	10.202	0.766	0.600	0.776	4.700	5.605	0.37	0.75	0.374	0.7490
41	P14770	FLLWATAEA	169	12.358	0.832	-2.480	-0.596	3.80	4.270	0.59	0.59	1.183	0.5917
42	O60486	FLVTVIHTL	1560	12.009	0.802	1.33	2.145	4.765	6.425	0.06	0.19	0.064	0.2564

43	Q00610	FVHDLVLYL	1667	8.045	0.725	1.940	1.049	4.635	6.235	1.26	0.66	0.479	0.4199
44	P33778	FVNDIFERI	118	6.080	0.620	-0.670	-0.200	5.95	6.78	3.39	1.69	55.932	0.8474
45	P12429	GIGTDEKML	315	-2.568	0.119	-1.310	-1.337	5.345	7.050	15.87	33.02	15.556	26.9841
46	P49720	GLATDVQTV	197	8.885	0.749	-0.390	0.127	5.240	5.785	2.54	0.51	0.507	1.0152
47	Q8NI35	GLFPWTPKL	1793	10.453	0.702	2.670	2.830	4.570	6.16	0.17	0.39	0.111	0.1115
48	O14737	GLIEILKKV	117	7.196	0.651	3.10	0.503	5.235	5.17	0.85	0.85	0.854	0.8547
49	P46821	GLSEFTEYL	2460	10.820	0.786	-0.510	0.519	5.485	6.550	0.12	0.08	0.008	0.0813
50	P04075	GLSERCAQY	356	-0.229	0.124	2.09	1.407	3.93	3.37	12.92	33.99	14.606	19.3820
51	P06731	GVLVGVALI	694	3.004	0.364	-0.340	0.129	5.96	6.24	5.48	5.62	1.873	2.8818
52	O76021	HIIENIVAV	482	7.273	0.717	1.67	0.758	5.58	5.585	1.24	0.62	0.207	0.6224
53	Q8NFD2	HLAVERGKV	757	-0.391	0.277	-1.49	-1.028	4.315	4.35	14.80	11.10	10.303	12.1532
54	1424926	HLGPEGRSV	184	1.333	0.289	-1.72	0.130	6.27	5.875	21.20	20.11	8.695	20.1086
55	Q5BJD5	HLINYIIFL	283	11.864	0.830	2.53	2.418	5.16	6.55	0.71	0.35	0.706	1.0600

56	Q16790	HLSTAFARV	451	8.263	0.679	-0.17	-0.143	5.085	5.11	1.33	1.33	0.665	1.9955
57	Q6FI81	HSAEILAEI	304	0.344	0.376	0.360	-0.496	5.125	5.225	10.86	4.28	4.605	2.9605
58	P04075	IAMATVTAL	356	4.996	0.490	0.840	0.075	6.040	6.425	3.09	4.49	5.617	3.6516
59	P49279	IIMPHNIYL	542	9.960	0.739	3.46	2.141	4.870	6.605	2.40	1.85	0.184	0.9225
60	Q9NYB9	ILDDIGHGV	505	9.052	0.774	-0.410	0.814	4.70	4.975	0.59	0.40	1.666	0.1980
61	P49189	ILDKFTEEV	486	10.299	0.799	-2.59	-0.633	2.79	3.42	0.21	0.21	1.639	0.2057
62	P05386	ILHDDEVTV	106	7.436	0.674	1.33	1.880	5.710	5.740	0.94	0.94	0.943	0.9433
63	Q12864	ILQAHLHSL	824	10.845	0.756	1.12	1.069	6.165	6.085	0.24	0.24	0.121	0.1213
64	P13639	ILTDITKGV	850	7.758	0.682	-0.010	0.930	4.950	5.63	1.41	1.18	0.705	0.8235
65	Q08209	ILYPKTLFL	513	12.351	0.724	2.950	1.843	5.410	6.555	0.39	0.58	0.194	0.3898
66	A8MWD9	IMLEALERV	68	9.900	0.794	7.60	0.067	na	na	1.47	1.47	1.470	1.4705
67	P25054	KIMDQVQQA	2835	7.802	0.680	1.050	0.353	4.775	5.750	0.42	0.32	0.246	0.5643

68	P46777	KIYEGQVEV	289	10.820	0.726	2.80	1.324	4.610	4.72	0.35	0.35	0.346	0.3460
69	P21283	KLDAFVEGV	374	10.308	0.825	-0.810	0.277	5.425	5.015	0.27	0.53	0.267	0.5347
70	Q92597	KLDPTKTTL	386	7.615	0.453	-0.010	0.732	4.275	5.370	1.04	3.63	0.777	2.331
71	Q9UNX4	KLFNEFIQL	935	9.411	0.710	2.61	1.721	5.325	6.76	0.64	0.86	0.106	0.2139
72	Q01478	KLFSDISAI	333	11.967	0.772	1.790	1.249	4.945	5.395	0.60	0.90	0.300	0.6006
73	P84077	KLGEIVTTI	173	10.022	0.711	0.190	0.250	4.525	4.595	1.16	1.16	1.156	1.1560
74	Q9BWF3	KLHGVNINV	356	10.398	0.632	1.53	1.488	4.340	4.880	0.28	1.40	0.280	0.2808
75	P33241	KLIDRTESL	331	10.384	0.751	2.43	2.486	5.165	7.255	0.30	0.30	0.302	0.3021
76	P23998	KLIIHNPEL	343	9.921	0.723	3.370	2.465	4.60	6.340	1.17	0.87	0.291	1.1661
77	P51589	KLLDEVTYL	494	11.764	0.821	1.290	0.517	4.775	6.085	0.61	0.40	0.202	0.4048
78	P42224	KLQELNYNL	742	10.639	0.732	2.560	2.14	5.575	6.475	0.54	0.54	0.269	0.2695
79	P19387	KLSDLQTQL	267	10.870	0.589	1.760	1.709	5.155	6.455	0.37	1.50	0.374	0.3745

80	Q9BUP0	KLSEIDVAL	231	8.873	0.650	2.08	1.409	6.405	7.575	0.43	0.87	0.432	0.4329
81	P05787	KLSELEAAL	475	8.645	0.593	1.89	1.326	5.745	6.720	0.63	1.26	0.631	0.6315
82	P63244	KTIKLWNTL	309	2.866	0.225	3.19	2.479	3.970	6.20	4.53	9.06	4.530	4.530
83	P12110	KTRVFAVVI	1011	-3.262	0.158	2.02	1.473	6.86	7.405	13.35	15.3	11.968	9.1988
84	Q9UL46	KVLERVNAV	231	5.559	0.523	2.04	0.610	4.850	5.125	4.33	3.90	1.298	1.7316
85	O94768	LATDFIQSL	364	4.872	0.586	2.67	1.265	5.035	7.705	3.02	1.65	7.967	10.4395
86	P05067	LLAAWTARA	762	8.995	0.749	0.16	-0.061	4.825	4.095	0.79	0.26	1.968	0.7874
87	P21980	LLAERDLYL	679	7.917	0.750	2.08	0.470	4.610	5.810	1.03	0.44	0.417	0.1472
88	Q9P2J5	LLAPFCPHL	1168	9.746	0.696	2.15	1.085	3.415	4.555	0.60	1.28	0.684	0.5993
89	Q96PU8	LLDEEISRV	333	8.864	0.767	1.44	-1.628	4.13	3.520	0.30	0.30	1.123	0.3003
90	Q14094	LLDRFLATV	369	11.424	0.795	0.420	0.233	3.850	4.555	0.27	0.27	0.757	0.5420
91	P52272	LLFDRPMHV	722	8.810	0.765	2.69	1.857	3.23	3.72	0.28	0.14	0.138	0.1385

