IEDB Analysis Resource

- Home
- Help
- Example
- Reference
- Contact

MHC-I processing prediction results

Input Sequences

#	Name	Sequence
1	sequence 1	MTLRVVPEGLAAASAAVEALTARLAAAHASAAPVITAVVPPAADPVSLQT AAGFSAQGVEHAVVTAEGVEELGRAGVGVGESGASYLAGDAAAAATYGVV GG

Predictions - High scores = high efficiency

Click on column headers for sorting

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*1517	1:46-54	9	VSLQTAAGF	1.27	1.09	-0.49	2.35	1.86	3.1
HLA B*5801	1:46-54	9	VSLQTAAGF	1.27	1.09	-1.51	2.35	0.84	32.4
HLA A*0250	1:86-94	9	YLAGDAAAA	1.33	-0.20	-0.44	1.13	0.69	2.8
HLA B*1517	1:64-72	9	VTAEGVEEL	1.39	0.46	-1.16	1.85	0.69	14.5
HLA B*1503	1:46-54	9	VSLQTAAGF	1.27	1.09	-1.70	2.35	0.66	49.6
HLA B*1501	1:78-86	9	GVGESGASY	1.21	1.20	-1.81	2.41	0.60	64.2
HLA A*0250	1:9-17	9	GLAAASAAV	1.01	0.00	-0.43	1.01	0.59	2.7
HLA A*0202	1:9-17	9	GLAAASAAV	1.01	0.00	-0.47	1.01	0.54	2.9
HLA A*0203	1:9-17	9	GLAAASAAV	1.01	0.00	-0.48	1.01	0.53	3.0
HLA A*0212	1:9-17	9	GLAAASAAV	1.01	0.00	-0.54	1.01	0.48	3.4
HLA A*0203	1:86-94	9	YLAGDAAAA	1.33	-0.20	-0.70	1.13	0.43	5.0
HLA A*0219	1:9-17	9	GLAAASAAV	1.01	0.00	-0.58	1.01	0.43	3.8
HLA A*0211	1:64-72	9	VTAEGVEEL	1.39	0.46	-1.46	1.85	0.39	28.9
HLA A*0211	1:9-17	9	GLAAASAAV	1.01	0.00	-0.63	1.01	0.39	4.2
HLA A*0211	1:86-94	9	YLAGDAAAA	1.33	-0.20	-0.76	1.13	0.37	5.7
HLA A*0202	1:64-72	9	VTAEGVEEL	1.39	0.46	-1.48	1.85	0.37	30.3
HLA A*0202	1:12-20	9	AASAAVEAL	1.45	0.57	-1.65	2.01	0.36	44.6
HLA A*0219	1:86-94	9	YLAGDAAAA	1.33	-0.20	-0.78	1.13	0.35	6.0
HLA A*0206	1:30-38	9	SAAPVITAV	0.96	0.26	-0.87	1.21	0.35	7.3
HLA A*0202	1:86-94	9	YLAGDAAAA	1.33	-0.20	-0.79	1.13	0.34	6.1
HLA A*6802	1:64-72	9	VTAEGVEEL	1.39	0.46	-1.51	1.85	0.34	32.4
HLA A*6802	1:30-38	9	SAAPVITAV	0.96	0.26	-0.88	1.21	0.33	7.6
HLA A*0203	1:23-31	9	RLAAAHASA	1.16	-0.04	-0.79	1.11	0.32	6.2
HLA A*6802	1:91-99	9	AAAAATYGV	1.05	0.17	-0.92	1.22	0.29	8.4
HLA A*0216	1:9-17	9	GLAAASAAV	1.01	0.00	-0.76	1.01	0.25	5.7
HLA A*0212	1:86-94	9	YLAGDAAAA	1.33	-0.20	-0.92	1.13	0.21	8.3

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*1517	1:78-86	9	GVGESGASY	1.21	1.20	-2.20	2.41	0.20	159.6
HLA A*2902	1:78-86	9	GVGESGASY	1.21	1.20	-2.24	2.41	0.17	174.1
HLA A*0206	1:64-72	9	VTAEGVEEL	1.39	0.46	-1.70	1.85	0.15	49.7
HLA A*3002	1:78-86	9	GVGESGASY	1.21	1.20	-2.26	2.41	0.15	180.9
HLA A*0202	1:91-99	9	AAAAATYGV	1.05	0.17	-1.08	1.22	0.14	11.9
HLA A*0250	1:23-31	9	RLAAAHASA	1.16	-0.04	-0.98	1.11	0.13	9.6
HLA A*0203	1:30-38	9	SAAPVITAV	0.96	0.26	-1.10	1.21	0.12	12.5
HLA A*0216	1:86-94	9	YLAGDAAAA	1.33	-0.20	-1.06	1.13	0.06	11.6
HLA A*0250	1:71-79	9	ELGRAGVGV	1.09	-0.09	-0.95	1.00	0.05	8.9
HLA A*0250	1:19-27	9	ALTARLAAA	1.01	-0.25	-0.71	0.76	0.05	5.2
HLA B*3901	1:27-35	9	AHASAAPVI	1.32	0.37	-1.65	1.69	0.04	44.7
HLA B*1502	1:78-86	9	GVGESGASY	1.21	1.20	-2.37	2.41	0.04	234.1
HLA A*0206	1:91-99	9	AAAAATYGV	1.05	0.17	-1.21	1.22	0.01	16.2
HLA A*0206	1:86-94	9	YLAGDAAAA	1.33	-0.20	-1.13	1.13	-0.00	13.5
HLA A*0203	1:19-27	9	ALTARLAAA	1.01	-0.25	-0.79	0.76	-0.03	6.2
HLA A*0206	1:5-13	9	VVPEGLAAA	1.10	-0.09	-1.05	1.01	-0.03	11.1
HLA A*2603	1:78-86	9	GVGESGASY	1.21	1.20	-2.45	2.41	-0.04	280.9
HLA A*0202	1:23-31	9	RLAAAHASA	1.16	-0.04	-1.18	1.11	-0.07	15.3
HLA A*0206	1:9-17	9	GLAAASAAV	1.01	0.00	-1.10	1.01	-0.09	12.6
HLA A*0250	1:30-38	9	SAAPVITAV	0.96	0.26	-1.32	1.21	-0.11	21.0
HLA A*0206	1:48-56	9	LQTAAGFSA	1.01	-0.19	-0.94	0.82	-0.12	8.7
HLA A*0211	1:30-38	9	SAAPVITAV	0.96	0.26	-1.35	1.21	-0.13	22.1
HLA A*0201	1:9-17	9	GLAAASAAV	1.01	0.00	-1.16	1.01	-0.15	14.5
HLA B*5701	1:46-54	9	VSLQTAAGF	1.27	1.09	-2.56	2.35	-0.21	364.5
HLA A*6901	1:91-99	9	AAAAATYGV	1.05	0.17	-1.44	1.22	-0.22	27.4
HLA A*0211	1:2-10	9	TLRVVPEGL	1.62	0.45	-2.32	2.07	-0.24	208.2
HLA A*0202	1:30-38	9	SAAPVITAV	0.96	0.26	-1.46	1.21	-0.24	28.7
HLA B*4501	1:80-88	9	GESGASYLA	1.31	-0.35	-1.21	0.96	-0.25	16.1
HLA A*0202	1:16-24	9	AVEALTARL	1.61	0.54	-2.43	2.15	-0.28	272.1
HLA A*0250	1:64-72	9	VTAEGVEEL	1.39	0.46	-2.13	1.85	-0.29	136.4
HLA A*0250	1:2-10	9	TLRVVPEGL	1.62	0.45	-2.37	2.07	-0.29	233.7
HLA A*0201	1:86-94	9	YLAGDAAAA	1.33	-0.20	-1.42	1.13	-0.30	26.5
HLA A*0250	1:91-99	9	AAAAATYGV	1.05	0.17	-1.52	1.22	-0.31	33.3
HLA A*0216	1:71-79	9	ELGRAGVGV	1.09	-0.09	-1.32	1.00	-0.32	20.9
HLA A*6802	1:38-46	9	VVPPAADPV	0.76	0.28	-1.36	1.04	-0.32	23.1
HLA B*1501	1:46-54	9	VSLQTAAGF	1.27	1.09	-2.68	2.35	-0.32	476.1
HLA A*0206	1:38-46	9	VVPPAADPV	0.76	0.28	-1.42	1.04	-0.37	26.0
HLA A*0219	1:71-79	9	ELGRAGVGV	1.09	-0.09	-1.37	1.00	-0.38	23.7
HLA A*0250	1:55-63	9	SAQGVEHAV	1.10	0.12	-1.60	1.22	-0.38	39.8
HLA A*0216	1:64-72	9	VTAEGVEEL	1.39	0.46	-2.24	1.85	-0.39	173.8
HLA A*2602	1:64-72	9	VTAEGVEEL	1.39	0.46	-2.24	1.85	-0.39	174.1
HLA A*0203	1:5-13	9	VVPEGLAAA	1.10	-0.09	-1.41	1.01	-0.40	25.7
HLA A*0203	1:64-72	9	VTAEGVEEL	1.39	0.46	-2.26	1.85	-0.41	181.6
HLA A*0211	1:71-79	9	ELGRAGVGV	1.09	-0.09	-1.41	1.00	-0.41	25.8
HLA A*3001	1:26-34	9	AAHASAAPV	0.61	0.30	-1.34	0.91	-0.42	21.7
HLA A*3001	1:21-29	9	TARLAAAHA	1.27	-0.18	-1.54	1.09	-0.45	35.0
HLA A*0216	1:30-38	9	SAAPVITAV	0.96	0.26	-1.68	1.21	-0.46	47.4
HLA A*2902	1:89-97	9	GDAAAAATY	1.41	1.13	-3.02	2.55	-0.48	1050.1
HLA A*0211	1:23-31	9	RLAAAHASA	1.16	-0.04	-1.60	1.11	-0.48	39.7

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*1517	1:12-20	9	AASAAVEAL	1.45	0.57	-2.50	2.01	-0.49	319.2
HLA A*0203	1:91-99	9	AAAAATYGV	1.05	0.17	-1.71	1.22	-0.49	51.0
HLA A*0250	1:16-24	9	AVEALTARL	1.61	0.54	-2.64	2.15	-0.49	441.2
HLA A*0219	1:91-99	9	AAAAATYGV	1.05	0.17	-1.72	1.22	-0.50	52.1
HLA A*6901	1:30-38	9	SAAPVITAV	0.96	0.26	-1.72	1.21	-0.51	52.9
HLA A*0206	1:12-20	9	AASAAVEAL	1.45	0.57	-2.54	2.01	-0.53	348.5
HLA A*0202	1:19-27	9	ALTARLAAA	1.01	-0.25	-1.33	0.76	-0.56	21.2
HLA A*6901	1:61-69	9	HAVVTAEGV	1.02	0.08	-1.67	1.10	-0.57	47.2
HLA A*0211	1:55-63	9	SAQGVEHAV	1.10	0.12	-1.81	1.22	-0.59	64.8
HLA A*6901	1:64-72	9	VTAEGVEEL	1.39	0.46	-2.44	1.85	-0.59	276.9
HLA A*3002	1:89-97	9	GDAAAAATY	1.41	1.13	-3.18	2.55	-0.63	1507.1
HLA A*3001	1:23-31	9	RLAAAHASA	1.16	-0.04	-1.77	1.11	-0.65	58.8
HLA A*0201	1:64-72	9	VTAEGVEEL	1.39	0.46	-2.50	1.85	-0.66	319.8
HLA A*3101	1:15-23	9	AAVEALTAR	0.88	0.79	-2.33	1.67	-0.67	215.3
HLA A*6801	1:15-23	9	AAVEALTAR	0.88	0.79	-2.36	1.67	-0.69	227.3
HLA A*0203	1:2-10	9	TLRVVPEGL	1.62	0.45	-2.78	2.07	-0.70	595.8
HLA A*6802	1:61-69	9	HAVVTAEGV	1.02	0.08	-1.81	1.10	-0.71	64.3
HLA B*1503	1:12-20	9	AASAAVEAL	1.45	0.57	-2.72	2.01	-0.71	530.2
HLA A*0250	1:38-46	9	VVPPAADPV	0.76	0.28	-1.76	1.04	-0.71	57.1
HLA A*0206	1:4-12	9	RVVPEGLAA	1.27	-0.01	-1.98	1.26	-0.72	94.4
HLA B*1517	1:26-34	9	AAHASAAPV	0.61	0.30	-1.63	0.91	-0.72	42.6
HLA B*1501	1:12-20	9	AASAAVEAL	1.45	0.57	-2.75	2.01	-0.73	556.9
HLA A*0201	1:91-99	9	AAAAATYGV	1.05	0.17	-1.97	1.22	-0.75	92.4
HLA B*3501	1:89-97	9	GDAAAAATY	1.41	1.13	-3.30	2.55	-0.76	2012.3
HLA A*3201	1:46-54	9	VSLQTAAGF	1.27	1.09	-3.12	2.35	-0.77	1324.0
HLA B*1501	1:89-97	9	GDAAAAATY	1.41	1.13	-3.33	2.55	-0.78	2126.5
HLA A*6802	1:31-39	9	AAPVITAVV	1.00	0.24	-2.03	1.24	-0.79	108.3
HLA A*0202	1:2-10	9	TLRVVPEGL	1.62	0.45	-2.87	2.07	-0.79	736.0
HLA B*5301	1:40-48	9	PPAADPVSL	1.65	0.10	-2.58	1.76	-0.82	379.0
HLA A*0216	1:91-99	9	AAAAATYGV	1.05	0.17	-2.04	1.22	-0.83	110.3
HLA A*0206	1:19-27	9	ALTARLAAA	1.01	-0.25	-1.62	0.76	-0.85	41.2
HLA B*3901	1:12-20	9	AASAAVEAL	1.45	0.57	-2.87	2.01	-0.85	737.2
HLA A*0203	1:26-34	9	AAHASAAPV	0.61	0.30	-1.77	0.91	-0.86	59.4
HLA A*2603	1:46-54	9	VSLQTAAGF	1.27	1.09	-3.24	2.35	-0.89	1751.6
HLA A*0211	1:91-99	9	AAAAATYGV	1.05	0.17	-2.11	1.22	-0.90	129.5
HLA A*2602	1:78-86	9	GVGESGASY	1.21	1.20	-3.31	2.41	-0.90	2037.4
HLA A*6802	1:12-20	9	AASAAVEAL	1.45	0.57	-2.93	2.01	-0.91	846.2
HLA A*0206	1:34-42	9	VITAVVPPA	1.03	-0.23	-1.72	0.81	-0.92	52.8
HLA A*3201	1:16-24	9	AVEALTARL	1.61	0.54	-3.07	2.15	-0.92	1183.1
HLA A*0203	1:92-100	9	AAAATYGVV	1.09	0.30	-2.32	1.39	-0.93	207.9
HLA A*0219	1:64-72	9	VTAEGVEEL	1.39	0.46	-2.78	1.85	-0.94	608.4
HLA B*5801	1:64-72	9	VTAEGVEEL	1.39	0.46	-2.80	1.85	-0.96	635.7
HLA A*6802	1:26-34	9	AAHASAAPV	0.61	0.30	-1.88	0.91	-0.97	76.2
HLA B*1501	1:23-31	9	RLAAAHASA	1.16	-0.04	-2.10	1.11	-0.98	124.6
HLA B*1517	1:16-24	9	AVEALTARL	1.61	0.54	-3.14	2.15	-0.98	1366.0
HLA B*0702	1:40-48	9	PPAADPVSL	1.65	0.10	-2.74	1.76	-0.99	551.3
HLA B*1503	1:27-35	9	AHASAAPVI	1.32	0.37	-2.68	1.69	-0.99	477.0
HLA A*0212	1:71-79	9	ELGRAGVGV	1.09	-0.09	-1.99	1.00	-1.00	98.9
HLA A*0206	1:23-31	9	RLAAAHASA	1.16	-0.04	-2.12	1.11	-1.01	132.7