92	P49755	LLGPRLVLA	211	5.014	0.534	1.22	-0.406	4.380	3.405	5.21	5.69	1.895	3.3175
93	Q70EL2	LLHYLLDAV	806	7.710	0.598	0.370	0.378	4.995	5.480	1.24	1.36	2.357	0.7444
94	P13284	LLLDVPTAA	253	9.371	0.712	0.430	-0.269	5.790	5.400	1.19	1.58	1.185	2.7667
95	Q93074	LLLEDLIRC	2169	3.58	0.454	1.45	0.986	5.54	5.445	5.49	3.92	0.875	1.8902
96	P21453	LLLLSIVIL	374	7.486	0.607	1.49	1.361	4.980	5.990	5.08	4.81	5.614	6.4171
97	Q9BTY2	LLPPPPCPA	459	4.837	0.382	0.500	0.831	3.89	4.06	3.70	6.97	4.357	3.9215
98	P40259	LLSAEPVPA	221	5.804	0.640	0.640	0.218	5.910	5.320	8.14	4.52	3.619	5.4298
99	P26006	LLYPTEITV	1058	11.131	0.711	3.65	2.867	3.820	4.22	0.38	0.57	0.378	0.3780
100	P01860	LMISRTPEV	369	11.60	0.805	1.84	1.044	4.13	4.67	0.27	0.27	0.271	0.2710
101	Q8N307	LMQQLHREL	701	2.407	0.255	1.41	0.706	4.035	6.52	4.28	7.42	5.278	2.9957
102	P06737	NLAENISRV	839	7.587	0.665	1.47	0.072	3.865	3.43	1.07	1.07	0.357	0.5959
103	Q9NUQ6	NLCPTRIEV	550	6.205	0.349	2.52	1.953	5.365	4.985	1.64	3.27	2.000	1.8181

104	Q9NZA1	NLLPKLHVV	402	6.435	0.484	1.94	1.614	6.67	6.49	1.49	2.99	0.497	0.7462
105	Q9BV36	NLPIFLPRV	592	8.418	0.626	3.01	2.020	6.16	6.39	0.68	0.68	0.337	1.5236
106	P15941	NLTISDVSV	1247	5.482	0.419	1.33	1.991	6.185	5.375	1.36	2.41	0.6415	1.5236
107	Q9BYC9	NLVKCQVEL	141	6.392	0.475	3.05	2.569	5.195	6.405	0.71	2.84	2.1276	0.7092
108	Q9UHD2	NTATIFHEL	721	4.677	0.385	2.37	0.521	4.905	6.575	5.55	7.07	6.1026	6.2413
109	Q9Y2Y1	NTCPYVHNI	100	3.47	0.255	2.06	1.389	4.03	3.845	2.00	5.00	5.00	5.00
110	P04637	PLDGEYFTL	385	4.488	0.362	-2.72	-1.616	4.515	6.54	3.12	4.94	1.8181	3.6363
111	Q92503	QLIDKVWQL	707	8.306	0.752	1.57	0.557	4.52	6.135	1.13	0.28	0.1414	0.1414
112	Q9UPQ0	QMFEGVARV	1075	8.914	0.765	0.770	-0.193	4.795	4.250	0.19	0.09	0.0930	0.0930
113	O43665	QMQEKAKEI	165	2.33	0.297	-0.930	-1.556	5.960	5.255	4.85	6.67	6.6666	7.8787
114	Q99613	QVCAIIERV	905	1.890	0.490	1.06	0.680	4.190	4.480	7.07	2.98	4.8618	5.4143
115	O15144	RIIEETLAL	292	7.748	0.592	3.01	0.984	5.995	6.71	1.03	2.05	0.6849	1.0273

116	P33993	RLAQHITYV	711	11.005	0.824	1.950	1.455	2.435	2.185	0.28	0.28	0.1406	0.1406
117	Q9P2B2	RLASRPLLL	871	8.258	0.645	3.19	1.218	8.24	8.045	0.69	0.92	0.8036	1.6073
118	P35527	RLASYLDKV	615	10.314	0.779	0.300	-1.419	4.835	5.645	0.16	0.16	0.1626	0.1626
119	P05783	RLASYLDRV	422	10.200	0.786	0.840	0.094	4.935	4.960	0.25	0.24	0.2369	0.2369
120	Q9Y5R8	RLDSYVRSL	137	8.603	0.615	0.840	0.857	5.60	6.395	2.19	2.92	0.7299	2.9197
121	O95715	RLLAAALLL	91	7.756	0.694	2.170	1.518	8.06	7.275	5.49	4.40	1.0989	3.2967
122	Q7Z460	RLLDGAFKL	1530	7.356	0.707	2.08	1.020	6.145	7.075	1.31	0.33	0.0653	0.0653
123	2920537	RLLDVLAPL	1328	12.501	0.808	1.84	1.506	7.005	7.385	0.08	0.08	0.2259	0.1506
124	Q6P2H3	RLQMEQMQL	754	5.685	0.442	2.06	1.246	4.08	6.025	1.46	2.39	1.0610	1.3262
125	O00507	RLWGEPVNL	2547	8.921	0.592	2.94	1.851	5.255	6.670	0.71	2.32	0.1963	0.6674
126	P11586	RMFGIPVVV	927	9.101	0.650	3.44	2.428	6.800	7.385	0.54	0.86	0.3236	0.3236
127	Q9BRB3	RMFPGEVAL	752	6.136	0.485	3.59	2.178	na	na	5.45	6.91	0.6648	1.8617

128	Q92769	RMLPHAPGV	480	8.438	0.742	3.41	2.661	4.450	4.340	0.63	0.43	0.2083	0.2083
129	Q15397	RTLDKVLEV	640	6.306	0.602	2.41	0.910	5.09	4.705	2.50	1.41	0.7812	1.0937
130	A5A3E0	RVAPEEHPV	1067	2.603	0.474	2.03	1.018	4.480	3.365	3.75	2.06	1.5932	1.8744
131	Q9UEE5	SAVDFIRTL	406	1.333	0.349	4.25	2.606	5.785	6.85	8.62	6.65	5.418	8.3743
132	Q9NS40	SIFGNVSAI	1188	7.990	0.417	0.830	-0.462	3.535	4.205	1.68	5.39	1.0942	1.6835
133	Q15366	SLAQYLINV	357	11.963	0.802	1.44	1.372	4.47	3.86	0.28	0.28	0.2801	0.2801
134	Q8WUM4	SLFGGSVKL	860	8.512	0.569	1.210	0.605	8.950	9.370	0.47	1.63	0.1162	0.3488
135	Q13045	SLFPGKLEV	1261	8.337	0.665	1.75	1.901	3.32	2.81	1.11	1.11	0.0793	0.4758
136	Q99832	SLHDAIMIV	535	9.38	0.767	2.27	1.627	5.38	4.445	0.75	0.56	0.5607	0.7490
137	Q16690	SLIGHLQTL	376	11.224	0.729	1.79	1.275	4.245	5.610	0.27	0.53	0.2659	0.5319
138	P62140	SLITRLLEV	319	10.913	0.791	1.75	1.660	4.805	4.935	0.31	0.31	0.3134	0.2557
139	P68314	SLKDVLVSV	55	10.471	0.716	1.32	1.760	4.50	4.905	1.82	1.82	1.8181	1.8181

140	P13747	SLKYFHTSV	350	7.876	0.563	1.30	1.973	3.615	3.870	1.14	2.29	2.2857	3.1428
141	Q6NZI2	SLLDKIIGA	382	8.784	0.764	2.41	2.159	5.915	5.615	0.52	0.26	0.2617	0.2617
142	O43324	SLLEKSLGL	166	9.533	0.681	2.32	1.385	5.895	7.04	1.20	1.20	1.2048	1.2048
143	0P0791	SLLENLEKI	298	8.109	0.65	-0.250	-0.063	5.095	5.510	0.67	1.34	0.3355	0.3355
144	Q9UI95	SLLSHVEQL	203	10.059	0.707	0.480	-0.047	5.740	6.63	0.99	1.48	0.4926	0.4926
145	Q9UNZ5	SLPKKLALL	91	8.705	0.559	1.20	0.723	6.03	7.515	1.10	1.10	1.0989	1.0989
146	Q96M43	SLVQIVTTL	115	9.635	0.606	2.48	2.263	4.895	6.065	0.87	0.87	0.8695	0.8695
147	P29400	SLWGQPAEA	1677	10.919	0.673	0.39	0.543	5.16	5.615	0.18	0.30	0.1192	0.2385
148	Q9BQB6	SLYALHVKA	155	6.554	0.602	2.05	1.857	6.350	6.650	10.32	6.45	3.8709	7.7419
149	Q5VTR2	SLYGGTITI	967	12.863	0.731	2.59	1.770	4.435	5.245	0.10	0.31	0.2068	1.2409
150	Q5SRE5	STADVIQHC	1741	0.030	0.227	0.580	0.410	3.685	3.720	16.71	18.67	9.3624	16.5422
151	P03141	STNRQSGRQ	392	-9.53	0.080	-1.70	-0.936	3.765	3.94	55.36	70.41	79.0816	86.479

152	Q9Y5K3	STSDIITRI	361	6.239	0.507	2.44	1.438	4.10	4.03	1.11	1.11	0.8310	1.9390
153	Q9Y6Q2	SVAGKIHTV	727	6.758	0.587	2.49	1.060	4.845	5.585	0.96	0.96	0.1375	0.4126
154	Q99541	SVASTITGV	429	8.540	0.700	1.50	0.920	6.145	5.205	2.10	1.40	0.9324	1.3986
155	Q9NZN4	SVLGRIWKL	535	5.794	0.551	3.11	1.390	5.495	6.910	2.62	2.06	1.1214	1.1214
156	Q14165	TAVALLRLL	284	-2.346	0.186	2.18	1.290	7.235	7.175	17.96	20.42	20.0704	15.4929
157	Q9Y4A5	TLADLVHHV	3851	9.287	0.763	0.82	0.336	4.425	5.06	1.169	0.55	0.0519	0.1298
158	Q9UBL3	TLADVLYHV	620	11.612	0.822	0.750	0.572	5.335	5.075	0.161	0.16	0.1612	0.1612
159	Q9Y679	TLAQRVKEV	468	4.643	0.464	-0.260	-0.309	4.13	4.455	5.77	5.13	0.0235	5.1282
160	Q8TEL6	TLIEDILGV	789	10.727	0.830	2.40	2.574	4.365	3.93	0.38	0.13	0.1267	0.2534
161	P30260	TLLGHEFVL	816	6.485	0.540	1.27	0.994	5.145	6.65	1.10	2.57	0.4901	0.3676
162	Q14643	TLLNVIKSV	2750	8.314	0.660	0.51	1.728	4.075	5.115	1.35	1.35	0.5090	1.1272
163	Q6NXT6	TLLPLRVFL	559	7.420	0.453	2.33	2.225	7.485	8.11	2.68	7.33	0.7155	1.9677

164	P63010	TLLTAIVKL	929	7.331	0.666	1.87	1.124	7.295	7.735	1.51	1.08	0.3229	1.2917
165	Q562E7	TLMDILPRI	882	10.634	0.816	3.020	2.371	5.415	4.845	0.57	0.23	0.1133	0.2267
166	|Q9BYN0	TLSDLRVYL	129	7.152	0.588	2.45	2.186	5.145	7.83	2.33	2.33	1.5503	1.5503
167	Q6UVK1	TMLARLASA	2314	8.909	0.695	0.44	0.983	6.55	6.250	0.56	0.69	1.7718	0.8210
168	P35222	TTSRVLKVL	773	-1.259	0.118	0.330	0.277	6.670	7.610	17.85	42.95	28.848	28.589
169	P08174	TVARPSVPA	373	0.033	0.241	1.110	0.761	7.405	6.370	10.72	10.72	9.9195	10.9919
170	Q9NYY3	VADTVARVL	677	-6.794	0.122	-0.930	-1.212	7.225	7.585	36.48	33.23	13.4416	20.5317
171	Q8TDN4	VALEFALHL	625	1.452	0.438	2.14	0.359	5.20	6.47	3.36	3.68	3.2	4.16
172	O15527	VLADQVWTL	337	10.048	0.801	2.50	1.286	3.825	5.820	0.30	0.30	0.2967	0.2967
173	Q99829	VLAEVPTQL	529	9.289	0.700	0.470	-0.282	4.970	5.625	0.57	0.38	0.1890	0.3780
174	Q15293	VLAPRVLRA	323	4.232	0.539	1.480	0.553	4.38	4.990	3.10	2.79	1.2383	2.1671
175	Q4KMQ2	VLDDKLVFV	902	9.936	0.807	-0.720	-0.502	5.265	5.825	0.78	0.11	0.1108	0.1108

176	Q92620	VLFGLLREV	1219	7.953	0.677	1.27	1.727	4.305	5.025	0.57	0.49	0.1640	0.0820
177	O14980	VLIDYQRNV	1063	7.519	0.682	1.51	2.430	4.265	4.185	2.16	1.22	0.4703	1.0348
178	Q8N138	VLIPKLPQL	145	7.892	0.652	2.64	2.094	5.245	6.485	4.14	2.76	0.6896	0.6896
179	Q6TFL4	VLLGKVYVV	592	8.147	0.687	1.23	1.055	4.14	5.035	0.68	0.51	0.1689	0.1689
180	P79483	VLSSRLAFA	258	9.165	0.683	-0.670	0.016	4.94	6.12	0.78	0.78	2.7131	1.1627
181	P42224	VLWDRTFSL	742	13.550	0.824	4.06	3.133	3.970	5.565	0.13	0.13	0.1347	0.1347
182	Q07000	VMAPRTLLL	358	8.377	0.652	2.58	1.018	5.585	5.165	0.84	0.84	0.8379	1.1173
183	P01892	VMAPRTLVL	357	5.848	0.474	2.49	1.018	6.195	5.70	1.96	3.08	0.8403	1.4005
184	Q31612	VMAPRTVLL	355	7.757	0.639	2.14	0.960	6.385	6.380	1.69	1.13	0.5633	0.8450
185	P52294	VMDSKIVQV	530	8.748	0.748	0.010	-0.467	7.185	5.995	1.32	0.75	0.3773	0.9433
186	Q9UJF2	VMLDVPIRL	1131	8.715	0.701	3.350	1.227	5.585	6.56	1.15	0.88	0.0884	0.7073
187	O15427	VVHTPETSV	457	1.926	0.243	2.260	2.094	na	na	14.66	22.10	14.2231	26.258

188	Q14627	WLPFGFILI	837	9.232	0.530	0.360	0.720	4.140	4.180	0.36	1.31	0.9557	0.7160
189	Q16531	YLDNGVVFV	1132	11.381	0.831	-3.02	-1.570	4.570	5.945	0.35	0.18	0.1766	0.1766
190	Q96S19	YLDPAQRGV	196	7.514	0.610	-1.44	0.066	5.40	6.09	2.04	1.02	0.5102	0.5102
191	Q96SK2	YLFERIKEL	553	10.510	0.756	1.51	1.301	4.905	6.345	0.36	0.72	0.1808	0.1808
192	Q9UBU8	YLHDFLKYL	354	11.364	0.793	0.590	0.308	7.030	8.545	0.28	0.28	0.2824	0.2824
193	P26196	YLIPLLERL	475	10.117	0.733	1.110	1.550	6.525	7.230	0.42	0.42	0.2105	0.4210
194	P35580	YLLEKSRAV	1968	8.535	0.694	-0.400	-0.291	5.635	4.765	0.61	0.41	0.0508	0.2540
195	Q6T310	YLLPKDIKL	234	7.873	0.583	1.080	0.697	8.145	8.805	2.56	3.42	0.4273	0.8547
196	P27694	YLMDTSGKV	608	11.696	0.790	-1.750	-0.394	5.010	4.16	0.16	0.16	0.1644	0.1644
197	O43187	YLPEDFIRV	617	12.359	0.798	0.360	0.092	4.880	4.990	0.32	0.16	0.1620	0.1620
198	P08581	YVDPVITSI	1382	10.314	0.633	-0.770	0.490	4.360	4.295	0.22	0.94	0.1447	0.7235
199	P13987	SLSEKTVLL	120	9.531	0.651	1.090	0.779	5.505	6.020	1.67	2.50	0.8333	1.666

200	P14923	NLMEQPIKV	737	8.844	0.709	2.94	1.872	3.450	3.260	1.09	1.09	0.1356	0.1356
201	Q9Y696	NLLPKLHIV	245	7.270	0.565	1.590	1.377	5.575	5.675	2.45	3.67	0.8163	0.8163
202	P26012	ALMEQQHYV	761	13.08	0.838	2.36	2.094	3.00	3.155	0.13	0.13	0.1314	0.1314
203	Q96AC1	ALSDLEITL	672	8.419	0.610	4.40	3.290	6.355	8.460	1.04	1.34	0.1488	0.7440
204	Q96FZ7	DAILEELSA	193	-6.138	0.099	-0.330	0.026	4.275	4.730	32.12	47.67	28.4974	29.015
205	O14896	GLYPGLIWL	459	11.980	0.742	3.30	2.246	4.780	5.880	0.218	0.44	0.2178	0.4357
206	P62249	KLLEPVLLL	138	10.745	0.724	3.37	1.828	4.80	6.810	0.725	2.17	0.7246	0.7246
207	O95236	ALANGIEEV	394	8.175	0.798	0.500	0.645	3.675	4.635	1.52	0.25	0.2538	0.2538
208	Q9NZN4	ALASHLIEA	535	10.021	0.785	1.340	0.018	5.720	5.33	0.37	0.19	0.5607	0.7476
209	P05783	ALLNIKVKL	422	4.506	0.545	2.99	2.123	5.62	7.14	2.61	1.42	0.7109	1.4218
210	P07686	ALVVQVAEA	548	5.884	0.534	0.520	1.065	6.230	6.015	4.38	4.56	2.5547	5.1094
211	P78371	EAAEVILRV	527	0.068	0.326	0.450	-0.939	4.710	4.765	13.09	10.06	6.4516	9.2979