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*3501	1:78-86	9	GVGESGASY	1.21	1.20	-3.42	2.41	-1.02	2641.8
HLA A*0203	1:12-20	9	AASAAVEAL	1.45	0.57	-3.03	2.01	-1.02	1074.4
HLA A*0216	1:34-42	9	VITAVVPPA	1.03	-0.23	-1.83	0.81	-1.02	67.0
HLA A*6901	1:71-79	9	ELGRAGVGV	1.09	-0.09	-2.02	1.00	-1.03	105.6
HLA A*0216	1:23-31	9	RLAAAHASA	1.16	-0.04	-2.14	1.11	-1.03	138.6
HLA B*3501	1:46-54	9	VSLQTAAGF	1.27	1.09	-3.39	2.35	-1.04	2478.6
HLA A*0203	1:34-42	9	VITAVVPPA	1.03	-0.23	-1.88	0.81	-1.08	76.3
HLA A*2602	1:46-54	9	VSLQTAAGF	1.27	1.09	-3.45	2.35	-1.09	2813.7
HLA A*0211	1:19-27	9	ALTARLAAA	1.01	-0.25	-1.87	0.76	-1.11	74.1
HLA B*4402	1:89-97	9	GDAAAAATY	1.41	1.13	-3.66	2.55	-1.11	4535.6
HLA B*1502	1:89-97	9	GDAAAAATY	1.41	1.13	-3.67	2.55	-1.12	4669.0
HLA A*1101	1:78-86	9	GVGESGASY	1.21	1.20	-3.55	2.41	-1.15	3576.7
HLA A*0206	1:26-34	9	AAHASAAPV	0.61	0.30	-2.06	0.91	-1.15	116.1
HLA B*3501	1:12-20	9	AASAAVEAL	1.45	0.57	-3.17	2.01	-1.15	1471.2
HLA A*0201	1:30-38	9	SAAPVITAV	0.96	0.26	-2.37	1.21	-1.15	233.3
HLA A*6802	1:54-62	9	FSAQGVEHA	1.07	-0.26	-1.98	0.81	-1.17	95.5
HLA A*0250	1:26-34	9	AAHASAAPV	0.61	0.30	-2.09	0.91	-1.18	122.9
HLA A*6802	1:55-63	9	SAQGVEHAV	1.10	0.12	-2.40	1.22	-1.18	249.6
HLA A*0211	1:34-42	9	VITAVVPPA	1.03	-0.23	-1.99	0.81	-1.18	96.7
HLA B*1503	1:78-86	9	GVGESGASY	1.21	1.20	-3.60	2.41	-1.19	3967.0
HLA A*0201	1:23-31	9	RLAAAHASA	1.16	-0.04	-2.33	1.11	-1.22	216.0
HLA A*2501	1:78-86	9	GVGESGASY	1.21	1.20	-3.65	2.41	-1.24	4416.8
HLA B*4501	1:17-25	9	VEALTARLA	1.29	-0.19	-2.34	1.10	-1.24	220.1
HLA A*8001	1:78-86	9	GVGESGASY	1.21	1.20	-3.65	2.41	-1.25	4518.5
HLA B*1501	1:9-17	9	GLAAASAAV	1.01	0.00	-2.27	1.01	-1.25	184.4
HLA A*0216	1:2-10	9	TLRVVPEGL	1.62	0.45	-3.33	2.07	-1.26	2146.6
HLA B*5401	1:44-52	9	DPVSLQTAA	1.05	-0.40	-1.91	0.65	-1.26	80.5
HLA A*0212	1:19-27	9	ALTARLAAA	1.01	-0.25	-2.02	0.76	-1.26	105.8
HLA A*6802	1:92-100	9	AAAATYGVV	1.09	0.30	-2.66	1.39	-1.27	461.2
HLA A*0250	1:5-13	9	VVPEGLAAA	1.10	-0.09	-2.29	1.01	-1.28	195.8
HLA A*0206	1:16-24	9	AVEALTARL	1.61	0.54	-3.44	2.15	-1.29	2765.5
HLA B*3901	1:40-48	9	PPAADPVSL	1.65	0.10	-3.05	1.76	-1.29	1121.4
HLA B*1503	1:89-97	9	GDAAAAATY	1.41	1.13	-3.85	2.55	-1.30	7047.2
HLA A*0301	1:78-86	9	GVGESGASY	1.21	1.20	-3.71	2.41	-1.31	5174.4
HLA A*3002	1:46-54	9	VSLQTAAGF	1.27	1.09	-3.66	2.35	-1.31	4617.7
HLA A*0211	1:5-13	9	VVPEGLAAA	1.10	-0.09	-2.34	1.01	-1.33	219.0
HLA B*4403	1:89-97	9	GDAAAAATY	1.41	1.13	-3.89	2.55	-1.34	7682.1
HLA A*0250	1:34-42	9	VITAVVPPA	1.03	-0.23	-2.15	0.81	-1.34	141.0
HLA B*1502	1:46-54	9	VSLQTAAGF	1.27	1.09	-3.70	2.35	-1.35	5021.8
HLA B*1801	1:89-97	9	GDAAAAATY	1.41	1.13	-3.90	2.55	-1.36	8016.0
HLA A*6901	1:18-26	9	EALTARLAA	1.39	-0.27	-2.48	1.12	-1.36	304.0
HLA B*1509	1:27-35	9	AHASAAPVI	1.32	0.37	-3.05	1.69	-1.36	1131.0
HLA B*1501	1:56-64	9	AQGVEHAVV	1.12	0.18	-2.67	1.30	-1.37	467.7
HLA A*0203	1:24-32	9	LAAAHASAA	0.90	-0.14	-2.12	0.75	-1.37	132.9
HLA A*6802	1:16-24	9	AVEALTARL	1.61	0.54	-3.53	2.15	-1.38	3356.5
HLA A*0203	1:38-46	9	VVPPAADPV	0.76	0.28	-2.42	1.04	-1.38	263.4
HLA A*2403	1:46-54	9	VSLQTAAGF	1.27	1.09	-3.74	2.35	-1.38	5436.9
HLA B*1517	1:89-97	9	GDAAAAATY	1.41	1.13	-3.93	2.55	-1.39	8530.2
HLA A*0212	1:2-10	9	TLRVVPEGL	1.62	0.45	-3.47	2.07	-1.40	2971.9

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*2601	1:78-86	9	GVGESGASY	1.21	1.20	-3.82	2.41	-1.42	6652.5
HLA A*0250	1:31-39	9	AAPVITAVV	1.00	0.24	-2.66	1.24	-1.42	458.6
HLA B*0702	1:16-24	9	AVEALTARL	1.61	0.54	-3.59	2.15	-1.43	3849.3
HLA A*0211	1:38-46	9	VVPPAADPV	0.76	0.28	-2.48	1.04	-1.44	300.8
HLA A*0201	1:19-27	9	ALTARLAAA	1.01	-0.25	-2.20	0.76	-1.44	158.4
HLA A*0212	1:91-99	9	AAAAATYGV	1.05	0.17	-2.66	1.22	-1.44	452.1
HLA B*3501	1:44-52	9	DPVSLQTAA	1.05	-0.40	-2.10	0.65	-1.46	126.2
HLA A*0216	1:38-46	9	VVPPAADPV	0.76	0.28	-2.50	1.04	-1.46	317.5
HLA B*4002	1:80-88	9	GESGASYLA	1.31	-0.35	-2.42	0.96	-1.46	263.7
HLA B*3501	1:40-48	9	PPAADPVSL	1.65	0.10	-3.22	1.76	-1.46	1657.3
HLA A*2301	1:46-54	9	VSLQTAAGF	1.27	1.09	-3.84	2.35	-1.48	6882.4
HLA A*0216	1:55-63	9	SAQGVEHAV	1.10	0.12	-2.70	1.22	-1.49	505.6
HLA A*0206	1:61-69	9	HAVVTAEGV	1.02	0.08	-2.58	1.10	-1.49	384.3
HLA A*0203	1:16-24	9	AVEALTARL	1.61	0.54	-3.64	2.15	-1.49	4328.2
HLA A*0250	1:51-59	9	AAGFSAQGV	1.07	0.15	-2.71	1.22	-1.49	512.2
HLA A*0211	1:12-20	9	AASAAVEAL	1.45	0.57	-3.51	2.01	-1.50	3268.8
HLA A*3001	1:4-12	9	RVVPEGLAA	1.27	-0.01	-2.77	1.26	-1.51	583.7
HLA A*0206	1:46-54	9	VSLQTAAGF	1.27	1.09	-3.86	2.35	-1.51	7310.6
HLA A*2902	1:46-54	9	VSLQTAAGF	1.27	1.09	-3.88	2.35	-1.52	7512.1
HLA B*3901	1:16-24	9	AVEALTARL	1.61	0.54	-3.67	2.15	-1.52	4721.5
HLA B*0702	1:12-20	9	AASAAVEAL	1.45	0.57	-3.55	2.01	-1.54	3574.7
HLA A*0219	1:23-31	9	RLAAAHASA	1.16	-0.04	-2.67	1.11	-1.55	465.6
HLA B*4001	1:69-77	9	VEELGRAGV	1.03	0.03	-2.62	1.06	-1.56	417.7
HLA B*1503	1:56-64	9	AQGVEHAVV	1.12	0.18	-2.87	1.30	-1.57	741.1
HLA A*8001	1:89-97	9	GDAAAAATY	1.41	1.13	-4.11	2.55	-1.57	13004.5
HLA A*0212	1:64-72	9	VTAEGVEEL	1.39	0.46	-3.42	1.85	-1.57	2624.2
HLA A*3201	1:64-72	9	VTAEGVEEL	1.39	0.46	-3.43	1.85	-1.58	2672.8
HLA A*0206	1:56-64	9	AQGVEHAVV	1.12	0.18	-2.89	1.30	-1.59	776.5
HLA B*4001	1:80-88	9	GESGASYLA	1.31	-0.35	-2.56	0.96	-1.60	362.0
HLA A*0201	1:34-42	9	VITAVVPPA	1.03	-0.23	-2.42	0.81	-1.62	265.8
HLA A*3201	1:12-20	9	AASAAVEAL	1.45	0.57	-3.64	2.01	-1.62	4321.6
HLA A*0211	1:26-34	9	AAHASAAPV	0.61	0.30	-2.53	0.91	-1.62	342.4
HLA A*2402	1:46-54	9	VSLQTAAGF	1.27	1.09	-3.98	2.35	-1.63	9574.4
HLA A*0212	1:23-31	9	RLAAAHASA	1.16	-0.04	-2.74	1.11	-1.63	552.2
HLA A*0206	1:31-39	9	AAPVITAVV	1.00	0.24	-2.87	1.24	-1.63	749.1
HLA A*0206	1:54-62	9	FSAQGVEHA	1.07	-0.26	-2.45	0.81	-1.64	281.7
HLA B*3501	1:24-32	9	LAAAHASAA	0.90	-0.14	-2.40	0.75	-1.65	250.9
HLA A*0201	1:16-24	9	AVEALTARL	1.61	0.54	-3.81	2.15	-1.66	6458.2
HLA A*6901	1:92-100	9	AAAATYGVV	1.09	0.30	-3.06	1.39	-1.67	1151.3
HLA A*0202	1:54-62	9	FSAQGVEHA	1.07	-0.26	-2.49	0.81	-1.68	308.8
HLA A*0211	1:16-24	9	AVEALTARL	1.61	0.54	-3.83	2.15	-1.68	6798.1
HLA A*3001	1:16-24	9	AVEALTARL	1.61	0.54	-3.84	2.15	-1.69	6865.2
HLA A*0219	1:2-10	9	TLRVVPEGL	1.62	0.45	-3.76	2.07	-1.69	5777.3
HLA B*5801	1:12-20	9	AASAAVEAL	1.45	0.57	-3.70	2.01	-1.69	5060.9
HLA B*4501	1:66-74	9	AEGVEELGR	1.14	0.58	-3.42	1.72	-1.69	2605.3
HLA A*0101	1:78-86	9	GVGESGASY	1.21	1.20	-4.10	2.41	-1.70	12682.7
HLA A*0250	1:92-100	9	AAAATYGVV	1.09	0.30	-3.10	1.39	-1.71	1256.4
HLA A*6802	1:2-10	9	TLRVVPEGL	1.62	0.45	-3.78	2.07	-1.71	6085.0
HLA A*6802	1:9-17	9	GLAAASAAV	1.01	0.00	-2.72	1.01	-1.71	528.3

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*1503	1:26-34	9	AAHASAAPV	0.61	0.30	-2.63	0.91	-1.71	422.1
HLA A*3001	1:78-86	9	GVGESGASY	1.21	1.20	-4.12	2.41	-1.71	13199.6
HLA A*3001	1:89-97	9	GDAAAAATY	1.41	1.13	-4.27	2.55	-1.72	18466.9
HLA A*6901	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.08	2.35	-1.73	12139.2
HLA A*2601	1:89-97	9	GDAAAAATY	1.41	1.13	-4.28	2.55	-1.73	18845.3
HLA B*0702	1:26-34	9	AAHASAAPV	0.61	0.30	-2.65	0.91	-1.74	447.9
HLA B*4601	1:78-86	9	GVGESGASY	1.21	1.20	-4.15	2.41	-1.74	14018.8
HLA B*1503	1:2-10	9	TLRVVPEGL	1.62	0.45	-3.81	2.07	-1.74	6523.3
HLA B*0702	1:92-100	9	AAAATYGVV	1.09	0.30	-3.13	1.39	-1.74	1352.3
HLA A*0206	1:55-63	9	SAQGVEHAV	1.10	0.12	-2.97	1.22	-1.75	924.8
HLA B*1517	1:61-69	9	HAVVTAEGV	1.02	0.08	-2.85	1.10	-1.75	708.5
HLA A*3301	1:15-23	9	AAVEALTAR	0.88	0.79	-3.42	1.67	-1.76	2655.2
HLA B*5801	1:89-97	9	GDAAAAATY	1.41	1.13	-4.31	2.55	-1.76	20239.4
HLA B*1801	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.12	2.35	-1.77	13227.0
HLA A*0211	1:56-64	9	AQGVEHAVV	1.12	0.18	-3.07	1.30	-1.77	1176.1
HLA A*6901	1:16-24	9	AVEALTARL	1.61	0.54	-3.92	2.15	-1.77	8301.6
HLA A*0211	1:92-100	9	AAAATYGVV	1.09	0.30	-3.16	1.39	-1.77	1445.6
HLA A*0301	1:89-97	9	GDAAAAATY	1.41	1.13	-4.32	2.55	-1.78	21087.2
HLA B*4601	1:89-97	9	GDAAAAATY	1.41	1.13	-4.33	2.55	-1.78	21213.4
HLA A*6801	1:89-97	9	GDAAAAATY	1.41	1.13	-4.33	2.55	-1.78	21333.7
HLA A*6901	1:12-20	9	AASAAVEAL	1.45	0.57	-3.80	2.01	-1.79	6323.7
HLA A*0206	1:2-10	9	TLRVVPEGL	1.62	0.45	-3.86	2.07	-1.79	7271.7
HLA A*0202	1:31-39	9	AAPVITAVV	1.00	0.24	-3.03	1.24	-1.79	1074.3
HLA A*0203	1:31-39	9	AAPVITAVV	1.00	0.24	-3.03	1.24	-1.79	1080.1
HLA B*5701	1:89-97	9	GDAAAAATY	1.41	1.13	-4.34	2.55	-1.80	21923.5
HLA B*4501	1:56-64	9	AQGVEHAVV	1.12	0.18	-3.10	1.30	-1.80	1260.2
HLA A*0101	1:89-97	9	GDAAAAATY	1.41	1.13	-4.35	2.55	-1.80	22163.8
HLA B*4001	1:89-97	9	GDAAAAATY	1.41	1.13	-4.35	2.55	-1.80	22291.7
HLA A*3201	1:78-86	9	GVGESGASY	1.21	1.20	-4.21	2.41	-1.81	16353.2
HLA A*0212	1:78-86	9	GVGESGASY	1.21	1.20	-4.21	2.41	-1.81	16377.3
HLA B*1501	1:86-94	9	YLAGDAAAA	1.33	-0.20	-2.93	1.13	-1.81	860.8
HLA A*6901	1:89-97	9	GDAAAAATY	1.41	1.13	-4.36	2.55	-1.81	22788.6
HLA A*1101	1:89-97	9	GDAAAAATY	1.41	1.13	-4.36	2.55	-1.81	22806.1
HLA A*6802	1:86-94	9	YLAGDAAAA	1.33	-0.20	-2.94	1.13	-1.81	872.4
HLA A*0250	1:12-20	9	AASAAVEAL	1.45	0.57	-3.83	2.01	-1.82	6777.2
HLA B*5801	1:78-86	9	GVGESGASY	1.21	1.20	-4.23	2.41	-1.82	17014.3
HLA B*1502	1:2-10	9	TLRVVPEGL	1.62	0.45	-3.90	2.07	-1.82	7920.3
HLA B*4801	1:89-97	9	GDAAAAATY	1.41	1.13	-4.37	2.55	-1.83	23495.9
HLA B*5701	1:78-86	9	GVGESGASY	1.21	1.20	-4.24	2.41	-1.83	17258.0
HLA B*3901	1:89-97	9	GDAAAAATY	1.41	1.13	-4.38	2.55	-1.83	23744.6
HLA A*3001	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.18	2.35	-1.83	15303.5
HLA A*0203	1:89-97	9	GDAAAAATY	1.41	1.13	-4.38	2.55	-1.83	23865.4
HLA B*0702	1:4-12	9	RVVPEGLAA	1.27	-0.01	-3.10	1.26	-1.84	1245.9
HLA B*4601	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.19	2.35	-1.84	15495.6
HLA B*1801	1:78-86	9	GVGESGASY	1.21	1.20	-4.24	2.41	-1.84	17496.8
HLA A*2501	1:89-97	9	GDAAAAATY	1.41	1.13	-4.38	2.55	-1.84	24150.3
HLA A*0212	1:89-97	9	GDAAAAATY	1.41	1.13	-4.38	2.55	-1.84	24195.3
HLA A*6801	1:78-86	9	GVGESGASY	1.21	1.20	-4.25	2.41	-1.84	17603.5
HLA A*0201	1:12-20	9	AASAAVEAL	1.45	0.57	-3.86	2.01	-1.84	7189.2