212	Q6PCB6	EVIDFSHGL	321	3.347	0.410	1.16	0.883	5.040	6.890	4.05	5.30	2.4922	4.0498
213	P05412	FAEGFVRAL	323	-0.550	0.225	-1.43	-1.675	6.710	7.915	11.46	13.93	7.7399	10.8591
214	O95372	FLEKLLPPV	223	9.631	0.809	-0.970	0.971	4.275	4.775	0.45	0.45	0.4484	0.4484
215	P78371	FLLDKKIGV	527	8.897	0.805	1.180	1.640	4.360	4.770	0.19	0.19	0.1897	0.1897
216	P08311	FLLPTGAEA	247	9.819	0.686	-2.780	0.050	5.365	5.810	0.40	0.81	0.4048	0.8097
217	Q99828	FLTKQEILL	183	6.658	0.656	0.530	1.105	4.790	5.950	1.64	0.55	0.5464	0.5464
218	Q02880	FLYDDNQRV	1618	13.093	0.857	1.230	1.105	3.085	3.725	0.06	0.06	0.0618	0.0618
219	P27708	GLADKVYFL	2217	10.220	0.777	1.700	0.506	5.510	6.940	0.41	0.14	0.0451	0.0451
220	P26358	GLIEKNIEL	1608	8.697	0.679	1.960	1.478	4.765	6.290	0.25	0.31	0.0621	0.0621
221	O14777	GLNEEIARV	634	8.905	0.746	-0.080	-0.087	4.835	3.585	0.63	0.32	0.1577	0.3154
222	Q8IYM9	HLANIVERV	490	5.956	0.747	-0.060	-0.140	4.380	4.950	1.22	0.20	0.2040	0.4081
223	Q14168	HVGDIIKEV	568	2.694	0.491	-0.590	-0.664	5.070	6.325	5.46	2.46	1.5845	3.8732

224	Q9UHE5	ILDTGTIQL	219	8.494	0.654	-1.57	-1.088	5.490	6.360	3.20	2.28	0.9132	1.8264
225	O14775	ILFGHENRV	387	6.656	0.588	1.42	1.187	4.795	5.590	1.03	0.78	0.2583	0.2583
226	Q07954	ILIEHLYGL	4536	11.932	0.834	2.84	2.477	4.345	5.085	0.04	0.02	0.0220	0.0220
227	P40227	IMRAGMSSL	523	7.806	0.453	0.370	0.126	4.745	6.305	0.76	3.63	4.5889	3.8240
228	P09601	KIAQKALDL	280	1.450	0.229	2.730	0.601	5.835	6.425	8.21	15.7	8.9285	13.9285
229	Q9BXD5	KLDQVIIHV	312	10.379	0.751	0.190	0.647	5.365	5.980	0.96	24.68	0.3205	1.2820
230	P51572	KLDVGNAEV	238	8.509	0.710	-1.96	-0.710	5.335	4.605	2.94	2.521	1.2605	2.1008
231	Q9Y4C2	KLGSVPVTV	913	9.523	0.699	-0.220	0.180	6.185	6.305	0.66	0.77	0.1095	0.8762
232	P32991	KLLDKTSLV	583	11.696	0.790	0.290	0.180	3.220	3.050	0.51	0.51	0.3430	0.8576
233	Q15427	KLYGKPIRV	416	10.142	0.715	4.160	1.735	5.270	5.23	0.72	0.96	0.2403	0.2403
234	Q9BX97	KVKTLEVEI	434	-0.019	0.194	2.050	1.721	6.565	7.685	10.83	15.67	7.6036	11.059
235	O15539	LAALPHSCL	173	-2.302	0.130	1.72	-0.741	4.845	5.555	10.40	27.75	27.7456	10.4046

236	Q9Y490	LLDHVLLTL	2533	8.999	0.665	0.530	0.475	4.910	6.750	0.28	0.51	0.3947	0.2368
237	Q99650	LLDPGEHYC	971	-0.008	0.276	-1.740	-0.501	4.150	4.560	11.33	11.43	1.4418	2.9866
238	O00560	LMDHTIPEV	290	10.216	0.786	0.360	0.487	4.125	4.800	0.69	0.34	0.3448	0.4784
239	P62906	NMVAKVDEV	209	5.795	0.532	1.250	0.458	4.545	5.170	1.91	3.35	2.3923	3.3492
240	P61289	QLVDIIEKV	246	7.521	0.752	1.090	1.437	4.390	5.455	2.03	0.41	0.4065	1.6260
241	Q9UH99	RIRPTAVTL	709	1.702	0.182	3.380	2.215	6.625	7.650	8.04	17.63	4.3723	9.1678
242	Q63ZY3	RLLDYVVNI	843	11.339	0.783	2.22	2.263	6.825	7.425	0.24	0.12	0.1186	0.1186
243	P62136	SIIGRLLEV	322	9.553	0.683	2.11	0.997	4.020	4.505	0.62	1.24	0.3105	0.3105
244	Q14444	SLLDEFYKL	701	10.433	0.759	1.880	0.951	5.725	7.080	0.14	0.14	0.1426	0.1426
245	P49815	SLLDIIEKV	1799	10.886	0.815	1.520	1.570	4.760	5.640	0.22	0.06	0.1111	0.1111
246	Q8N461	SLRLLSLAG	471	-4.416	0.113	0.130	-0.034	4.720	5.080	34.18	43.95	39.0658	25.0530
247	Q9P2P1	TLADIIARL	1890	9.307	0.770	2.62	1.092	5.685	7.640	0.74	0.32	0.0529	0.1587

248	P21100	TLLDHIRTA	173	5.283	0.623	1.230	1.736	4.715	4.670	4.05	1.16	0.5780	1.1560
249	Q8WXG6	TLVDFPLHL	1639	8.267	0.674	2.64	1.735	7.120	6.565	1.28	0.98	0.3050	0.5491
250	P62906	TLYEAVREV	209	8.716	0.737	1.820	0.779	4.085	4.465	0.48	0.48	0.4784	0.4784
251	Q96QK1	TTVEIFNKL	788	2.171	0.232	1.790	0.534	5.420	6.895	9.26	15.10	6.5989	9.3908
252	Q9H6Z9	YIVPCLHEV	231	11.328	0.790	0.680	0.556	3.550	3.705	0.43	0.87	1.7316	1.2987
253	P78536	YLIELIDRV	816	11.537	0.833	0.690	1.139	5.230	5.240	0.25	0.25	0.1225	0.1225
254	O75367	YLTAEILEL	364	11.175	0.805	0.180	0.540	7.410	8.290	0.55	0.55	0.2747	0.5494

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S.No.	**Protein accession number**	**Epitope sequence**	**Total no. of peptides**	**MHC binding score**		**TAP binding score**		**C-terminal cleavage score**		**Average relative rank of epitopes in their source antigen (%)**			
				PSSM	**ANN**	**TAP-2003**	**TAP-2004**	**Constitutive proteasome**	**Immuno-proteasome**	**PSSM**	**ANN**	**NetMHCpan4.0 (E)**	**NetMHCpan4.0 (BA)**

1	P14209	AVQRTLLEK	177	7.946	0.832	2.23	1.434	na	na	1.13	0.56	0.5649	0.5649
2	Q9C0B1	GTLDYILQR	497	5.881	0.648	2.92	2.175	4.72	3.76	1.81	1.41	0.4024	0.4024
3	P06340	GTYVSSVPR	242	6.905	0.753	2.26	1.843	na	na	0.83	0.83	0.4132	0.4132
4	Q04637	GVIDLIFEK	1592	7.066	0.807	2.67	2.886	5.780	6.355	0.50	0.06	0.0628	0.0628
5	Q8WVV9	SVSPVVHVR	534	6.267	0.722	2.20	1.536	4.795	5.085	1.69	1.12	0.3745	0.3745
6	Q67863	YVNVNMGLK	351	5.271	0.717	-3.04	-1.253	2.615	2.03	1.71	0.57	0.5698	1.7094
7	Q96NU0	ASVAWAVLK	1280	5.515	0.754	3.710	2.947	6.845	5.030	1.56	0.23	0.0781	0.0781
8	Q9P1Y6	GSSDVIIHR	1641	4.080	0.559	2.580	1.930	4.410	5.050	3.29	2.01	0.1828	0.2437
9	Q5SRD1	GTMTGMLYK	249	8.549	0.834	0.310	0.675	3.720	3.945	0.40	0.40	0.4016	0.4016
10	Q460N5	GVFGFPLGR	**1793**	5.371	0.774	3.790	2.870	4.800	4.525	3.04	0.53	0.1617	0.2788
11	Q9NP97	SLMHSFILK	88	8.579	0.798	2.110	2.334	4.200	4.560	1.14	1.14	1.1363	1.1363

12	P05019	SSLPTQLFK	187	7.803	0.765	1.710	1.765	2.270	2.400	1.07	0.53	0.5347	0.5347
13	O43826	STAAFFLLR	421	7.285	0.804	2.83	1.090	5.010	4.395	0.71	0.24	0.2375	0.2375
14	Q99541	TSALPIIQK	429	5.680	0.729	3.050	1.633	4.105	4.515	5.13	1.63	0.4662	0.2331

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S.No.	Protein accession number	Epitope sequence	Total no. of peptides	MHC binding score		TAP binding score		C-terminal cleavage score		Average relative rank of epitopes in their source antigen (%)			
				PSSM	ANN	TAP-2003	TAP-2004	Constitutive proteasome	Immuno-proteasome	PSSM	ANN	NetMHCpan4.0 (E)	NetMHCpan4.0 (BA)
1	P22626	DTIEIITDR	345	5.520	0.772	1.14	1.049	4.250	4.09	0.29	0.58	0.2898	00.2898
2	P62736	EAGPSIVHR	369	3.113	0.727	-1.390	-1.052	na	na	6.78	1.90	1.8970	2.4390
3	Q9H299	EVTRILDGK	85	3.603	0.702	-1.150	0.158	4.115	4.320	4.71	4.71	2.3529	2.3529
4	P08133	TIIDIITHR	665	6.559	0.769	3.32	2.132	3.880	3.720	0.60	0.60	0.1503	00.1503

5	P01833	VAVGVARAR	756	2.316	0.434	2.02	0.573	4.565	5.235	9.26	18.92	1.5873	1.3227
6	P30499	DTAAQITQR	358	5.041	0.775	-0.050	-0.386	4.945	4.050	1.12	0.28	0.2793	00.2793
7	P04075	ESTGSIAKR	356	4.499	0.745	-0.810	-0.668	3.715	3.625	1.97	0.56	0.2808	00.2808
8	P43308	NVSHTVVLR	175	5.610	0.749	3.370	2.451	5.100	4.660	1.71	0.57	0.5714	00.5714
9	Q15437	STIEYVIQR	759	6.747	0.743	3.440	1.783	4.040	5.280	0.53	0.40	0.1317	00.1317
10	P07355	TIVNILTNR	331	6.714	0.734	2.090	1.655	3.545	3.465	3.02	0.91	0.3021	00.3021
11	P07148	TLGDIVFKR	119	5.242	0.640	0.850	0.210	3.220	4.280	4.20	7.56	1.6806	1.6806
12	P62736	TTAEREIVR	369	5.070	0.790	2.940	1.008	5.240	5.075	2.44	0.27	1.6260	1.0840
HLA-A* 03:01													
S.No.	**Protein accession number**	**Epitope sequence**	**Total no. of peptides**	**MHC binding score**		**TAP binding score**		**C-terminal cleavage score**		**Average relative rank of epitopes in their source antigen (%)**			
				PSSM	**ANN**	**TAP-2003**	**TAP-2004**	**Constitutive proteasome**	**Immuno-proteasome**	**PSSM**	**ANN**	**NetMHCpan4.0 (E)**	**NetMHCpan4.0 (BA)**

1	P08670	ALRDVRQQY	458	4.158	0.421	4.810	2.443	4.970	4.985	3.71	4.158	0.6550	1.0917
2	P78527	ATDPNILGR	4120	4.936	0.296	2.650	1.603	3.715	3.195	3.33	20.33	1.2864	1.2135
3	P23229	ATFPDTLTY	1122	7.061	0.460	5.970	3.805	4.190	4.145	0.62	3.03	0.0891	0.0891
4	O00159	FLDHVRTSF	1055	0.573	0.291	0.280	1.767	3.660	4.195	22.75	19.15	15.0710	13.270
5	P01833	FSVVINQLR	756	2.609	0.320	1.56	1.829	3.015	3.255	8.47	11.77	10.0529	11.1111
6	P56378	GLMGFIVYK	50	7.142	0.717	1.49	2.386	4.33	4.805	2.00	2.00	2.00	2.00
7	Q13287	GVADKILKK	299	6.390	0.528	2.44	0.993	4.280	3.655	2.01	2.01	0.3344	0.3344
8	P24001	GVLAWVKEK	226	5.237	0.358	0.460	0.862	4.795	5.945	2.21	9.73	0.4424	0.4424
9	Q14669	HLEDIVRQK	1984	5.019	0.440	-0.860	-0.116	4.080	4.435	3.13	4.59	1.3608	0.7056
10	P18074	ILENIQRNK	752	5.961	0.564	-1.170	1.051	3.445	2.825	1.197	0.93	1.0638	0.7978
11	P27449	IVALILSTK	147	5.681	0.642	1.040	0.722	na	na	2.041	0.68	1.3605	1.3605
12	Q9H3M7	KIKSFEVVF	383	0.536	0.252	4.26	2.635	6.415	7.245	21.93	26.11	11.7493	10.9660
13	Q9BZZ5	KLFDKLLEY	502	8.093	0.609	5.480	3.087	4.910	5.375	0.60	1.79	0.1992	0.1992

14	P51991	KLFIGGLSF	370	3.022	0.460	5.060	4.478	4.865	5.150	4.86	2.16	1.3513	1.5957
15	Q9NZN4	KLPNSVLGR	535	6.952	0.502	2.490	2.176	4.00	3.350	0.75	1.68	1.1214	0.9345
16	Q9H0A9	KLRELTQRY	332	5.978	0.575	4.12	2.017	5.065	5.17	1.51	0.60	0.6024	0.9036
17	O95298	KTYGEIFEK	111	9.439	0.648	3.14	1.912	na	na	0.90	0.90	0.9090	0.9090
18	P07711	KVFQEPLFY	325	7.586	0.571	5.49	2.979	4.45	4.32	0.31	0.62	0.3076	0.3076
19	O75718	KVMQQNLVY	393	7.037	0.492	5.62	3.815	2.995	2.810	1.02	3.31	1.0178	0.7633
20	Q9NUV9	QIASFILLR	321	5.981	0.658	3.05	1.006	na	na	1.87	0.93	2.1806	1.5576
21	O75643	QTYVGITEK	2128	8.393	0.632	0.810	0.844	3.645	4.47	0.09	0.52	0.0902	0.1409
22	Q71U36	RIHFPLATY	443	5.196	0.519	6.36	3.584	5.695	5.810	1.13	1.58	0.2257	0.2257
23	Q8NBM4	RLFPPLRQR	336	6.480	0.569	4.34	3.471	3.735	3.505	1.79	2.38	0.5952	0.5952
24	O43390	RLFVGSIPK	625	10.442	0.732	2.42	2.536	4.25	4.26	0.16	0.16	0.16	0.16
25	Q5PRF9	RLLQKVLAY	686	5.334	0.463	4.95	2.592	5.325	5.425	2.04	3.50	0.2915	0.2915
26	P25787	RVASVMQEY	226	4.771	0.504	3.13	0.685	3.120	4.20	2.21	2.21	0.8849	0.8849