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*0206	1:92-100	9	AAAATYGVV	1.09	0.30	-3.23	1.39	-1.84	1708.0
HLA B*5301	1:89-97	9	GDAAAAATY	1.41	1.13	-4.39	2.55	-1.84	24473.6
HLA B*1501	1:48-56	9	LQTAAGFSA	1.01	-0.19	-2.66	0.82	-1.84	460.0
HLA A*0201	1:89-97	9	GDAAAAATY	1.41	1.13	-4.39	2.55	-1.84	24519.4
HLA B*1501	1:64-72	9	VTAEGVEEL	1.39	0.46	-3.69	1.85	-1.85	4936.9
HLA B*1509	1:89-97	9	GDAAAAATY	1.41	1.13	-4.39	2.55	-1.85	24659.5
HLA B*2705	1:89-97	9	GDAAAAATY	1.41	1.13	-4.39	2.55	-1.85	24721.6
HLA B*0702	1:89-97	9	GDAAAAATY	1.41	1.13	-4.40	2.55	-1.85	24831.5
HLA B*4403	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.20	2.35	-1.85	16006.1
HLA B*0802	1:89-97	9	GDAAAAATY	1.41	1.13	-4.40	2.55	-1.85	24914.9
HLA B*3801	1:89-97	9	GDAAAAATY	1.41	1.13	-4.40	2.55	-1.85	25071.1
HLA A*2603	1:89-97	9	GDAAAAATY	1.41	1.13	-4.40	2.55	-1.86	25288.6
HLA A*3101	1:89-97	9	GDAAAAATY	1.41	1.13	-4.40	2.55	-1.86	25294.8
HLA B*0801	1:2-10	9	TLRVVPEGL	1.62	0.45	-3.94	2.07	-1.86	8675.8
HLA B*4402	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.22	2.35	-1.87	16617.8
HLA A*6901	1:26-34	9	AAHASAAPV	0.61	0.30	-2.78	0.91	-1.87	604.1
HLA A*0201	1:2-10	9	TLRVVPEGL	1.62	0.45	-3.94	2.07	-1.87	8772.9
HLA A*3001	1:2-10	9	TLRVVPEGL	1.62	0.45	-3.94	2.07	-1.87	8777.0
HLA A*0219	1:89-97	9	GDAAAAATY	1.41	1.13	-4.41	2.55	-1.87	25982.6
HLA A*0211	1:78-86	9	GVGESGASY	1.21	1.20	-4.28	2.41	-1.87	18952.7
HLA A*0203	1:78-86	9	GVGESGASY	1.21	1.20	-4.28	2.41	-1.87	19054.4
HLA A*0216	1:19-27	9	ALTARLAAA	1.01	-0.25	-2.64	0.76	-1.87	432.9
HLA B*1503	1:64-72	9	VTAEGVEEL	1.39	0.46	-3.73	1.85	-1.88	5310.0
HLA A*2403	1:89-97	9	GDAAAAATY	1.41	1.13	-4.42	2.55	-1.88	26532.0
HLA A*0216	1:78-86	9	GVGESGASY	1.21	1.20	-4.29	2.41	-1.88	19333.9
HLA B*0803	1:89-97	9	GDAAAAATY	1.41	1.13	-4.43	2.55	-1.88	26790.3
HLA B*0801	1:89-97	9	GDAAAAATY	1.41	1.13	-4.43	2.55	-1.88	26843.6
HLA A*0216	1:89-97	9	GDAAAAATY	1.41	1.13	-4.43	2.55	-1.89	27044.3
HLA A*6802	1:11-19	9	AAASAAVEA	1.20	-0.12	-2.97	1.08	-1.89	928.5
HLA A*6802	1:89-97	9	GDAAAAATY	1.41	1.13	-4.43	2.55	-1.89	27066.2
HLA A*2602	1:89-97	9	GDAAAAATY	1.41	1.13	-4.43	2.55	-1.89	27107.0
HLA A*0202	1:92-100	9	AAAATYGVV	1.09	0.30	-3.28	1.39	-1.89	1901.8
HLA A*0206	1:11-19	9	AAASAAVEA	1.20	-0.12	-2.97	1.08	-1.89	941.2
HLA B*4001	1:12-20	9	AASAAVEAL	1.45	0.57	-3.92	2.01	-1.90	8232.7
HLA A*0202	1:38-46	9	VVPPAADPV	0.76	0.28	-2.95	1.04	-1.90	882.1
HLA B*0702	1:24-32	9	LAAAHASAA	0.90	-0.14	-2.66	0.75	-1.91	462.0
HLA B*2705	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.27	2.35	-1.91	18439.5
HLA B*1501	1:4-12	9	RVVPEGLAA	1.27	-0.01	-3.17	1.26	-1.91	1484.9
HLA B*5101	1:89-97	9	GDAAAAATY	1.41	1.13	-4.46	2.55	-1.91	28697.9
HLA B*5401	1:24-32	9	LAAAHASAA	0.90	-0.14	-2.67	0.75	-1.91	466.7
HLA B*4402	1:78-86	9	GVGESGASY	1.21	1.20	-4.32	2.41	-1.92	21000.7
HLA A*6901	1:78-86	9	GVGESGASY	1.21	1.20	-4.32	2.41	-1.92	21009.6
HLA A*0206	1:78-86	9	GVGESGASY	1.21	1.20	-4.32	2.41	-1.92	21010.9
HLA B*1501	1:2-10	9	TLRVVPEGL	1.62	0.45	-3.99	2.07	-1.92	9871.9
HLA B*0702	1:78-86	9	GVGESGASY	1.21	1.20	-4.33	2.41	-1.92	21349.9
HLA A*6802	1:29-37	9	ASAAPVITA	1.21	-0.15	-2.98	1.06	-1.92	955.5
HLA B*3901	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.28	2.35	-1.92	19011.2
HLA A*8001	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.28	2.35	-1.93	19043.0
HLA A*0250	1:78-86	9	GVGESGASY	1.21	1.20	-4.33	2.41	-1.93	21506.5

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*5301	1:78-86	9	GVGESGASY	1.21	1.20	-4.33	2.41	-1.93	21601.6
HLA A*0219	1:78-86	9	GVGESGASY	1.21	1.20	-4.34	2.41	-1.93	21631.1
HLA A*3101	1:78-86	9	GVGESGASY	1.21	1.20	-4.34	2.41	-1.93	21682.8
HLA B*4801	1:12-20	9	AASAAVEAL	1.45	0.57	-3.95	2.01	-1.93	8867.6
HLA A*2602	1:16-24	9	AVEALTARL	1.61	0.54	-4.09	2.15	-1.93	12161.9
HLA B*2705	1:78-86	9	GVGESGASY	1.21	1.20	-4.34	2.41	-1.93	21929.8
HLA A*2602	1:12-20	9	AASAAVEAL	1.45	0.57	-3.95	2.01	-1.94	8923.5
HLA B*4001	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.29	2.35	-1.94	19532.0
HLA A*0219	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.29	2.35	-1.94	19589.3
HLA A*0101	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.30	2.35	-1.94	19736.9
HLA A*6901	1:9-17	9	GLAAASAAV	1.01	0.00	-2.95	1.01	-1.94	895.2
HLA A*0212	1:56-64	9	AQGVEHAVV	1.12	0.18	-3.25	1.30	-1.94	1760.9
HLA A*6901	1:86-94	9	YLAGDAAAA	1.33	-0.20	-3.07	1.13	-1.94	1180.2
HLA A*0206	1:89-97	9	GDAAAAATY	1.41	1.13	-4.50	2.55	-1.95	31301.0
HLA A*0202	1:89-97	9	GDAAAAATY	1.41	1.13	-4.50	2.55	-1.95	31499.8
HLA A*0212	1:16-24	9	AVEALTARL	1.61	0.54	-4.11	2.15	-1.96	12764.7
HLA A*3201	1:89-97	9	GDAAAAATY	1.41	1.13	-4.50	2.55	-1.96	31843.1
HLA B*0802	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.31	2.35	-1.96	20532.0
HLA B*4002	1:89-97	9	GDAAAAATY	1.41	1.13	-4.50	2.55	-1.96	31891.8
HLA B*4501	1:89-97	9	GDAAAAATY	1.41	1.13	-4.50	2.55	-1.96	31909.0
HLA B*1501	1:16-24	9	AVEALTARL	1.61	0.54	-4.12	2.15	-1.96	13035.5
HLA A*0202	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.32	2.35	-1.96	20862.3
HLA B*4001	1:78-86	9	GVGESGASY	1.21	1.20	-4.37	2.41	-1.97	23627.7
HLA A*0211	1:51-59	9	AAGFSAQGV	1.07	0.15	-3.19	1.22	-1.97	1538.4
HLA B*4801	1:78-86	9	GVGESGASY	1.21	1.20	-4.37	2.41	-1.97	23672.6
HLA B*1509	1:78-86	9	GVGESGASY	1.21	1.20	-4.38	2.41	-1.97	23770.9
HLA B*0702	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.32	2.35	-1.97	21111.8
HLA A*0203	1:4-12	9	RVVPEGLAA	1.27	-0.01	-3.23	1.26	-1.97	1701.6
HLA A*0211	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.33	2.35	-1.97	21195.7
HLA A*0211	1:89-97	9	GDAAAAATY	1.41	1.13	-4.52	2.55	-1.97	32958.4
HLA A*2501	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.33	2.35	-1.97	21253.2
HLA A*6802	1:5-13	9	VVPEGLAAA	1.10	-0.09	-2.98	1.01	-1.97	962.6
HLA B*0801	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.33	2.35	-1.97	21272.8
HLA A*3101	1:16-24	9	AVEALTARL	1.61	0.54	-4.13	2.15	-1.97	13342.9
HLA A*0216	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.33	2.35	-1.98	21380.7
HLA B*3801	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.33	2.35	-1.98	21385.6
HLA A*3101	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.33	2.35	-1.98	21390.0
HLA A*0212	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.33	2.35	-1.98	21477.7
HLA A*3001	1:12-20	9	AASAAVEAL	1.45	0.57	-3.99	2.01	-1.98	9816.5
HLA A*0201	1:78-86	9	GVGESGASY	1.21	1.20	-4.39	2.41	-1.98	24268.0
HLA B*0803	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.34	2.35	-1.98	21688.0
HLA B*0801	1:78-86	9	GVGESGASY	1.21	1.20	-4.39	2.41	-1.98	24482.4
HLA A*0301	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.34	2.35	-1.98	21767.3
HLA A*2301	1:89-97	9	GDAAAAATY	1.41	1.13	-4.53	2.55	-1.98	33788.3
HLA A*2403	1:78-86	9	GVGESGASY	1.21	1.20	-4.39	2.41	-1.99	24724.5
HLA A*2601	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.34	2.35	-1.99	21968.1
HLA B*1509	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.07	2.07	-2.00	11744.7
HLA A*3201	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.07	2.07	-2.00	11769.3
HLA B*0802	1:78-86	9	GVGESGASY	1.21	1.20	-4.40	2.41	-2.00	25305.1

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*0803	1:78-86	9	GVGESGASY	1.21	1.20	-4.41	2.41	-2.00	25431.6
HLA B*5401	1:89-97	9	GDAAAAATY	1.41	1.13	-4.55	2.55	-2.00	35331.8
HLA B*4403	1:66-74	9	AEGVEELGR	1.14	0.58	-3.73	1.72	-2.01	5352.2
HLA B*3801	1:78-86	9	GVGESGASY	1.21	1.20	-4.41	2.41	-2.01	25827.4
HLA A*2402	1:89-97	9	GDAAAAATY	1.41	1.13	-4.55	2.55	-2.01	35537.5
HLA B*0802	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.08	2.07	-2.01	12033.4
HLA B*5301	1:12-20	9	AASAAVEAL	1.45	0.57	-4.02	2.01	-2.01	10506.6
HLA A*0203	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.36	2.35	-2.01	23026.7
HLA A*0202	1:11-19	9	AAASAAVEA	1.20	-0.12	-3.09	1.08	-2.01	1230.0
HLA B*3901	1:78-86	9	GVGESGASY	1.21	1.20	-4.42	2.41	-2.01	26067.6
HLA B*1502	1:9-17	9	GLAAASAAV	1.01	0.00	-3.02	1.01	-2.01	1050.7
HLA B*1501	1:54-62	9	FSAQGVEHA	1.07	-0.26	-2.82	0.81	-2.01	666.3
HLA A*0202	1:48-56	9	LQTAAGFSA	1.01	-0.19	-2.84	0.82	-2.02	685.9
HLA B*4801	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.37	2.35	-2.02	23596.7
HLA A*0201	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.38	2.35	-2.02	23775.4
HLA A*0219	1:12-20	9	AASAAVEAL	1.45	0.57	-4.04	2.01	-2.02	10901.0
HLA B*1509	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.38	2.35	-2.02	23943.8
HLA A*6802	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.38	2.35	-2.03	24196.4
HLA A*0219	1:16-24	9	AVEALTARL	1.61	0.54	-4.18	2.15	-2.03	15229.8
HLA B*1503	1:48-56	9	LQTAAGFSA	1.01	-0.19	-2.85	0.82	-2.03	709.6
HLA A*1101	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.39	2.35	-2.03	24440.6
HLA A*6802	1:78-86	9	GVGESGASY	1.21	1.20	-4.44	2.41	-2.03	27574.4
HLA B*5101	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.39	2.35	-2.04	24599.4
HLA A*0250	1:89-97	9	GDAAAAATY	1.41	1.13	-4.58	2.55	-2.04	38204.8
HLA A*0216	1:16-24	9	AVEALTARL	1.61	0.54	-4.19	2.15	-2.04	15425.2
HLA B*5301	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.39	2.35	-2.04	24745.8
HLA B*3501	1:16-24	9	AVEALTARL	1.61	0.54	-4.19	2.15	-2.04	15561.8
HLA A*0202	1:78-86	9	GVGESGASY	1.21	1.20	-4.45	2.41	-2.05	28419.4
HLA B*1517	1:51-59	9	AAGFSAQGV	1.07	0.15	-3.27	1.22	-2.05	1861.3
HLA B*5101	1:78-86	9	GVGESGASY	1.21	1.20	-4.46	2.41	-2.05	28638.1
HLA A*0202	1:26-34	9	AAHASAAPV	0.61	0.30	-2.96	0.91	-2.05	918.8
HLA A*2602	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-2.83	0.77	-2.05	670.3
HLA B*1503	1:15-23	9	AAVEALTAR	0.88	0.79	-3.72	1.67	-2.05	5250.6
HLA A*2403	1:85-93	9	SYLAGDAAA	1.15	-0.02	-3.19	1.13	-2.06	1551.5
HLA B*0801	1:16-24	9	AVEALTARL	1.61	0.54	-4.21	2.15	-2.06	16185.7
HLA B*7301	1:89-97	9	GDAAAAATY	1.41	1.13	-4.61	2.55	-2.06	40461.5
HLA B*0803	1:16-24	9	AVEALTARL	1.61	0.54	-4.22	2.15	-2.07	16491.5
HLA A*6901	1:51-59	9	AAGFSAQGV	1.07	0.15	-3.29	1.22	-2.07	1955.0
HLA A*6801	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-2.85	0.77	-2.08	712.0
HLA B*1517	1:20-28	9	LTARLAAAH	1.06	-0.16	-2.97	0.89	-2.08	932.4
HLA A*6901	1:55-63	9	SAQGVEHAV	1.10	0.12	-3.30	1.22	-2.08	1984.1
HLA A*2603	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-2.86	0.77	-2.08	717.3
HLA A*2603	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.16	2.07	-2.08	14356.0
HLA A*3301	1:89-97	9	GDAAAAATY	1.41	1.13	-4.63	2.55	-2.09	42922.4
HLA A*2603	1:16-24	9	AVEALTARL	1.61	0.54	-4.24	2.15	-2.09	17345.2
HLA A*6901	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.16	2.07	-2.09	14547.7
HLA A*3002	1:16-24	9	AVEALTARL	1.61	0.54	-4.24	2.15	-2.09	17448.7
HLA B*1503	1:23-31	9	RLAAAHASA	1.16	-0.04	-3.21	1.11	-2.09	1611.8
HLA A*2403	1:64-72	9	VTAEGVEEL	1.39	0.46	-3.94	1.85	-2.09	8725.4