27	Q03164	RVFPWFSVK	3961	9.667	0.691	3.110	2.821	3.620	3.495	0.03	0.15	0.0252	0.0252
28	Q9NZN4	RVHAYIISY	535	7.865	0.512	7.07	4.802	3.745	3.575	0.37	1.50	0.1869	0.1869
29	P18085	SLFSRLFGK	172	8.744	0.769	2.88	2.863	3.560	3.790	0.58	0.58	0.5813	0.5813
30	Q8NF91	SVYDSVLQK	8789	10.90	0.661	3.58	1.780	3.425	2.925	0.01	0.20	0.0113	0.0113
31	P58876	SVYVYKVLK	118	9.075	0.617	3.71	3.178	2.905	3.285	1.69	0.85	0.8474	0.8474
32	O43324	TLADILLYY	166	6.682	0.620	4.38	2.042	3.76	4.210	1.81	1.20	0.6024	0.6024
33	Q99541	TSALPIIQK	429	7.10	0.523	3.05	1.633	4.105	4.515	0.70	1.17	0.6993	1.6317
34	Q9BUN8	TVAVPLVGK	243	5.076	0.486	2.27	1.946	5.96	4.995	4.53	4.12	0.4115	0.4115
35	Q9UHB9	VLYDRVLKY	619	8.271	0.618	6.29	3.01	5.940	5.950	0.16	0.48	0.1615	0.1615
36	O00476	YLADFLLTK	412	7.320	0.583	1.62	1.479	4.075	4.585	0.24	0.73	0.2427	0.2427
37	P63241	AVAIKAMAK	146	5.467	0.576	3.25	0.831	4.375	5.035	2.74	1.37	1.3698	0.1369
38	P26358	ESYEALPQH	1608	2.32	0.261	0.520	-0.356	4.610	3.850	9.89	22.01	10.9452	6.7786
39	O60506	GLTDVILYH	615	3.043	0.455	-0.030	0.849	3.925	4.125	5.53	2.44	1.7886	0.9756

40	Q8IWX8	GLYEFFRAK	908	7.578	0.593	2.070	1.667	3.520	3.620	0.11	0.33	0.1101	0.1101
41	P37088	GTLPHPLQR	661	4.307	0.335	2.090	1.148	4.20	2.475	4.84	14.37	0.1512	0.1512
42	Q5SRD1	GTMTGMLYK	249	8.120	0.744	0.310	0.675	3.720	3.945	0.80	0.40	0.4016	0.8032
43	P06396	IIYKGGTSR	774	6.422	0.610	3.440	2.661	5.115	5.330	0.78	0.65	0.3875	0.3875
44	O75400	IVAGSLITK	949	6.766	0.635	1.640	1.035	4.840	4.645	0.84	0.74	0.1053	0.1053
45	P61968	KIADRFLLY	157	6.755	0.669	5.720	2.066	4.570	4.390	1.27	1.27	0.6369	0.6369
46	Q14004	KLADFGLAR	1504	5.101	0.467	3.61	1.947	5.150	4.830	2.19	2.79	0.1329	0.2659
47	P56559	KLYEMILKR	184	9.909	0.678	5.750	3.393	4.160	3.685	0.54	0.54	0.5434	0.5434
48	Q13094	KVYNIQIRY	525	8.942	0.576	-7.710	4.042	3.025	4.210	0.19	0.76	0.3809	0.3809
49	P26373	LTGPVMPVR	203	1.204	0.298	0.420	0.099	4.945	4.945	20.20	21.18	5.4187	5.4187
50	O60449	QIPKGRTPK	1714	7.155	0.594	0.150	0.248	2.695	2.475	0.82	0.82	3.2672	2.0420
51	Q96TA1	QISIPFLLK	725	8.316	0.770	1.810	1.158	4.710	3.495	0.28	0.14	0.6896	0.55517
52	P62273	QLYWSHPRK	48	9.054	0.775	2.740	2.377	2.645	2.800	2.08	2.08	2.0833	2.0833

53	P48556	RILFFNTPK	249	9.834	0.678	3.000	2.478	2.345	3.310	0.40	0.80	1.2048	0.8032
54	P52895	RLLEMILNK	315	9.449	0.751	3.140	3.018	5.205	4.535	0.32	0.63	0.3174	0.3174
55	Q86XP3	RMFDMGFEY	930	7.312	0.621	6.190	4.169	3.905	5.310	1.18	0.54	0.2150	0.5376
56	Q00325	RQIPYTMMK	354	8.319	0.601	3.810	3.155	2.330	2.290	0.56	1.69	0.2824	0.5649
57	Q9UBB5	SIFKQPVTK	403	7.724	0.667	3.510	2.993	4.215	4.495	0.99	0.50	0.4962	0.4962
58	Q9Y4A5	SITSVFITK	3851	8.074	0.622	1.750	1.096	5.015	4.645	0.44	0.93	0.3895	2.8564
59	O95373	SLAEILLKK	1030	8.058	0.696	1.950	0.776	4.490	4.100	0.29	0.19	0.0970	0.0970
60	Q9NP97	SLMHSFILK	88	10.713	0.806	2.110	2.334	4.200	4.560	1.14	1.14	1.1363	1.1363
61	P33121	SLWDRLIFH	690	3.500	0.610	2.870	1.642	4.505	5.335	5.65	0.43	0.8695	0.1449
62	Q12929	SVLSPLLNK	814	8.480	0.665	2.450	1.638	4.400	4.195	0.12	0.12	0.1228	0.1228
63	Q8WVX9	SVYVLVRQK	507	7.595	0.551	3.230	2.281	4.910	5.170	0.39	1.58	0.3944	0.1972
64	Q96DT5	TLADLLALR	4515	4.356	0.547	1.87	1.205	4.835	4.555	4.10	1.62	1.9269	2.2812
65	P19367	TLIDIMTRF	909	2.878	0.288	3.55	2.647	4.165	4.610	8.69	19.36	7.0407	8.8008
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S.No.	Protein accession number	Epitope sequence	Total no. of peptides	MHC binding score		TAP binding score		C-terminal cleavage score		Average relative rank of epitopes in their source antigen (%)			
				PSSM	ANN	TAP-2003	TAP-2004	Constitutive proteasome	Immuno-proteasome	PSSM	ANN	NetMHCpan4.0 (E)	NetMHCpan4.0 (BA)
1	Q9ULT8	MPRGVVVTL	2604	11.590	0.471	-1.31	-1.248	5.460	7.520	0.08	1.42	0.0384	0.0384
2	O60895	RPAALRLLL	167	11.942	0.495	0.950	-2.220	6.915	8.035	0.60	1.80	0.5988	0.5988
3	P31431	APARLFALL	190	8.422	0.426	-0.150	-0.986	5.570	6.485	0.53	3.16	0.5263	0.5263
4	Q31612	APRTVLLLL	355	10.616	0.473	0.020	-0.827	7.060	7.495	0.28	1.41	0.2816	0.2816
5	O75179	APRVPVQAL	2595	12.53	0.487	0.050	-1.193	5.500	6.155	0.08	1.31	0.0385	0.0385
6	Q6NUT3	APSPRPLSL	472	11.130	0.479	1.120	0.544	4.905	5.685	0.21	1.48	0.2118	0.2118
7	P43355	FPSLREAAL	301	10.824	0.490	-3.130	-2.215	5.985	7.045	0.33	1.0	0.3322	0.3322

8	Q9H1B7	FVIETARQL	788	1.998	0.367	0.180	0.241	5.485	5.645	14.97	37.18	4.1878	7.3604
9	P57086	GPREAFRQL	171	10.465	0.483	-2.150	-2.246	6.180	6.745	0.58	2.92	0.5847	0.5847
10	Q15393	GPRSSLRVL	1209	10.561	0.488	-2.670	-2.178	6.985	7.370	0.08	0.50	0.0827	0.0827
11	P29401	HASDRIIAL	615	3.352	0.379	3.110	1.034	5.870	6.620	5.37	17.40	1.1382	1.7886
12	Q99541	IARNLTQQL	429	4.487	0.379	3.110	0.077	3.490	5.290	2.56	5.128	0.4662	0.6993
13	Q8N6M6	IVPANFPSL	811	3.098	0.382	1.870	1.645	5.550	7.525	6.04	17.88	2.5893	5.1787
14	P17931	KPNANRIAL	242	11.148	0.486	-1.080	-1.847	5.235	6.100	0.83	1.24	0.4132	0.4132
15	Q8N531	LPKPPGRGV	531	10.034	0.443	-1.180	-0.287	5.945	5.555	1.13	5.84	0.9416	1.6949
16	P62701	LPRGKGIRL	255	10.461	0.479	-0.270	-1.751	5.820	7.070	0.78	2.35	0.3921	0.3921
17	Q04828	RPELVRPAL	315	12.650	0.515	-1.120	-1.206	5.465	6.195	0.32	0.32	0.3174	0.3174
18	Q14332	RPRSALPRL	557	13.447	0.510	0.770	-1.062	6.715	6.455	0.18	0.36	0.1795	0.1795
19	Q9NTK1	RPSSVLRTL	204	11.963	0.502	-0.940	-0.775	5.350	6.550	0.98	0.98	0.4901	0.4901