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*0206	1:24-32	9	LAAAHASAA	0.90	-0.14	-2.85	0.75	-2.09	703.4
HLA A*0250	1:56-64	9	AQGVEHAVV	1.12	0.18	-3.40	1.30	-2.09	2491.6
HLA A*2403	1:16-24	9	AVEALTARL	1.61	0.54	-4.25	2.15	-2.10	17630.4
HLA A*2902	1:16-24	9	AVEALTARL	1.61	0.54	-4.25	2.15	-2.10	17832.8
HLA A*0206	1:87-95	9	LAGDAAAAA	1.17	-0.30	-2.97	0.87	-2.10	943.1
HLA B*1517	1:79-87	9	VGESGASYL	1.43	0.25	-3.78	1.68	-2.10	6080.6
HLA B*1503	1:92-100	9	AAAATYGVV	1.09	0.30	-3.50	1.39	-2.11	3142.0
HLA A*3001	1:85-93	9	SYLAGDAAA	1.15	-0.02	-3.24	1.13	-2.11	1757.6
HLA B*0702	1:23-31	9	RLAAAHASA	1.16	-0.04	-3.23	1.11	-2.11	1683.4
HLA B*1501	1:26-34	9	AAHASAAPV	0.61	0.30	-3.02	0.91	-2.11	1057.9
HLA B*4001	1:16-24	9	AVEALTARL	1.61	0.54	-4.26	2.15	-2.11	18328.9
HLA A*0216	1:12-20	9	AASAAVEAL	1.45	0.57	-4.13	2.01	-2.11	13442.0
HLA A*2301	1:78-86	9	GVGESGASY	1.21	1.20	-4.53	2.41	-2.12	33558.4
HLA A*0212	1:55-63	9	SAQGVEHAV	1.10	0.12	-3.34	1.22	-2.12	2179.2
HLA A*8001	1:16-24	9	AVEALTARL	1.61	0.54	-4.27	2.15	-2.12	18725.4
HLA A*0202	1:55-63	9	SAQGVEHAV	1.10	0.12	-3.34	1.22	-2.12	2202.2
HLA A*6801	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.48	2.35	-2.13	30167.7
HLA A*2403	1:12-20	9	AASAAVEAL	1.45	0.57	-4.14	2.01	-2.13	13859.3
HLA A*1101	1:15-23	9	AAVEALTAR	0.88	0.79	-3.80	1.67	-2.13	6257.4
HLA B*4403	1:78-86	9	GVGESGASY	1.21	1.20	-4.54	2.41	-2.13	34440.5
HLA A*6802	1:71-79	9	ELGRAGVGV	1.09	-0.09	-3.13	1.00	-2.13	1348.2
HLA B*0801	1:12-20	9	AASAAVEAL	1.45	0.57	-4.15	2.01	-2.13	14095.3
HLA A*0101	1:16-24	9	AVEALTARL	1.61	0.54	-4.29	2.15	-2.14	19351.4
HLA A*2501	1:64-72	9	VTAEGVEEL	1.39	0.46	-3.98	1.85	-2.14	9638.8
HLA B*4501	1:7-15	9	PEGLAAASA	1.26	-0.55	-2.85	0.71	-2.14	704.0
HLA A*2402	1:78-86	9	GVGESGASY	1.21	1.20	-4.55	2.41	-2.14	35339.1
HLA B*0802	1:16-24	9	AVEALTARL	1.61	0.54	-4.29	2.15	-2.14	19660.2
HLA B*1517	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.22	2.07	-2.14	16513.6
HLA B*4601	1:64-72	9	VTAEGVEEL	1.39	0.46	-3.99	1.85	-2.14	9820.8
HLA B*3801	1:16-24	9	AVEALTARL	1.61	0.54	-4.30	2.15	-2.15	19853.5
HLA B*3501	1:86-94	9	YLAGDAAAA	1.33	-0.20	-3.27	1.13	-2.15	1882.0
HLA B*1503	1:16-24	9	AVEALTARL	1.61	0.54	-4.30	2.15	-2.15	19880.8
HLA B*5401	1:78-86	9	GVGESGASY	1.21	1.20	-4.56	2.41	-2.15	36154.8
HLA B*5801	1:16-24	9	AVEALTARL	1.61	0.54	-4.30	2.15	-2.15	20117.1
HLA A*0212	1:12-20	9	AASAAVEAL	1.45	0.57	-4.17	2.01	-2.16	14855.5
HLA A*3301	1:78-86	9	GVGESGASY	1.21	1.20	-4.57	2.41	-2.16	36757.5
HLA A*2601	1:16-24	9	AVEALTARL	1.61	0.54	-4.31	2.15	-2.16	20431.0
HLA A*0301	1:16-24	9	AVEALTARL	1.61	0.54	-4.31	2.15	-2.16	20549.6
HLA B*0803	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.24	2.07	-2.16	17238.4
HLA A*6802	1:18-26	9	EALTARLAA	1.39	-0.27	-3.28	1.12	-2.16	1919.2
HLA B*4501	1:69-77	9	VEELGRAGV	1.03	0.03	-3.22	1.06	-2.17	1672.0
HLA A*0202	1:34-42	9	VITAVVPPA	1.03	-0.23	-2.97	0.81	-2.17	942.9
HLA A*0211	1:31-39	9	AAPVITAVV	1.00	0.24	-3.41	1.24	-2.17	2591.7
HLA B*4601	1:12-20	9	AASAAVEAL	1.45	0.57	-4.19	2.01	-2.17	15419.8
HLA A*0216	1:92-100	9	AAAATYGVV	1.09	0.30	-3.57	1.39	-2.18	3674.9
HLA B*2705	1:16-24	9	AVEALTARL	1.61	0.54	-4.33	2.15	-2.18	21441.2
HLA B*4801	1:16-24	9	AVEALTARL	1.61	0.54	-4.33	2.15	-2.18	21459.3
HLA B*5301	1:16-24	9	AVEALTARL	1.61	0.54	-4.33	2.15	-2.18	21580.4
HLA A*2603	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.03	1.85	-2.18	10771.8

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*1101	1:16-24	9	AVEALTARL	1.61	0.54	-4.34	2.15	-2.19	21770.1
HLA B*3501	1:18-26	9	EALTARLAA	1.39	-0.27	-3.31	1.12	-2.19	2029.6
HLA B*3501	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.04	1.85	-2.20	11079.8
HLA B*3501	1:87-95	9	LAGDAAAAA	1.17	-0.30	-3.07	0.87	-2.20	1174.7
HLA B*4402	1:12-20	9	AASAAVEAL	1.45	0.57	-4.21	2.01	-2.20	16361.6
HLA B*5401	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.56	2.35	-2.20	35914.8
HLA A*0202	1:24-32	9	LAAAHASAA	0.90	-0.14	-2.96	0.75	-2.20	906.8
HLA B*7301	1:78-86	9	GVGESGASY	1.21	1.20	-4.61	2.41	-2.20	40746.2
HLA A*0250	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.56	2.35	-2.21	36281.1
HLA A*6802	1:35-43	9	ITAVVPPAA	1.01	-0.20	-3.01	0.81	-2.21	1030.1
HLA A*3001	1:29-37	9	ASAAPVITA	1.21	-0.15	-3.26	1.06	-2.21	1840.1
HLA A*0201	1:5-13	9	VVPEGLAAA	1.10	-0.09	-3.22	1.01	-2.21	1654.2
HLA B*4501	1:78-86	9	GVGESGASY	1.21	1.20	-4.62	2.41	-2.21	41422.5
HLA B*0702	1:30-38	9	SAAPVITAV	0.96	0.26	-3.42	1.21	-2.21	2657.4
HLA A*3001	1:92-100	9	AAAATYGVV	1.09	0.30	-3.60	1.39	-2.21	4004.6
HLA A*2402	1:27-35	9	AHASAAPVI	1.32	0.37	-3.90	1.69	-2.22	8030.5
HLA B*0802	1:12-20	9	AASAAVEAL	1.45	0.57	-4.23	2.01	-2.22	17016.0
HLA A*0203	1:54-62	9	FSAQGVEHA	1.07	-0.26	-3.03	0.81	-2.22	1068.5
HLA B*4601	1:16-24	9	AVEALTARL	1.61	0.54	-4.37	2.15	-2.22	23439.0
HLA B*3501	1:28-36	9	HASAAPVIT	1.18	-0.26	-3.14	0.92	-2.22	1377.6
HLA A*3002	1:79-87	9	VGESGASYL	1.43	0.25	-3.90	1.68	-2.22	8003.7
HLA B*4002	1:78-86	9	GVGESGASY	1.21	1.20	-4.63	2.41	-2.22	42630.1
HLA B*5701	1:16-24	9	AVEALTARL	1.61	0.54	-4.37	2.15	-2.22	23704.9
HLA A*3101	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.30	2.07	-2.22	19883.7
HLA B*4402	1:66-74	9	AEGVEELGR	1.14	0.58	-3.95	1.72	-2.22	8870.3
HLA A*2301	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.30	2.07	-2.22	19905.2
HLA B*7301	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.58	2.35	-2.23	38222.0
HLA A*0203	1:51-59	9	AAGFSAQGV	1.07	0.15	-3.45	1.22	-2.23	2811.2
HLA A*3301	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.58	2.35	-2.23	38330.1
HLA B*1501	1:24-32	9	LAAAHASAA	0.90	-0.14	-2.98	0.75	-2.23	963.1
HLA B*1517	1:4-12	9	RVVPEGLAA	1.27	-0.01	-3.49	1.26	-2.23	3102.3
HLA B*2705	1:22-30	9	ARLAAAHAS	1.08	-0.81	-2.50	0.27	-2.23	318.9
HLA B*4002	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.59	2.35	-2.23	38651.0
HLA B*5701	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.31	2.07	-2.24	20402.4
HLA A*0301	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.31	2.07	-2.24	20436.3
HLA A*2501	1:16-24	9	AVEALTARL	1.61	0.54	-4.39	2.15	-2.24	24534.8
HLA B*1503	1:40-48	9	PPAADPVSL	1.65	0.10	-4.00	1.76	-2.24	9901.0
HLA B*0801	1:19-27	9	ALTARLAAA	1.01	-0.25	-3.00	0.76	-2.24	1009.6
HLA B*1503	1:30-38	9	SAAPVITAV	0.96	0.26	-3.46	1.21	-2.24	2858.6
HLA B*4402	1:16-24	9	AVEALTARL	1.61	0.54	-4.40	2.15	-2.24	24857.3
HLA B*3901	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.32	2.07	-2.25	20909.0
HLA A*6901	1:38-46	9	VVPPAADPV	0.76	0.28	-3.29	1.04	-2.25	1947.9
HLA B*3501	1:30-38	9	SAAPVITAV	0.96	0.26	-3.47	1.21	-2.25	2924.0
HLA B*5801	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.33	2.07	-2.26	21481.4
HLA A*3002	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.11	1.85	-2.26	12774.4
HLA B*4501	1:46-54	9	VSLQTAAGF	1.27	1.09	-4.61	2.35	-2.26	41034.2
HLA B*4403	1:80-88	9	GESGASYLA	1.31	-0.35	-3.22	0.96	-2.26	1654.0
HLA B*1517	1:29-37	9	ASAAPVITA	1.21	-0.15	-3.32	1.06	-2.26	2084.6
HLA B*1509	1:16-24	9	AVEALTARL	1.61	0.54	-4.42	2.15	-2.26	26031.5