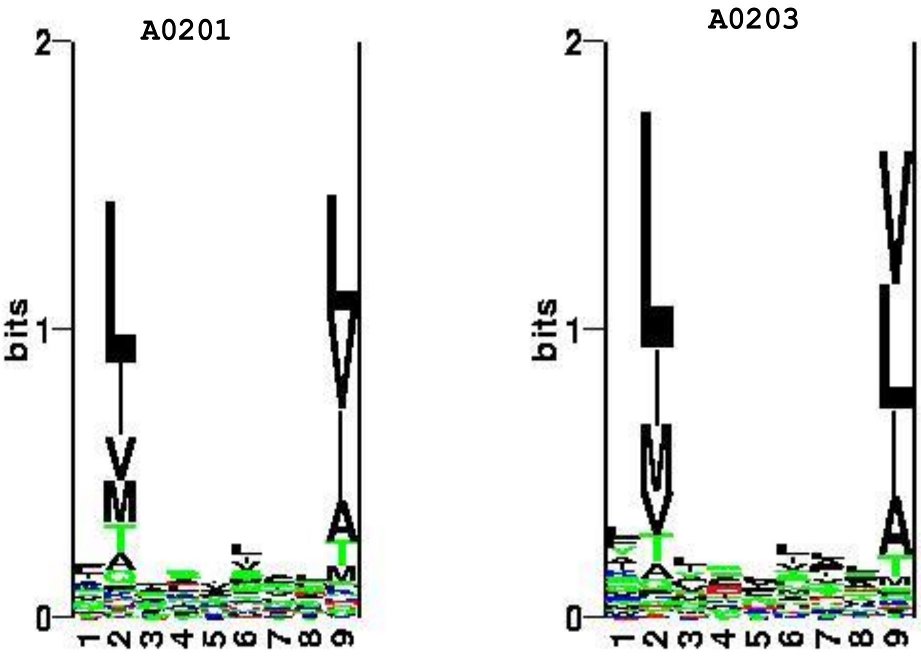
20	P17936	RPTLWAAAL	283	11.334	0.483	-0.920	-1.180	7.975	7.750	0.35	1.77	0.3533	0.3533
21	Q99856	SPKLPVSSL	585	10.853	0.478	-1.320	-1.427	6.170	7.800	0.17	1.71	0.1709	0.1709
22	P37023	SPRKGLLML	495	10.773	0.498	-0.690	-1.418	5.045	5.725	0.20	0.81	0.2020	0.2020
23	Q14669	SPRLPVGGF	1984	8.872	0.465	0.100	0.097	5.035	5.525	0.71	2.22	0.1008	0.2016
24	O00214	TPMGPGRTV	308	9.457	0.460	-1.300	-0.143	5.165	4.645	1.30	1.95	0.6493	0.6493
25	P21810	WPLWRLVSL	360	10.819	0.431	-1.210	-0.264	5.985	7.915	1.11	5.56	1.6666	0.2777
HLA-B* 45:01													
S.No.	**Protein accession number**	**Epitope sequence**	**Total no. of peptides**	**MHC binding score**		**TAP binding score**		**C-terminal cleavage score**		**Average relative rank of epitopes in their source antigen (%)**			
				PSSM	**ANN**	**TAP-2003**	**TAP-2004**	**Constitutive proteasome**	**Immuno-proteasome**	**PSSM**	**ANN**	**NetMHCpan4.0 (E)**	**NetMHCpan4.0 (BA)**

1	Q9UJZ1	AEAIRILAA	348	14.703	0.538	2.98	0.766	6.910	5.365	0.29	0.29	0.2873	0.2873
2	P14923	AELATRALP	737	8.025	0.413	1.54	0.836	5.375	3.445	1.76	8.41	0.9497	0.8141
3	Q14258	AEMPQNYRP	622	6.027	0.412	3.66	2.396	2.265	2.560	1.61	8.04	0.4823	0.4823
4	P25205	EEMPQVHTP	800	0.628	0.408	-0.440	0.110	3.850	4.320	11.63	6.63	0.50	0.50
5	P34896	EENARLFHP	475	9.633	0.444	-2.42	-1.609	5.575	4.230	1.05	4.63	2.3157	2.5263
6	Q9Y2Y0	EENKLIYTP	155	6.898	0.458	0.060	0.924	2.750	3.705	2.58	2.58	1.9354	1.2903
7	Q16665	MEDIKILIA	818	9.796	0.485	-0.820	-0.855	4.27	3.855	0.37	0.24	0.3667	0.4889
8	P08670	MEENFAVEA	458	12.803	0.519	-2.14	-0.928	5.86	6.28	0.44	0.22	0.6550	0.2183
9	Q95604	NEDLRSWTA	364	6.006	0.456	-0.110	-0.299	6.650	6.810	3.02	3.57	0.2747	0.8241
10	P13639	NEIKDSVVA	850	11.910	0.496	1.26	1.151	5.270	5.255	0.24	0.59	0.2352	0.3529
11	P05107	QEQSFVIRA	761	11.508	0.504	-0.060	-1.259	4.290	4.705	0.26	0.26	0.1314	0.1314

12	Q96AD5	REHAPFLVA	496	15.694	0.537	2.03	1.220	5.275	5.235	0.20	0.20	0.2016	0.2016
13	P13760	VEHPSLTSP	258	0.339	0.379	0.480	0.742	3.935	3.485	12.79	15.12	1.1627	1.9379
14	P17931	VEPDHFKVA	242	2.990	0.486	-0.580	-0.826	6.090	5.795	3.31	0.41	0.4132	1.6528

na- not available for prediction

Figure S1: The logo visualizations of peptide binding motifs for 22 HLA-A and B alleles. The peptide binding motif specificities were generated from the binders of the MHCIPREDS-IEDB training set using the EasyPred matrix modeler. The height of a column in the logo is proportional to the relative information content in the sequence motif, and the letter height is proportional to the amino acid frequency.



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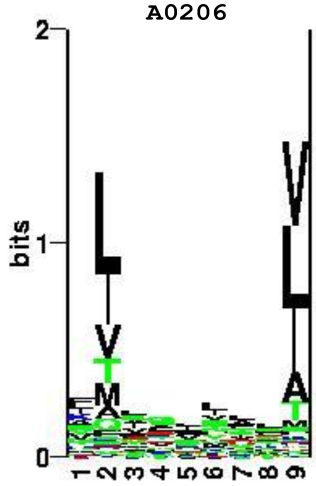

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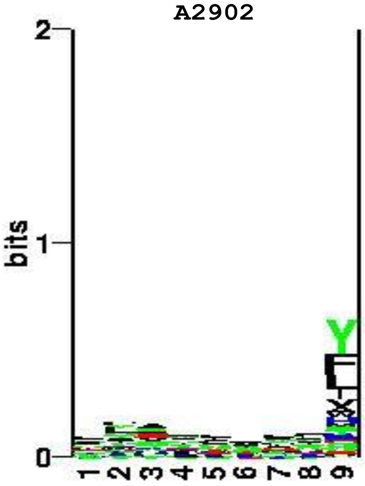

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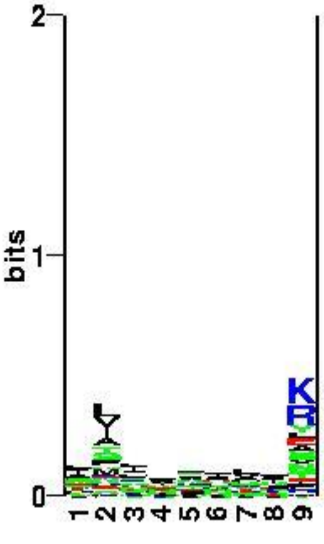