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*0206	1:14-22	9	SAAVEALTA	1.39	-0.11	-3.54	1.28	-2.26	3493.3
HLA B*5701	1:12-20	9	AASAAVEAL	1.45	0.57	-4.28	2.01	-2.27	19026.0
HLA A*0206	1:35-43	9	ITAVVPPAA	1.01	-0.20	-3.07	0.81	-2.27	1179.8
HLA B*0801	1:40-48	9	PPAADPVSL	1.65	0.10	-4.03	1.76	-2.28	10750.6
HLA A*0212	1:38-46	9	VVPPAADPV	0.76	0.28	-3.32	1.04	-2.28	2082.4
HLA A*0203	1:56-64	9	AQGVEHAVV	1.12	0.18	-3.58	1.30	-2.28	3800.4
HLA A*2402	1:16-24	9	AVEALTARL	1.61	0.54	-4.43	2.15	-2.28	26908.3
HLA B*5101	1:40-48	9	PPAADPVSL	1.65	0.10	-4.04	1.76	-2.28	10864.3
HLA A*2601	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.35	2.07	-2.28	22600.0
HLA B*4601	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.36	2.07	-2.28	22683.1
HLA B*3901	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.13	1.85	-2.28	13529.7
HLA B*3801	1:27-35	9	AHASAAPVI	1.32	0.37	-3.97	1.69	-2.28	9428.9
HLA B*1509	1:12-20	9	AASAAVEAL	1.45	0.57	-4.30	2.01	-2.29	20001.8
HLA A*0219	1:38-46	9	VVPPAADPV	0.76	0.28	-3.33	1.04	-2.29	2144.9
HLA A*8001	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.36	2.07	-2.29	23147.6
HLA A*2403	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.37	2.07	-2.29	23292.0
HLA A*3101	1:12-20	9	AASAAVEAL	1.45	0.57	-4.31	2.01	-2.29	20305.5
HLA A*0206	1:15-23	9	AAVEALTAR	0.88	0.79	-3.96	1.67	-2.29	9154.3
HLA B*1502	1:16-24	9	AVEALTARL	1.61	0.54	-4.45	2.15	-2.29	27866.6
HLA A*0101	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.37	2.07	-2.30	23524.1
HLA A*2301	1:16-24	9	AVEALTARL	1.61	0.54	-4.45	2.15	-2.30	28075.6
HLA A*0206	1:51-59	9	AAGFSAQGV	1.07	0.15	-3.52	1.22	-2.30	3299.7
HLA B*4801	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.37	2.07	-2.30	23586.8
HLA B*5101	1:16-24	9	AVEALTARL	1.61	0.54	-4.45	2.15	-2.30	28243.2
HLA B*4601	1:30-38	9	SAAPVITAV	0.96	0.26	-3.51	1.21	-2.30	3273.0
HLA B*4001	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.38	2.07	-2.30	23802.8
HLA B*0702	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.38	2.07	-2.30	23855.9
HLA B*2705	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.38	2.07	-2.31	23984.7
HLA A*0212	1:30-38	9	SAAPVITAV	0.96	0.26	-3.52	1.21	-2.31	3344.0
HLA B*1801	1:16-24	9	AVEALTARL	1.61	0.54	-4.46	2.15	-2.31	29065.3
HLA B*1502	1:86-94	9	YLAGDAAAA	1.33	-0.20	-3.44	1.13	-2.31	2763.9
HLA B*1501	1:92-100	9	AAAATYGVV	1.09	0.30	-3.70	1.39	-2.31	5056.7
HLA B*5101	1:12-20	9	AASAAVEAL	1.45	0.57	-4.33	2.01	-2.32	21359.6
HLA A*0216	1:51-59	9	AAGFSAQGV	1.07	0.15	-3.54	1.22	-2.32	3434.2
HLA B*3501	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.39	2.07	-2.32	24563.5
HLA A*2402	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.39	2.07	-2.32	24577.8
HLA B*1801	1:12-20	9	AASAAVEAL	1.45	0.57	-4.33	2.01	-2.32	21434.2
HLA A*0212	1:5-13	9	VVPEGLAAA	1.10	-0.09	-3.33	1.01	-2.32	2128.7
HLA A*2902	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.40	2.07	-2.32	24919.2
HLA A*0216	1:56-64	9	AQGVEHAVV	1.12	0.18	-3.63	1.30	-2.32	4217.3
HLA A*0101	1:12-20	9	AASAAVEAL	1.45	0.57	-4.34	2.01	-2.33	21858.9
HLA B*0801	1:24-32	9	LAAAHASAA	0.90	-0.14	-3.08	0.75	-2.33	1212.2
HLA B*1503	1:29-37	9	ASAAPVITA	1.21	-0.15	-3.39	1.06	-2.33	2433.8
HLA A*6801	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.18	1.85	-2.33	15193.3
HLA A*2501	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-3.11	0.77	-2.33	1284.7
HLA A*0301	1:12-20	9	AASAAVEAL	1.45	0.57	-4.35	2.01	-2.33	22345.3
HLA B*5701	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.18	1.85	-2.34	15237.4
HLA A*6802	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-3.11	0.77	-2.34	1291.4
HLA B*3801	1:12-20	9	AASAAVEAL	1.45	0.57	-4.35	2.01	-2.34	22507.1

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*5401	1:40-48	9	PPAADPVSL	1.65	0.10	-4.10	1.76	-2.34	12460.2
HLA B*4002	1:12-20	9	AASAAVEAL	1.45	0.57	-4.35	2.01	-2.34	22600.8
HLA A*0219	1:51-59	9	AAGFSAQGV	1.07	0.15	-3.56	1.22	-2.34	3637.4
HLA A*2501	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.41	2.07	-2.34	25994.8
HLA A*2601	1:12-20	9	AASAAVEAL	1.45	0.57	-4.36	2.01	-2.34	22663.1
HLA B*1509	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.19	1.85	-2.34	15459.7
HLA B*4402	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.42	2.07	-2.35	26400.1
HLA B*1801	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.42	2.07	-2.35	26485.5
HLA B*2705	1:12-20	9	AASAAVEAL	1.45	0.57	-4.36	2.01	-2.35	23081.4
HLA A*0203	1:48-56	9	LQTAAGFSA	1.01	-0.19	-3.17	0.82	-2.35	1475.7
HLA A*0202	1:71-79	9	ELGRAGVGV	1.09	-0.09	-3.35	1.00	-2.35	2229.0
HLA B*1509	1:40-48	9	PPAADPVSL	1.65	0.10	-4.11	1.76	-2.35	12904.7
HLA B*1517	1:91-99	9	AAAAATYGV	1.05	0.17	-3.57	1.22	-2.36	3732.2
HLA B*1503	1:84-92	9	ASYLAGDAA	1.27	-0.08	-3.55	1.19	-2.36	3531.5
HLA B*0803	1:12-20	9	AASAAVEAL	1.45	0.57	-4.37	2.01	-2.36	23567.3
HLA B*3501	1:15-23	9	AAVEALTAR	0.88	0.79	-4.03	1.67	-2.36	10625.1
HLA A*0202	1:5-13	9	VVPEGLAAA	1.10	-0.09	-3.37	1.01	-2.36	2337.0
HLA A*2402	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.21	1.85	-2.36	16168.3
HLA A*3301	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.44	2.07	-2.36	27433.2
HLA A*1101	1:12-20	9	AASAAVEAL	1.45	0.57	-4.38	2.01	-2.37	24065.0
HLA B*1503	1:11-19	9	AAASAAVEA	1.20	-0.12	-3.45	1.08	-2.37	2809.9
HLA B*5101	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.45	2.07	-2.37	27941.4
HLA A*6801	1:16-24	9	AVEALTARL	1.61	0.54	-4.52	2.15	-2.37	33459.4
HLA B*3901	1:26-34	9	AAHASAAPV	0.61	0.30	-3.29	0.91	-2.38	1941.0
HLA A*3002	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.45	2.07	-2.38	28420.7
HLA A*0219	1:30-38	9	SAAPVITAV	0.96	0.26	-3.59	1.21	-2.38	3925.8
HLA A*6801	1:20-28	9	LTARLAAAH	1.06	-0.16	-3.27	0.89	-2.38	1877.3
HLA A*0206	1:85-93	9	SYLAGDAAA	1.15	-0.02	-3.52	1.13	-2.38	3288.1
HLA A*0201	1:55-63	9	SAQGVEHAV	1.10	0.12	-3.60	1.22	-2.38	3991.3
HLA A*6802	1:24-32	9	LAAAHASAA	0.90	-0.14	-3.14	0.75	-2.38	1371.1
HLA A*3001	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.24	1.85	-2.39	17199.0
HLA B*3801	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.46	2.07	-2.39	29051.2
HLA A*8001	1:12-20	9	AASAAVEAL	1.45	0.57	-4.41	2.01	-2.39	25430.8
HLA B*4501	1:12-20	9	AASAAVEAL	1.45	0.57	-4.41	2.01	-2.39	25527.5
HLA A*0212	1:51-59	9	AAGFSAQGV	1.07	0.15	-3.61	1.22	-2.39	4104.3
HLA A*3002	1:12-20	9	AASAAVEAL	1.45	0.57	-4.41	2.01	-2.39	25622.6
HLA A*2902	1:12-20	9	AASAAVEAL	1.45	0.57	-4.41	2.01	-2.39	25651.2
HLA A*2601	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.24	1.85	-2.40	17527.4
HLA A*3002	1:27-35	9	AHASAAPVI	1.32	0.37	-4.09	1.69	-2.40	12198.4
HLA A*0206	1:29-37	9	ASAAPVITA	1.21	-0.15	-3.45	1.06	-2.40	2848.3
HLA A*1101	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.47	2.07	-2.40	29666.3
HLA B*1502	1:12-20	9	AASAAVEAL	1.45	0.57	-4.41	2.01	-2.40	25849.0
HLA B*1801	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.25	1.85	-2.40	17635.1
HLA A*0202	1:79-87	9	VGESGASYL	1.43	0.25	-4.08	1.68	-2.40	12026.0
HLA B*3501	1:20-28	9	LTARLAAAH	1.06	-0.16	-3.29	0.89	-2.40	1952.2
HLA B*5301	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.25	1.85	-2.40	17672.3
HLA A*2403	1:27-35	9	AHASAAPVI	1.32	0.37	-4.09	1.69	-2.40	12322.9
HLA A*6901	1:40-48	9	PPAADPVSL	1.65	0.10	-4.16	1.76	-2.40	14398.3
HLA B*5401	1:32-40	9	APVITAVVP	0.92	0.08	-3.40	0.99	-2.40	2487.4

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*0101	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.25	1.85	-2.40	17821.9
HLA B*4402	1:80-88	9	GESGASYLA	1.31	-0.35	-3.36	0.96	-2.40	2302.6
HLA B*5401	1:16-24	9	AVEALTARL	1.61	0.54	-4.56	2.15	-2.41	35975.1
HLA A*2602	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.48	2.07	-2.41	30277.9
HLA A*3301	1:16-24	9	AVEALTARL	1.61	0.54	-4.56	2.15	-2.41	36346.9
HLA A*2501	1:12-20	9	AASAAVEAL	1.45	0.57	-4.42	2.01	-2.41	26539.9
HLA A*2402	1:12-20	9	AASAAVEAL	1.45	0.57	-4.43	2.01	-2.42	26898.4
HLA B*4002	1:66-74	9	AEGVEELGR	1.14	0.58	-4.14	1.72	-2.42	13776.4
HLA A*3101	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.27	1.85	-2.42	18582.7
HLA B*1503	1:4-12	9	RVVPEGLAA	1.27	-0.01	-3.68	1.26	-2.42	4806.9
HLA B*4002	1:16-24	9	AVEALTARL	1.61	0.54	-4.58	2.15	-2.42	37584.3
HLA A*3001	1:15-23	9	AAVEALTAR	0.88	0.79	-4.09	1.67	-2.43	12388.2
HLA A*6901	1:35-43	9	ITAVVPPAA	1.01	-0.20	-3.23	0.81	-2.43	1703.5
HLA A*0211	1:35-43	9	ITAVVPPAA	1.01	-0.20	-3.23	0.81	-2.43	1703.9
HLA B*4501	1:29-37	9	ASAAPVITA	1.21	-0.15	-3.49	1.06	-2.43	3067.0
HLA A*6802	1:23-31	9	RLAAAHASA	1.16	-0.04	-3.55	1.11	-2.43	3521.4
HLA A*2902	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.29	1.85	-2.44	19275.7
HLA B*0702	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.29	1.85	-2.44	19323.5
HLA B*4501	1:16-24	9	AVEALTARL	1.61	0.54	-4.59	2.15	-2.44	38876.8
HLA B*3801	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.29	1.85	-2.44	19503.0
HLA B*4001	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.29	1.85	-2.45	19668.1
HLA A*8001	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.30	1.85	-2.45	19869.8
HLA B*3901	1:79-87	9	VGESGASYL	1.43	0.25	-4.13	1.68	-2.45	13538.0
HLA A*0206	1:84-92	9	ASYLAGDAA	1.27	-0.08	-3.64	1.19	-2.45	4396.6
HLA B*3501	1:79-87	9	VGESGASYL	1.43	0.25	-4.13	1.68	-2.45	13621.6
HLA B*1517	1:15-23	9	AAVEALTAR	0.88	0.79	-4.12	1.67	-2.45	13235.0
HLA B*4403	1:16-24	9	AVEALTARL	1.61	0.54	-4.61	2.15	-2.46	40582.5
HLA B*5101	1:27-35	9	AHASAAPVI	1.32	0.37	-4.15	1.69	-2.46	14117.2
HLA A*0203	1:11-19	9	AAASAAVEA	1.20	-0.12	-3.54	1.08	-2.46	3497.9
HLA A*3001	1:27-35	9	AHASAAPVI	1.32	0.37	-4.16	1.69	-2.47	14423.9
HLA B*4601	1:15-23	9	AAVEALTAR	0.88	0.79	-4.14	1.67	-2.47	13753.6
HLA B*1502	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.32	1.85	-2.47	20858.1
HLA A*0206	1:79-87	9	VGESGASYL	1.43	0.25	-4.15	1.68	-2.47	14233.0
HLA B*5401	1:87-95	9	LAGDAAAAA	1.17	-0.30	-3.35	0.87	-2.47	2219.0
HLA B*7301	1:16-24	9	AVEALTARL	1.61	0.54	-4.62	2.15	-2.47	42081.3
HLA A*0202	1:56-64	9	AQGVEHAVV	1.12	0.18	-3.78	1.30	-2.48	5998.4
HLA A*0203	1:58-66	9	GVEHAVVTA	1.37	-0.33	-3.52	1.04	-2.48	3304.0
HLA A*2301	1:12-20	9	AASAAVEAL	1.45	0.57	-4.49	2.01	-2.48	31152.7
HLA B*4801	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.33	1.85	-2.48	21280.5
HLA A*3001	1:91-99	9	AAAAATYGV	1.05	0.17	-3.70	1.22	-2.48	4983.2
HLA A*0202	1:27-35	9	AHASAAPVI	1.32	0.37	-4.17	1.69	-2.48	14864.3
HLA A*6801	1:12-20	9	AASAAVEAL	1.45	0.57	-4.50	2.01	-2.48	31394.3
HLA A*2602	1:15-23	9	AAVEALTAR	0.88	0.79	-4.15	1.67	-2.48	14202.0
HLA B*4402	1:17-25	9	VEALTARLA	1.29	-0.19	-3.59	1.10	-2.48	3857.2
HLA B*1517	1:14-22	9	SAAVEALTA	1.39	-0.11	-3.76	1.28	-2.48	5794.2
HLA A*0216	1:31-39	9	AAPVITAVV	1.00	0.24	-3.73	1.24	-2.49	5336.9
HLA B*0702	1:91-99	9	AAAAATYGV	1.05	0.17	-3.70	1.22	-2.49	5032.2
HLA B*5401	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.56	2.07	-2.49	36640.9
HLA B*3901	1:55-63	9	SAQGVEHAV	1.10	0.12	-3.71	1.22	-2.49	5127.4

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*0802	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.34	1.85	-2.49	22003.2
HLA B*4501	1:92-100	9	AAAATYGVV	1.09	0.30	-3.89	1.39	-2.50	7711.7
HLA A*0219	1:5-13	9	VVPEGLAAA	1.10	-0.09	-3.51	1.01	-2.50	3228.1
HLA A*2301	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.35	1.85	-2.50	22249.0
HLA A*6801	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.57	2.07	-2.50	37485.8
HLA B*1501	1:30-38	9	SAAPVITAV	0.96	0.26	-3.71	1.21	-2.50	5186.0
HLA A*2603	1:12-20	9	AASAAVEAL	1.45	0.57	-4.52	2.01	-2.50	32797.6
HLA A*0203	1:71-79	9	ELGRAGVGV	1.09	-0.09	-3.50	1.00	-2.50	3162.4
HLA B*5101	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.35	1.85	-2.50	22439.8
HLA A*0206	1:71-79	9	ELGRAGVGV	1.09	-0.09	-3.50	1.00	-2.50	3175.8
HLA B*4501	1:26-34	9	AAHASAAPV	0.61	0.30	-3.42	0.91	-2.50	2611.0
HLA B*4403	1:12-20	9	AASAAVEAL	1.45	0.57	-4.52	2.01	-2.50	33044.2
HLA A*0216	1:5-13	9	VVPEGLAAA	1.10	-0.09	-3.52	1.01	-2.51	3275.5
HLA A*0301	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.35	1.85	-2.51	22563.2
HLA B*5301	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.58	2.07	-2.51	38052.8
HLA A*0301	1:15-23	9	AAVEALTAR	0.88	0.79	-4.18	1.67	-2.51	14963.4
HLA B*5401	1:12-20	9	AASAAVEAL	1.45	0.57	-4.52	2.01	-2.51	33406.6
HLA B*1503	1:79-87	9	VGESGASYL	1.43	0.25	-4.19	1.68	-2.51	15565.3
HLA B*0801	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.36	1.85	-2.51	22934.1
HLA B*0702	1:79-87	9	VGESGASYL	1.43	0.25	-4.19	1.68	-2.51	15625.6
HLA B*1501	1:84-92	9	ASYLAGDAA	1.27	-0.08	-3.71	1.19	-2.51	5074.4
HLA B*7301	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.59	2.07	-2.51	38819.9
HLA A*0203	1:35-43	9	ITAVVPPAA	1.01	-0.20	-3.32	0.81	-2.52	2091.6
HLA B*1502	1:79-87	9	VGESGASYL	1.43	0.25	-4.20	1.68	-2.52	15898.9
HLA B*4001	1:27-35	9	AHASAAPVI	1.32	0.37	-4.21	1.69	-2.52	16264.0
HLA B*1503	1:9-17	9	GLAAASAAV	1.01	0.00	-3.53	1.01	-2.52	3421.7
HLA A*0219	1:31-39	9	AAPVITAVV	1.00	0.24	-3.77	1.24	-2.52	5827.9
HLA A*6802	1:34-42	9	VITAVVPPA	1.03	-0.23	-3.33	0.81	-2.53	2148.1
HLA B*0803	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.38	1.85	-2.53	23876.8
HLA A*3002	1:55-63	9	SAQGVEHAV	1.10	0.12	-3.75	1.22	-2.53	5625.6
HLA A*0201	1:38-46	9	VVPPAADPV	0.76	0.28	-3.57	1.04	-2.53	3751.1
HLA B*4801	1:40-48	9	PPAADPVSL	1.65	0.10	-4.29	1.76	-2.53	19506.8
HLA A*3001	1:84-92	9	ASYLAGDAA	1.27	-0.08	-3.73	1.19	-2.53	5316.9
HLA B*4002	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.61	2.07	-2.54	40807.7
HLA B*3901	1:92-100	9	AAAATYGVV	1.09	0.30	-3.93	1.39	-2.54	8443.6
HLA A*3001	1:40-48	9	PPAADPVSL	1.65	0.10	-4.30	1.76	-2.54	19725.2
HLA A*0203	1:14-22	9	SAAVEALTA	1.39	-0.11	-3.82	1.28	-2.54	6585.1
HLA A*1101	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.39	1.85	-2.54	24461.5
HLA A*0206	1:27-35	9	AHASAAPVI	1.32	0.37	-4.23	1.69	-2.54	17003.0
HLA B*4402	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.39	1.85	-2.54	24674.3
HLA B*4403	1:17-25	9	VEALTARLA	1.29	-0.19	-3.65	1.10	-2.55	4440.6
HLA A*3201	1:23-31	9	RLAAAHASA	1.16	-0.04	-3.66	1.11	-2.55	4611.7
HLA B*2705	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.40	1.85	-2.55	25022.3
HLA B*0801	1:23-31	9	RLAAAHASA	1.16	-0.04	-3.67	1.11	-2.55	4632.1
HLA A*3001	1:79-87	9	VGESGASYL	1.43	0.25	-4.23	1.68	-2.55	17106.1
HLA A*0250	1:79-87	9	VGESGASYL	1.43	0.25	-4.24	1.68	-2.56	17234.0
HLA B*3501	1:14-22	9	SAAVEALTA	1.39	-0.11	-3.84	1.28	-2.56	6858.0
HLA A*3101	1:66-74	9	AEGVEELGR	1.14	0.58	-4.28	1.72	-2.56	19166.3
HLA A*0202	1:61-69	9	HAVVTAEGV	1.02	0.08	-3.66	1.10	-2.56	4575.6

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*0211	1:79-87	9	VGESGASYL	1.43	0.25	-4.24	1.68	-2.56	17492.2
HLA A*3001	1:66-74	9	AEGVEELGR	1.14	0.58	-4.29	1.72	-2.56	19350.9
HLA B*4001	1:66-74	9	AEGVEELGR	1.14	0.58	-4.29	1.72	-2.56	19418.9
HLA A*0216	1:27-35	9	AHASAAPVI	1.32	0.37	-4.26	1.69	-2.57	18048.5
HLA A*6901	1:14-22	9	SAAVEALTA	1.39	-0.11	-3.85	1.28	-2.57	7004.2
HLA A*6901	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-3.34	0.77	-2.57	2198.4
HLA B*0702	1:27-35	9	AHASAAPVI	1.32	0.37	-4.26	1.69	-2.57	18160.3
HLA B*3501	1:27-35	9	AHASAAPVI	1.32	0.37	-4.26	1.69	-2.57	18198.1
HLA B*4501	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.65	2.07	-2.57	44452.3
HLA A*2301	1:27-35	9	AHASAAPVI	1.32	0.37	-4.26	1.69	-2.57	18395.0
HLA A*3001	1:35-43	9	ITAVVPPAA	1.01	-0.20	-3.38	0.81	-2.58	2403.3
HLA B*4402	1:27-35	9	AHASAAPVI	1.32	0.37	-4.27	1.69	-2.58	18443.1
HLA A*0211	1:61-69	9	HAVVTAEGV	1.02	0.08	-3.68	1.10	-2.58	4756.3
HLA A*0211	1:4-12	9	RVVPEGLAA	1.27	-0.01	-3.84	1.26	-2.58	6896.3
HLA A*0203	1:55-63	9	SAQGVEHAV	1.10	0.12	-3.80	1.22	-2.58	6284.6
HLA B*0801	1:18-26	9	EALTARLAA	1.39	-0.27	-3.70	1.12	-2.58	5014.9
HLA A*3001	1:1-9	9	MTLRVVPEG	0.78	-0.59	-2.77	0.19	-2.58	586.3
HLA B*4403	1:2-10	9	TLRVVPEGL	1.62	0.45	-4.66	2.07	-2.58	45313.1
HLA A*0201	1:48-56	9	LQTAAGFSA	1.01	-0.19	-3.40	0.82	-2.58	2519.0
HLA A*0203	1:27-35	9	AHASAAPVI	1.32	0.37	-4.27	1.69	-2.59	18827.3
HLA B*1501	1:27-35	9	AHASAAPVI	1.32	0.37	-4.27	1.69	-2.59	18828.7
HLA B*4501	1:27-35	9	AHASAAPVI	1.32	0.37	-4.28	1.69	-2.59	18868.4
HLA A*3301	1:12-20	9	AASAAVEAL	1.45	0.57	-4.61	2.01	-2.59	40472.6
HLA A*0250	1:61-69	9	HAVVTAEGV	1.02	0.08	-3.69	1.10	-2.59	4926.6
HLA B*3801	1:79-87	9	VGESGASYL	1.43	0.25	-4.27	1.68	-2.59	18815.2
HLA A*6802	1:40-48	9	PPAADPVSL	1.65	0.10	-4.35	1.76	-2.60	22473.3
HLA B*1501	1:87-95	9	LAGDAAAAA	1.17	-0.30	-3.47	0.87	-2.60	2952.7
HLA B*2705	1:27-35	9	AHASAAPVI	1.32	0.37	-4.29	1.69	-2.60	19391.1
HLA B*5801	1:40-48	9	PPAADPVSL	1.65	0.10	-4.36	1.76	-2.60	22814.9
HLA A*0203	1:15-23	9	AAVEALTAR	0.88	0.79	-4.27	1.67	-2.60	18623.7
HLA B*7301	1:12-20	9	AASAAVEAL	1.45	0.57	-4.62	2.01	-2.60	41377.0
HLA A*3201	1:91-99	9	AAAAATYGV	1.05	0.17	-3.82	1.22	-2.61	6644.6
HLA B*1501	1:15-23	9	AAVEALTAR	0.88	0.79	-4.28	1.67	-2.61	18843.5
HLA A*6802	1:51-59	9	AAGFSAQGV	1.07	0.15	-3.83	1.22	-2.61	6741.7
HLA A*0203	1:29-37	9	ASAAPVITA	1.21	-0.15	-3.67	1.06	-2.61	4627.2
HLA A*0301	1:40-48	9	PPAADPVSL	1.65	0.10	-4.37	1.76	-2.61	23247.8
HLA B*3501	1:11-19	9	AAASAAVEA	1.20	-0.12	-3.69	1.08	-2.61	4911.9
HLA B*1501	1:79-87	9	VGESGASYL	1.43	0.25	-4.29	1.68	-2.61	19582.2
HLA B*4001	1:79-87	9	VGESGASYL	1.43	0.25	-4.29	1.68	-2.61	19610.3
HLA A*6901	1:15-23	9	AAVEALTAR	0.88	0.79	-4.28	1.67	-2.61	19027.2
HLA A*0301	1:66-74	9	AEGVEELGR	1.14	0.58	-4.34	1.72	-2.61	21672.1
HLA B*0802	1:40-48	9	PPAADPVSL	1.65	0.10	-4.37	1.76	-2.61	23471.0
HLA A*0219	1:27-35	9	AHASAAPVI	1.32	0.37	-4.30	1.69	-2.61	20164.8
HLA B*4501	1:84-92	9	ASYLAGDAA	1.27	-0.08	-3.81	1.19	-2.62	6418.4
HLA B*1501	1:40-48	9	PPAADPVSL	1.65	0.10	-4.37	1.76	-2.62	23661.9
HLA B*1509	1:79-87	9	VGESGASYL	1.43	0.25	-4.30	1.68	-2.62	19915.3
HLA B*5801	1:27-35	9	AHASAAPVI	1.32	0.37	-4.31	1.69	-2.62	20334.5
HLA B*0801	1:79-87	9	VGESGASYL	1.43	0.25	-4.30	1.68	-2.62	19996.2
HLA A*0203	1:79-87	9	VGESGASYL	1.43	0.25	-4.30	1.68	-2.62	20013.7

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*3901	1:30-38	9	SAAPVITAV	0.96	0.26	-3.83	1.21	-2.62	6825.0
HLA A*0203	1:40-48	9	PPAADPVSL	1.65	0.10	-4.38	1.76	-2.62	23815.1
HLA A*0212	1:61-69	9	HAVVTAEGV	1.02	0.08	-3.72	1.10	-2.62	5259.3
HLA A*0219	1:40-48	9	PPAADPVSL	1.65	0.10	-4.38	1.76	-2.62	23881.3
HLA A*0101	1:40-48	9	PPAADPVSL	1.65	0.10	-4.38	1.76	-2.62	23914.2
HLA B*4501	1:11-19	9	AAASAAVEA	1.20	-0.12	-3.70	1.08	-2.62	5051.2
HLA B*3501	1:6-14	9	VPEGLAAAS	1.10	-1.12	-2.60	-0.03	-2.62	394.9
HLA A*2601	1:15-23	9	AAVEALTAR	0.88	0.79	-4.29	1.67	-2.62	19552.4
HLA B*4001	1:40-48	9	PPAADPVSL	1.65	0.10	-4.38	1.76	-2.62	23981.7
HLA B*1503	1:91-99	9	AAAAATYGV	1.05	0.17	-3.84	1.22	-2.62	6923.1
HLA A*0219	1:79-87	9	VGESGASYL	1.43	0.25	-4.31	1.68	-2.63	20256.5
HLA A*6901	1:54-62	9	FSAQGVEHA	1.07	-0.26	-3.44	0.81	-2.63	2749.7
HLA A*0201	1:92-100	9	AAAATYGVV	1.09	0.30	-4.02	1.39	-2.63	10412.5
HLA A*6901	1:79-87	9	VGESGASYL	1.43	0.25	-4.31	1.68	-2.63	20421.5
HLA B*5801	1:66-74	9	AEGVEELGR	1.14	0.58	-4.35	1.72	-2.63	22604.0
HLA B*0803	1:40-48	9	PPAADPVSL	1.65	0.10	-4.39	1.76	-2.63	24381.3
HLA B*1501	1:20-28	9	LTARLAAAH	1.06	-0.16	-3.52	0.89	-2.63	3330.6
HLA A*6901	1:27-35	9	AHASAAPVI	1.32	0.37	-4.32	1.69	-2.63	20987.9
HLA A*0206	1:58-66	9	GVEHAVVTA	1.37	-0.33	-3.67	1.04	-2.63	4705.5
HLA B*1503	1:24-32	9	LAAAHASAA	0.90	-0.14	-3.39	0.75	-2.63	2438.1
HLA A*6901	1:5-13	9	VVPEGLAAA	1.10	-0.09	-3.64	1.01	-2.63	4401.4
HLA A*0211	1:27-35	9	AHASAAPVI	1.32	0.37	-4.32	1.69	-2.63	21053.2
HLA A*2601	1:40-48	9	PPAADPVSL	1.65	0.10	-4.39	1.76	-2.63	24537.9
HLA B*4601	1:40-48	9	PPAADPVSL	1.65	0.10	-4.39	1.76	-2.64	24624.3
HLA A*0201	1:40-48	9	PPAADPVSL	1.65	0.10	-4.39	1.76	-2.64	24657.9
HLA A*3101	1:40-48	9	PPAADPVSL	1.65	0.10	-4.39	1.76	-2.64	24664.2
HLA A*0216	1:79-87	9	VGESGASYL	1.43	0.25	-4.32	1.68	-2.64	20766.2
HLA B*5701	1:40-48	9	PPAADPVSL	1.65	0.10	-4.39	1.76	-2.64	24686.6
HLA B*3501	1:91-99	9	AAAAATYGV	1.05	0.17	-3.85	1.22	-2.64	7120.4
HLA B*4402	1:40-48	9	PPAADPVSL	1.65	0.10	-4.40	1.76	-2.64	24878.7
HLA B*5801	1:79-87	9	VGESGASYL	1.43	0.25	-4.32	1.68	-2.64	20987.3
HLA B*3901	1:9-17	9	GLAAASAAV	1.01	0.00	-3.65	1.01	-2.64	4493.4
HLA B*4801	1:27-35	9	AHASAAPVI	1.32	0.37	-4.33	1.69	-2.64	21466.8
HLA A*8001	1:40-48	9	PPAADPVSL	1.65	0.10	-4.40	1.76	-2.64	25083.7
HLA A*0202	1:80-88	9	GESGASYLA	1.31	-0.35	-3.60	0.96	-2.64	3999.1
HLA A*0201	1:26-34	9	AAHASAAPV	0.61	0.30	-3.56	0.91	-2.64	3600.1
HLA B*1503	1:66-74	9	AEGVEELGR	1.14	0.58	-4.37	1.72	-2.65	23382.5
HLA B*1501	1:91-99	9	AAAAATYGV	1.05	0.17	-3.86	1.22	-2.65	7283.6
HLA B*1501	1:29-37	9	ASAAPVITA	1.21	-0.15	-3.70	1.06	-2.65	5053.2
HLA A*0203	1:61-69	9	HAVVTAEGV	1.02	0.08	-3.75	1.10	-2.65	5583.1
HLA B*4601	1:79-87	9	VGESGASYL	1.43	0.25	-4.33	1.68	-2.65	21557.2
HLA B*1801	1:69-77	9	VEELGRAGV	1.03	0.03	-3.71	1.06	-2.65	5132.6
HLA A*2501	1:40-48	9	PPAADPVSL	1.65	0.10	-4.41	1.76	-2.66	25797.6
HLA A*0216	1:40-48	9	PPAADPVSL	1.65	0.10	-4.41	1.76	-2.66	25850.6
HLA A*2902	1:53-61	9	GFSAQGVEH	1.21	-0.17	-3.70	1.04	-2.66	4975.8
HLA A*8001	1:66-74	9	AEGVEELGR	1.14	0.58	-4.38	1.72	-2.66	24095.8
HLA A*0212	1:40-48	9	PPAADPVSL	1.65	0.10	-4.41	1.76	-2.66	25996.4
HLA B*1517	1:92-100	9	AAAATYGVV	1.09	0.30	-4.05	1.39	-2.66	11193.3
HLA A*0206	1:40-48	9	PPAADPVSL	1.65	0.10	-4.42	1.76	-2.66	26095.0