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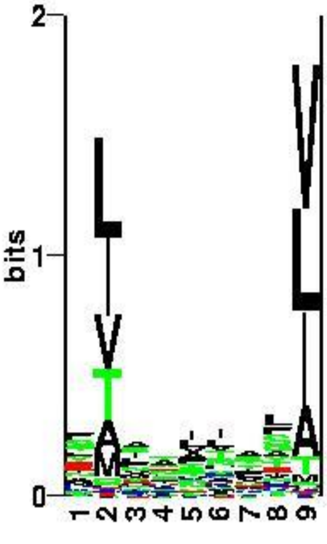

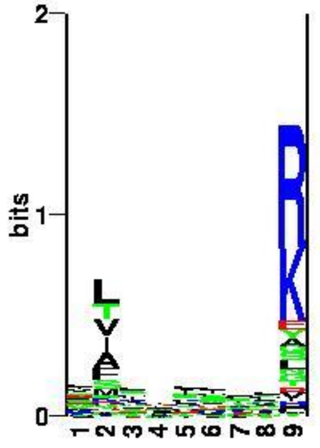
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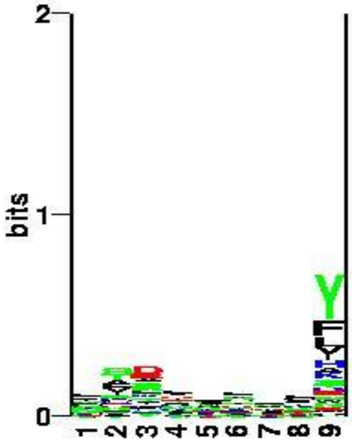
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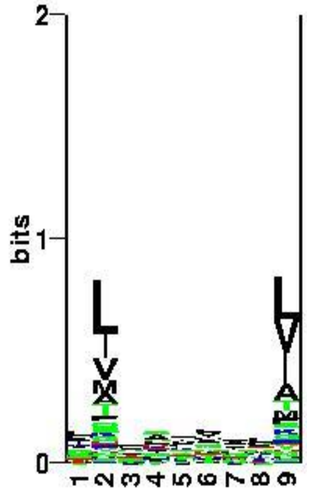
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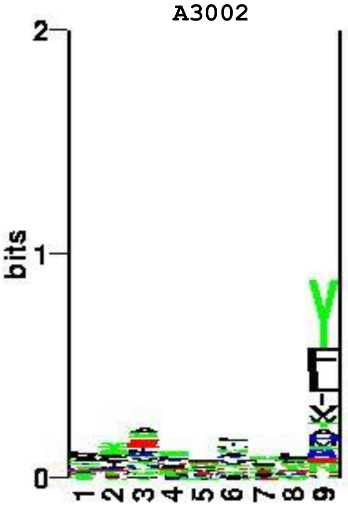
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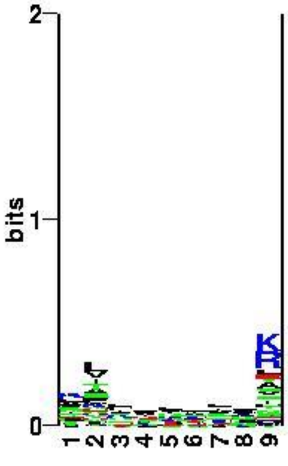

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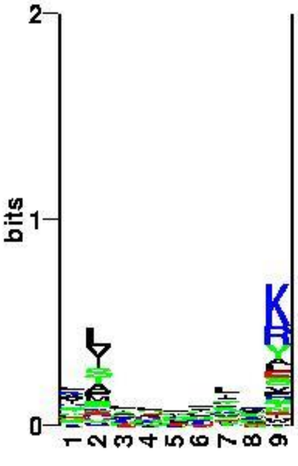

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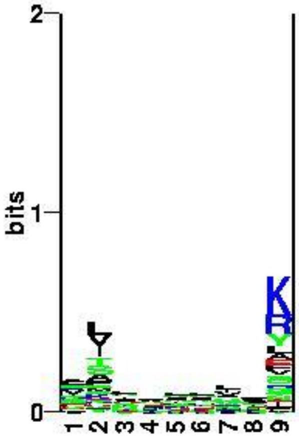

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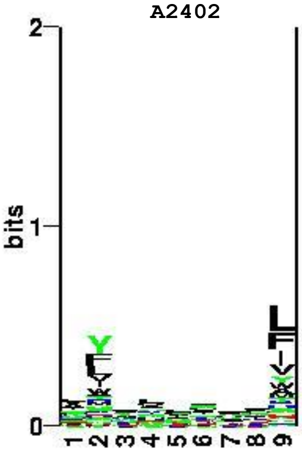

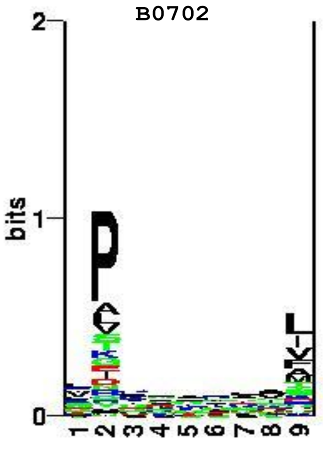
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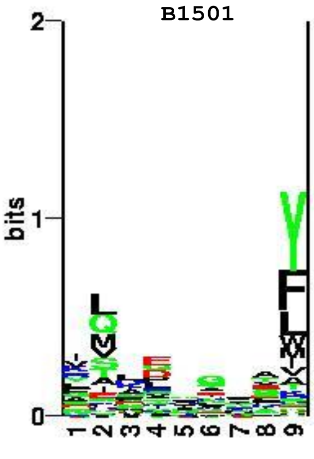
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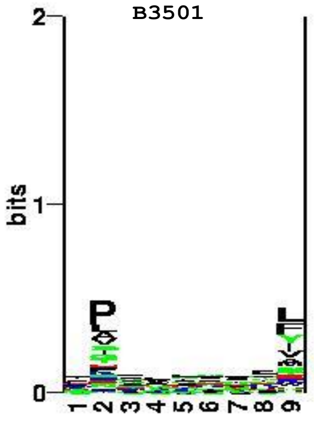
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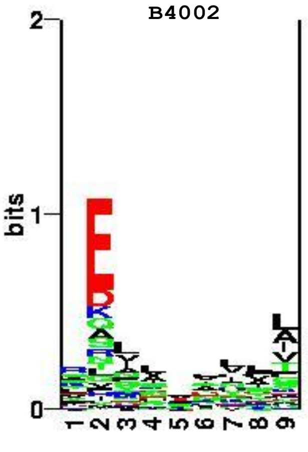
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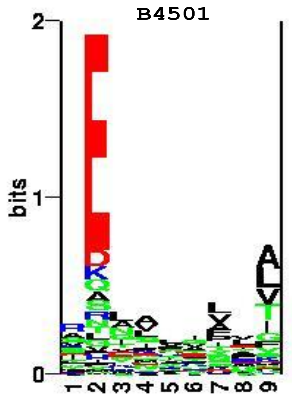
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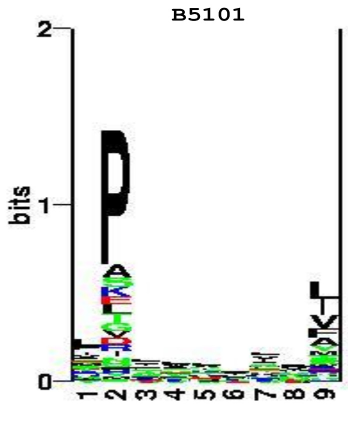
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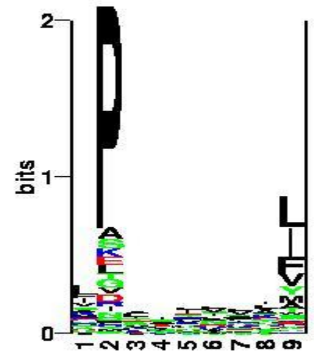
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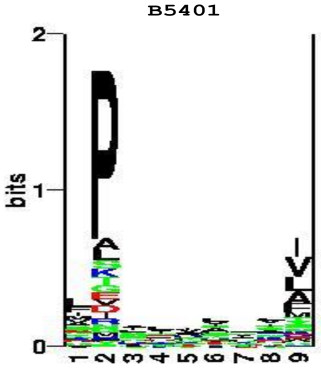
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