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*6901	1:66-74	9	AEGVEELGR	1.14	0.58	-4.38	1.72	-2.66	24199.4
HLA B*3801	1:40-48	9	PPAADPVSL	1.65	0.10	-4.42	1.76	-2.66	26153.9
HLA A*0101	1:66-74	9	AEGVEELGR	1.14	0.58	-4.39	1.72	-2.66	24290.5
HLA A*2403	1:40-48	9	PPAADPVSL	1.65	0.10	-4.42	1.76	-2.66	26254.2
HLA A*0201	1:31-39	9	AAPVITAVV	1.00	0.24	-3.91	1.24	-2.67	8079.4
HLA B*1801	1:40-48	9	PPAADPVSL	1.65	0.10	-4.42	1.76	-2.67	26423.1
HLA A*0101	1:79-87	9	VGESGASYL	1.43	0.25	-4.35	1.68	-2.67	22258.8
HLA B*1501	1:66-74	9	AEGVEELGR	1.14	0.58	-4.39	1.72	-2.67	24666.6
HLA B*2705	1:15-23	9	AAVEALTAR	0.88	0.79	-4.34	1.67	-2.67	21747.1
HLA A*2601	1:66-74	9	AEGVEELGR	1.14	0.58	-4.39	1.72	-2.67	24759.3
HLA A*2902	1:40-48	9	PPAADPVSL	1.65	0.10	-4.43	1.76	-2.67	26729.8
HLA A*3101	1:79-87	9	VGESGASYL	1.43	0.25	-4.35	1.68	-2.67	22524.1
HLA A*2902	1:79-87	9	VGESGASYL	1.43	0.25	-4.35	1.68	-2.67	22531.6
HLA A*6901	1:11-19	9	AAASAAVEA	1.20	-0.12	-3.75	1.08	-2.67	5659.9
HLA A*0201	1:66-74	9	AEGVEELGR	1.14	0.58	-4.40	1.72	-2.67	24861.7
HLA B*3501	1:55-63	9	SAQGVEHAV	1.10	0.12	-3.89	1.22	-2.67	7783.3
HLA A*3301	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.52	1.85	-2.67	33212.3
HLA B*0801	1:27-35	9	AHASAAPVI	1.32	0.37	-4.36	1.69	-2.67	23087.9
HLA A*0301	1:27-35	9	AHASAAPVI	1.32	0.37	-4.36	1.69	-2.67	23091.2
HLA A*6901	1:87-95	9	LAGDAAAAA	1.17	-0.30	-3.55	0.87	-2.67	3525.9
HLA B*5801	1:15-23	9	AAVEALTAR	0.88	0.79	-4.34	1.67	-2.68	22033.4
HLA A*0201	1:27-35	9	AHASAAPVI	1.32	0.37	-4.37	1.69	-2.68	23228.9
HLA A*0202	1:51-59	9	AAGFSAQGV	1.07	0.15	-3.90	1.22	-2.68	7904.4
HLA A*0301	1:79-87	9	VGESGASYL	1.43	0.25	-4.36	1.68	-2.68	22847.6
HLA B*1517	1:30-38	9	SAAPVITAV	0.96	0.26	-3.89	1.21	-2.68	7827.1
HLA A*0201	1:56-64	9	AQGVEHAVV	1.12	0.18	-3.98	1.30	-2.68	9625.3
HLA B*4002	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.53	1.85	-2.68	33797.8
HLA B*4801	1:79-87	9	VGESGASYL	1.43	0.25	-4.36	1.68	-2.68	23042.9
HLA A*0212	1:79-87	9	VGESGASYL	1.43	0.25	-4.36	1.68	-2.68	23048.2
HLA B*3901	1:56-64	9	AQGVEHAVV	1.12	0.18	-3.98	1.30	-2.68	9640.6
HLA B*0802	1:66-74	9	AEGVEELGR	1.14	0.58	-4.41	1.72	-2.68	25432.8
HLA B*4801	1:66-74	9	AEGVEELGR	1.14	0.58	-4.41	1.72	-2.68	25491.5
HLA A*0201	1:79-87	9	VGESGASYL	1.43	0.25	-4.36	1.68	-2.68	23157.4
HLA A*0202	1:29-37	9	ASAAPVITA	1.21	-0.15	-3.74	1.06	-2.68	5505.0
HLA A*2501	1:15-23	9	AAVEALTAR	0.88	0.79	-4.35	1.67	-2.68	22528.4
HLA A*0202	1:40-48	9	PPAADPVSL	1.65	0.10	-4.44	1.76	-2.69	27666.3
HLA B*4801	1:15-23	9	AAVEALTAR	0.88	0.79	-4.35	1.67	-2.69	22628.5
HLA B*1517	1:27-35	9	AHASAAPVI	1.32	0.37	-4.38	1.69	-2.69	23816.6
HLA A*2602	1:40-48	9	PPAADPVSL	1.65	0.10	-4.44	1.76	-2.69	27769.4
HLA A*0219	1:55-63	9	SAQGVEHAV	1.10	0.12	-3.91	1.22	-2.69	8071.0
HLA A*2601	1:27-35	9	AHASAAPVI	1.32	0.37	-4.38	1.69	-2.69	23944.5
HLA B*4601	1:27-35	9	AHASAAPVI	1.32	0.37	-4.38	1.69	-2.69	23954.1
HLA B*1801	1:15-23	9	AAVEALTAR	0.88	0.79	-4.36	1.67	-2.69	22785.2
HLA B*4402	1:15-23	9	AAVEALTAR	0.88	0.79	-4.36	1.67	-2.69	22824.3
HLA A*0212	1:27-35	9	AHASAAPVI	1.32	0.37	-4.38	1.69	-2.69	24013.1
HLA B*5701	1:66-74	9	AEGVEELGR	1.14	0.58	-4.41	1.72	-2.69	25968.8
HLA A*2902	1:27-35	9	AHASAAPVI	1.32	0.37	-4.38	1.69	-2.69	24097.0
HLA B*5701	1:27-35	9	AHASAAPVI	1.32	0.37	-4.38	1.69	-2.69	24113.8
HLA A*2601	1:79-87	9	VGESGASYL	1.43	0.25	-4.37	1.68	-2.69	23697.2

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*0212	1:66-74	9	AEGVEELGR	1.14	0.58	-4.42	1.72	-2.69	26126.5
HLA B*2705	1:40-48	9	PPAADPVSL	1.65	0.10	-4.45	1.76	-2.70	28266.4
HLA A*0211	1:29-37	9	ASAAPVITA	1.21	-0.15	-3.75	1.06	-2.70	5648.3
HLA A*8001	1:79-87	9	VGESGASYL	1.43	0.25	-4.38	1.68	-2.70	23807.0
HLA A*2402	1:40-48	9	PPAADPVSL	1.65	0.10	-4.45	1.76	-2.70	28331.9
HLA B*4601	1:66-74	9	AEGVEELGR	1.14	0.58	-4.42	1.72	-2.70	26402.6
HLA A*0202	1:15-23	9	AAVEALTAR	0.88	0.79	-4.37	1.67	-2.70	23241.0
HLA B*5401	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.55	1.85	-2.70	35180.8
HLA B*1517	1:40-48	9	PPAADPVSL	1.65	0.10	-4.46	1.76	-2.70	28510.3
HLA A*6802	1:15-23	9	AAVEALTAR	0.88	0.79	-4.37	1.67	-2.70	23307.4
HLA A*3101	1:27-35	9	AHASAAPVI	1.32	0.37	-4.39	1.69	-2.70	24525.1
HLA A*3201	1:27-35	9	AHASAAPVI	1.32	0.37	-4.39	1.69	-2.70	24539.4
HLA B*5801	1:92-100	9	AAAATYGVV	1.09	0.30	-4.09	1.39	-2.70	12309.4
HLA A*6901	1:31-39	9	AAPVITAVV	1.00	0.24	-3.94	1.24	-2.70	8776.1
HLA A*2301	1:40-48	9	PPAADPVSL	1.65	0.10	-4.46	1.76	-2.70	28676.6
HLA A*2403	1:79-87	9	VGESGASYL	1.43	0.25	-4.38	1.68	-2.70	24135.5
HLA A*0101	1:27-35	9	AHASAAPVI	1.32	0.37	-4.39	1.69	-2.70	24628.7
HLA B*0702	1:66-74	9	AEGVEELGR	1.14	0.58	-4.43	1.72	-2.70	26631.5
HLA A*3201	1:29-37	9	ASAAPVITA	1.21	-0.15	-3.76	1.06	-2.70	5739.6
HLA B*1503	1:61-69	9	HAVVTAEGV	1.02	0.08	-3.80	1.10	-2.70	6336.7
HLA B*0803	1:79-87	9	VGESGASYL	1.43	0.25	-4.38	1.68	-2.70	24226.2
HLA A*6802	1:27-35	9	AHASAAPVI	1.32	0.37	-4.39	1.69	-2.70	24743.7
HLA A*2403	1:66-74	9	AEGVEELGR	1.14	0.58	-4.43	1.72	-2.70	26741.0
HLA A*3201	1:55-63	9	SAQGVEHAV	1.10	0.12	-3.92	1.22	-2.70	8368.5
HLA A*1101	1:40-48	9	PPAADPVSL	1.65	0.10	-4.46	1.76	-2.70	28877.4
HLA B*7301	1:3-11	9	LRVVPEGLA	1.05	-0.10	-3.65	0.95	-2.70	4511.2
HLA A*0211	1:40-48	9	PPAADPVSL	1.65	0.10	-4.46	1.76	-2.71	28937.5
HLA B*5101	1:79-87	9	VGESGASYL	1.43	0.25	-4.39	1.68	-2.71	24367.7
HLA A*3002	1:92-100	9	AAAATYGVV	1.09	0.30	-4.10	1.39	-2.71	12477.0
HLA A*8001	1:27-35	9	AHASAAPVI	1.32	0.37	-4.40	1.69	-2.71	24966.5
HLA B*0702	1:86-94	9	YLAGDAAAA	1.33	-0.20	-3.84	1.13	-2.71	6844.1
HLA A*6901	1:29-37	9	ASAAPVITA	1.21	-0.15	-3.76	1.06	-2.71	5817.5
HLA A*6802	1:79-87	9	VGESGASYL	1.43	0.25	-4.39	1.68	-2.71	24504.6
HLA A*3001	1:11-19	9	AAASAAVEA	1.20	-0.12	-3.79	1.08	-2.71	6152.9
HLA B*1517	1:84-92	9	ASYLAGDAA	1.27	-0.08	-3.90	1.19	-2.71	7960.5
HLA A*0250	1:4-12	9	RVVPEGLAA	1.27	-0.01	-3.97	1.26	-2.71	9345.3
HLA B*4001	1:15-23	9	AAVEALTAR	0.88	0.79	-4.38	1.67	-2.71	23938.8
HLA A*0201	1:15-23	9	AAVEALTAR	0.88	0.79	-4.38	1.67	-2.71	24004.8
HLA B*0801	1:66-74	9	AEGVEELGR	1.14	0.58	-4.44	1.72	-2.71	27340.9
HLA A*0101	1:15-23	9	AAVEALTAR	0.88	0.79	-4.38	1.67	-2.71	24096.8
HLA B*0803	1:27-35	9	AHASAAPVI	1.32	0.37	-4.40	1.69	-2.71	25377.9
HLA B*0801	1:15-23	9	AAVEALTAR	0.88	0.79	-4.39	1.67	-2.72	24452.2
HLA B*0802	1:79-87	9	VGESGASYL	1.43	0.25	-4.40	1.68	-2.72	25206.6
HLA B*1501	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-3.50	0.77	-2.72	3128.9
HLA A*6802	1:66-74	9	AEGVEELGR	1.14	0.58	-4.45	1.72	-2.72	27865.4
HLA A*0202	1:87-95	9	LAGDAAAAA	1.17	-0.30	-3.60	0.87	-2.72	3937.1
HLA B*7301	1:27-35	9	AHASAAPVI	1.32	0.37	-4.41	1.69	-2.72	25821.4
HLA A*0203	1:66-74	9	AEGVEELGR	1.14	0.58	-4.45	1.72	-2.72	27911.6
HLA A*1101	1:66-74	9	AEGVEELGR	1.14	0.58	-4.45	1.72	-2.72	28025.7

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*0216	1:66-74	9	AEGVEELGR	1.14	0.58	-4.45	1.72	-2.72	28044.3
HLA A*2501	1:27-35	9	AHASAAPVI	1.32	0.37	-4.41	1.69	-2.72	25956.5
HLA A*3201	1:40-48	9	PPAADPVSL	1.65	0.10	-4.48	1.76	-2.73	30345.6
HLA B*2705	1:66-74	9	AEGVEELGR	1.14	0.58	-4.45	1.72	-2.73	28166.3
HLA A*0219	1:66-74	9	AEGVEELGR	1.14	0.58	-4.45	1.72	-2.73	28179.9
HLA A*0202	1:84-92	9	ASYLAGDAA	1.27	-0.08	-3.92	1.19	-2.73	8281.6
HLA A*0250	1:87-95	9	LAGDAAAAA	1.17	-0.30	-3.60	0.87	-2.73	3983.7
HLA B*5701	1:79-87	9	VGESGASYL	1.43	0.25	-4.41	1.68	-2.73	25659.8
HLA B*4402	1:79-87	9	VGESGASYL	1.43	0.25	-4.41	1.68	-2.73	25716.5
HLA B*7301	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.58	1.85	-2.73	37791.7
HLA A*3002	1:91-99	9	AAAAATYGV	1.05	0.17	-3.95	1.22	-2.73	8834.7
HLA B*4403	1:27-35	9	AHASAAPVI	1.32	0.37	-4.42	1.69	-2.73	26377.4
HLA A*3001	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.01	1.28	-2.73	10239.2
HLA A*2902	1:66-74	9	AEGVEELGR	1.14	0.58	-4.46	1.72	-2.73	28565.9
HLA B*3501	1:66-74	9	AEGVEELGR	1.14	0.58	-4.46	1.72	-2.73	28625.0
HLA B*5701	1:15-23	9	AAVEALTAR	0.88	0.79	-4.40	1.67	-2.73	25202.3
HLA B*1502	1:40-48	9	PPAADPVSL	1.65	0.10	-4.49	1.76	-2.73	30884.1
HLA B*1517	1:21-29	9	TARLAAAHA	1.27	-0.18	-3.83	1.09	-2.73	6694.1
HLA B*2705	1:79-87	9	VGESGASYL	1.43	0.25	-4.41	1.68	-2.73	25994.5
HLA A*0212	1:92-100	9	AAAATYGVV	1.09	0.30	-4.12	1.39	-2.73	13292.3
HLA B*5301	1:27-35	9	AHASAAPVI	1.32	0.37	-4.42	1.69	-2.73	26557.6
HLA B*3901	1:15-23	9	AAVEALTAR	0.88	0.79	-4.40	1.67	-2.74	25361.3
HLA A*6901	1:23-31	9	RLAAAHASA	1.16	-0.04	-3.85	1.11	-2.74	7107.7
HLA A*1101	1:79-87	9	VGESGASYL	1.43	0.25	-4.42	1.68	-2.74	26242.9
HLA A*0212	1:15-23	9	AAVEALTAR	0.88	0.79	-4.41	1.67	-2.74	25668.9
HLA B*0802	1:15-23	9	AAVEALTAR	0.88	0.79	-4.41	1.67	-2.74	25694.9
HLA B*0802	1:27-35	9	AHASAAPVI	1.32	0.37	-4.43	1.69	-2.74	27027.5
HLA B*3901	1:86-94	9	YLAGDAAAA	1.33	-0.20	-3.87	1.13	-2.74	7404.6
HLA A*0216	1:85-93	9	SYLAGDAAA	1.15	-0.02	-3.88	1.13	-2.74	7536.2
HLA B*0702	1:15-23	9	AAVEALTAR	0.88	0.79	-4.41	1.67	-2.74	25730.0
HLA A*6801	1:66-74	9	AEGVEELGR	1.14	0.58	-4.47	1.72	-2.74	29279.8
HLA A*1101	1:27-35	9	AHASAAPVI	1.32	0.37	-4.43	1.69	-2.74	27104.6
HLA A*0219	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.05	1.30	-2.74	11135.3
HLA B*3901	1:91-99	9	AAAAATYGV	1.05	0.17	-3.96	1.22	-2.75	9171.1
HLA A*3201	1:31-39	9	AAPVITAVV	1.00	0.24	-3.99	1.24	-2.75	9753.0
HLA B*5101	1:92-100	9	AAAATYGVV	1.09	0.30	-4.14	1.39	-2.75	13731.6
HLA B*0803	1:66-74	9	AEGVEELGR	1.14	0.58	-4.47	1.72	-2.75	29668.1
HLA B*1517	1:66-74	9	AEGVEELGR	1.14	0.58	-4.47	1.72	-2.75	29710.2
HLA A*0250	1:40-48	9	PPAADPVSL	1.65	0.10	-4.51	1.76	-2.75	32090.1
HLA B*4403	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.60	1.85	-2.75	39652.8
HLA B*5301	1:79-87	9	VGESGASYL	1.43	0.25	-4.43	1.68	-2.75	27018.1
HLA B*1801	1:79-87	9	VGESGASYL	1.43	0.25	-4.43	1.68	-2.75	27025.7
HLA A*0216	1:15-23	9	AAVEALTAR	0.88	0.79	-4.42	1.67	-2.75	26254.4
HLA A*2403	1:15-23	9	AAVEALTAR	0.88	0.79	-4.42	1.67	-2.75	26296.1
HLA A*0250	1:27-35	9	AHASAAPVI	1.32	0.37	-4.44	1.69	-2.75	27801.6
HLA A*0301	1:23-31	9	RLAAAHASA	1.16	-0.04	-3.87	1.11	-2.75	7405.9
HLA B*5401	1:48-56	9	LQTAAGFSA	1.01	-0.19	-3.57	0.82	-2.76	3754.2
HLA A*6901	1:34-42	9	VITAVVPPA	1.03	-0.23	-3.57	0.81	-2.76	3672.8
HLA B*5401	1:15-23	9	AAVEALTAR	0.88	0.79	-4.43	1.67	-2.76	26729.7

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*3501	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.02	1.26	-2.76	10472.0
HLA B*1801	1:66-74	9	AEGVEELGR	1.14	0.58	-4.48	1.72	-2.76	30529.2
HLA A*2501	1:66-74	9	AEGVEELGR	1.14	0.58	-4.49	1.72	-2.76	30578.6
HLA A*2301	1:79-87	9	VGESGASYL	1.43	0.25	-4.44	1.68	-2.76	27843.4
HLA A*0212	1:26-34	9	AAHASAAPV	0.61	0.30	-3.68	0.91	-2.76	4746.5
HLA A*0203	1:84-92	9	ASYLAGDAA	1.27	-0.08	-3.96	1.19	-2.76	9031.4
HLA A*0211	1:15-23	9	AAVEALTAR	0.88	0.79	-4.43	1.67	-2.76	27068.9
HLA A*2902	1:15-23	9	AAVEALTAR	0.88	0.79	-4.43	1.67	-2.76	27091.7
HLA A*0219	1:15-23	9	AAVEALTAR	0.88	0.79	-4.43	1.67	-2.77	27195.0
HLA A*2602	1:20-28	9	LTARLAAAH	1.06	-0.16	-3.66	0.89	-2.77	4550.5
HLA A*0212	1:31-39	9	AAPVITAVV	1.00	0.24	-4.01	1.24	-2.77	10207.6
HLA B*3901	1:66-74	9	AEGVEELGR	1.14	0.58	-4.49	1.72	-2.77	30941.9
HLA B*1509	1:66-74	9	AEGVEELGR	1.14	0.58	-4.49	1.72	-2.77	30953.8
HLA A*0219	1:92-100	9	AAAATYGVV	1.09	0.30	-4.16	1.39	-2.77	14383.5
HLA A*0202	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.03	1.26	-2.77	10692.6
HLA A*3001	1:31-39	9	AAPVITAVV	1.00	0.24	-4.01	1.24	-2.77	10261.8
HLA B*5401	1:92-100	9	AAAATYGVV	1.09	0.30	-4.16	1.39	-2.77	14419.2
HLA B*1801	1:27-35	9	AHASAAPVI	1.32	0.37	-4.46	1.69	-2.77	29148.8
HLA B*4501	1:64-72	9	VTAEGVEEL	1.39	0.46	-4.62	1.85	-2.78	42044.2
HLA B*5101	1:15-23	9	AAVEALTAR	0.88	0.79	-4.45	1.67	-2.78	27864.8
HLA B*1501	1:25-33	9	AAAHASAAP	0.72	0.16	-3.66	0.88	-2.78	4535.3
HLA B*5401	1:84-92	9	ASYLAGDAA	1.27	-0.08	-3.97	1.19	-2.78	9388.3
HLA A*8001	1:15-23	9	AAVEALTAR	0.88	0.79	-4.45	1.67	-2.78	28198.9
HLA B*4501	1:91-99	9	AAAAATYGV	1.05	0.17	-4.00	1.22	-2.78	9991.3
HLA A*0219	1:34-42	9	VITAVVPPA	1.03	-0.23	-3.59	0.81	-2.78	3885.9
HLA A*0203	1:87-95	9	LAGDAAAAA	1.17	-0.30	-3.66	0.87	-2.78	4536.4
HLA B*3501	1:92-100	9	AAAATYGVV	1.09	0.30	-4.18	1.39	-2.79	14990.6
HLA A*2602	1:5-13	9	VVPEGLAAA	1.10	-0.09	-3.80	1.01	-2.79	6260.6
HLA B*4002	1:27-35	9	AHASAAPVI	1.32	0.37	-4.48	1.69	-2.79	30043.8
HLA A*0216	1:26-34	9	AAHASAAPV	0.61	0.30	-3.70	0.91	-2.79	5021.2
HLA A*0250	1:11-19	9	AAASAAVEA	1.20	-0.12	-3.87	1.08	-2.79	7422.9
HLA B*0702	1:11-19	9	AAASAAVEA	1.20	-0.12	-3.87	1.08	-2.79	7423.4
HLA A*3002	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-3.57	0.77	-2.79	3682.9
HLA B*4601	1:31-39	9	AAPVITAVV	1.00	0.24	-4.04	1.24	-2.79	10849.5
HLA A*2501	1:79-87	9	VGESGASYL	1.43	0.25	-4.47	1.68	-2.79	29848.5
HLA B*5101	1:66-74	9	AEGVEELGR	1.14	0.58	-4.52	1.72	-2.79	32911.5
HLA A*3002	1:40-48	9	PPAADPVSL	1.65	0.10	-4.55	1.76	-2.80	35616.8
HLA A*0212	1:58-66	9	GVEHAVVTA	1.37	-0.33	-3.84	1.04	-2.80	6864.3
HLA B*1503	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.02	1.22	-2.80	10408.6
HLA A*0202	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.08	1.28	-2.80	11911.9
HLA B*5401	1:27-35	9	AHASAAPVI	1.32	0.37	-4.49	1.69	-2.80	30915.6
HLA A*2603	1:40-48	9	PPAADPVSL	1.65	0.10	-4.56	1.76	-2.80	36041.9
HLA A*3001	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.02	1.22	-2.80	10504.7
HLA A*3001	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.10	1.30	-2.80	12714.1
HLA B*4501	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.03	1.22	-2.81	10621.7
HLA B*1503	1:31-39	9	AAPVITAVV	1.00	0.24	-4.05	1.24	-2.81	11171.7
HLA A*3101	1:30-38	9	SAAPVITAV	0.96	0.26	-4.02	1.21	-2.81	10469.9
HLA B*0803	1:15-23	9	AAVEALTAR	0.88	0.79	-4.48	1.67	-2.81	29915.5
HLA A*6901	1:24-32	9	LAAAHASAA	0.90	-0.14	-3.56	0.75	-2.81	3669.7

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*0206	1:66-74	9	AEGVEELGR	1.14	0.58	-4.53	1.72	-2.81	34243.9
HLA B*3801	1:66-74	9	AEGVEELGR	1.14	0.58	-4.53	1.72	-2.81	34261.2
HLA A*0211	1:85-93	9	SYLAGDAAA	1.15	-0.02	-3.95	1.13	-2.81	8849.2
HLA A*2301	1:66-74	9	AEGVEELGR	1.14	0.58	-4.54	1.72	-2.81	34521.6
HLA A*2402	1:79-87	9	VGESGASYL	1.43	0.25	-4.50	1.68	-2.82	31389.5
HLA A*3001	1:34-42	9	VITAVVPPA	1.03	-0.23	-3.62	0.81	-2.82	4192.2
HLA A*3201	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.08	1.26	-2.82	11944.2
HLA A*2603	1:15-23	9	AAVEALTAR	0.88	0.79	-4.49	1.67	-2.82	30644.1
HLA A*3301	1:66-74	9	AEGVEELGR	1.14	0.58	-4.54	1.72	-2.82	34822.5
HLA A*3101	1:92-100	9	AAAATYGVV	1.09	0.30	-4.21	1.39	-2.82	16163.3
HLA A*2902	1:86-94	9	YLAGDAAAA	1.33	-0.20	-3.95	1.13	-2.82	8844.3
HLA A*0211	1:66-74	9	AEGVEELGR	1.14	0.58	-4.54	1.72	-2.82	34973.0
HLA B*5801	1:20-28	9	LTARLAAAH	1.06	-0.16	-3.71	0.89	-2.82	5163.3
HLA B*0702	1:9-17	9	GLAAASAAV	1.01	0.00	-3.83	1.01	-2.82	6818.8
HLA A*2602	1:27-35	9	AHASAAPVI	1.32	0.37	-4.52	1.69	-2.83	33068.0
HLA B*0801	1:92-100	9	AAAATYGVV	1.09	0.30	-4.22	1.39	-2.83	16567.9
HLA B*5401	1:3-11	9	LRVVPEGLA	1.05	-0.10	-3.78	0.95	-2.83	6022.6
HLA B*0702	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.05	1.22	-2.83	11207.1
HLA B*0801	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.11	1.28	-2.83	12866.5
HLA A*3001	1:19-27	9	ALTARLAAA	1.01	-0.25	-3.59	0.76	-2.83	3918.2
HLA B*3801	1:15-23	9	AAVEALTAR	0.88	0.79	-4.50	1.67	-2.83	31743.2
HLA A*0250	1:15-23	9	AAVEALTAR	0.88	0.79	-4.50	1.67	-2.84	31886.8
HLA B*1801	1:17-25	9	VEALTARLA	1.29	-0.19	-3.94	1.10	-2.84	8668.7
HLA A*6802	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.12	1.28	-2.84	13095.4
HLA B*1502	1:27-35	9	AHASAAPVI	1.32	0.37	-4.53	1.69	-2.84	33787.4
HLA B*1503	1:25-33	9	AAAHASAAP	0.72	0.16	-3.72	0.88	-2.84	5193.2
HLA A*6802	1:21-29	9	TARLAAAHA	1.27	-0.18	-3.93	1.09	-2.84	8547.7
HLA A*2403	1:92-100	9	AAAATYGVV	1.09	0.30	-4.23	1.39	-2.84	16970.2
HLA B*4002	1:17-25	9	VEALTARLA	1.29	-0.19	-3.94	1.10	-2.84	8801.0
HLA B*3501	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.04	1.19	-2.85	10880.3
HLA B*5401	1:66-74	9	AEGVEELGR	1.14	0.58	-4.57	1.72	-2.85	37212.2
HLA B*1509	1:15-23	9	AAVEALTAR	0.88	0.79	-4.52	1.67	-2.85	32801.7
HLA B*4601	1:92-100	9	AAAATYGVV	1.09	0.30	-4.24	1.39	-2.85	17327.4
HLA B*1503	1:18-26	9	EALTARLAA	1.39	-0.27	-3.97	1.12	-2.85	9324.1
HLA B*4501	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.07	1.22	-2.85	11732.7
HLA B*7301	1:40-48	9	PPAADPVSL	1.65	0.10	-4.61	1.76	-2.85	40496.3
HLA A*6901	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.11	1.26	-2.85	12985.0
HLA A*3002	1:85-93	9	SYLAGDAAA	1.15	-0.02	-3.99	1.13	-2.85	9736.3
HLA A*3002	1:15-23	9	AAVEALTAR	0.88	0.79	-4.52	1.67	-2.85	33279.6
HLA B*5801	1:91-99	9	AAAAATYGV	1.05	0.17	-4.07	1.22	-2.85	11767.5
HLA A*0211	1:54-62	9	FSAQGVEHA	1.07	-0.26	-3.67	0.81	-2.86	4659.2
HLA A*2402	1:66-74	9	AEGVEELGR	1.14	0.58	-4.58	1.72	-2.86	38175.3
HLA A*3002	1:66-74	9	AEGVEELGR	1.14	0.58	-4.58	1.72	-2.86	38308.7
HLA A*0216	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.14	1.28	-2.86	13798.1
HLA A*2301	1:15-23	9	AAVEALTAR	0.88	0.79	-4.53	1.67	-2.86	33913.0
HLA A*0212	1:34-42	9	VITAVVPPA	1.03	-0.23	-3.67	0.81	-2.86	4666.8
HLA A*3201	1:15-23	9	AAVEALTAR	0.88	0.79	-4.53	1.67	-2.86	34027.7
HLA B*1501	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.14	1.28	-2.86	13878.3
HLA A*3002	1:23-31	9	RLAAAHASA	1.16	-0.04	-3.98	1.11	-2.87	9580.3

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*0202	1:35-43	9	ITAVVPPAA	1.01	-0.20	-3.67	0.81	-2.87	4697.3
HLA B*5401	1:79-87	9	VGESGASYL	1.43	0.25	-4.55	1.68	-2.87	35349.4
HLA A*0202	1:66-74	9	AEGVEELGR	1.14	0.58	-4.59	1.72	-2.87	38993.5
HLA B*7301	1:66-74	9	AEGVEELGR	1.14	0.58	-4.59	1.72	-2.87	39014.8
HLA A*0250	1:66-74	9	AEGVEELGR	1.14	0.58	-4.59	1.72	-2.87	39120.9
HLA A*0201	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.13	1.26	-2.87	13466.4
HLA A*3001	1:18-26	9	EALTARLAA	1.39	-0.27	-3.99	1.12	-2.87	9793.6
HLA A*2601	1:30-38	9	SAAPVITAV	0.96	0.26	-4.08	1.21	-2.87	12149.2
HLA B*1509	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.17	1.30	-2.87	14910.9
HLA A*3001	1:58-66	9	GVEHAVVTA	1.37	-0.33	-3.91	1.04	-2.87	8151.0
HLA B*3901	1:22-30	9	ARLAAAHAS	1.08	-0.81	-3.14	0.27	-2.87	1390.8
HLA A*3301	1:40-48	9	PPAADPVSL	1.65	0.10	-4.63	1.76	-2.87	42629.7
HLA A*2602	1:79-87	9	VGESGASYL	1.43	0.25	-4.56	1.68	-2.88	36098.7
HLA A*0212	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.14	1.26	-2.88	13725.8
HLA A*0201	1:29-37	9	ASAAPVITA	1.21	-0.15	-3.93	1.06	-2.88	8595.2
HLA A*0216	1:48-56	9	LQTAAGFSA	1.01	-0.19	-3.70	0.82	-2.88	4976.3
HLA B*5301	1:15-23	9	AAVEALTAR	0.88	0.79	-4.55	1.67	-2.88	35177.7
HLA B*5301	1:66-74	9	AEGVEELGR	1.14	0.58	-4.60	1.72	-2.88	40017.8
HLA B*4002	1:43-51	9	ADPVSLQTA	1.35	-0.24	-3.98	1.11	-2.88	9644.8
HLA B*1503	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.01	1.13	-2.88	10151.9
HLA B*4002	1:40-48	9	PPAADPVSL	1.65	0.10	-4.64	1.76	-2.88	43283.8
HLA B*4501	1:15-23	9	AAVEALTAR	0.88	0.79	-4.55	1.67	-2.88	35370.3
HLA A*6801	1:30-38	9	SAAPVITAV	0.96	0.26	-4.09	1.21	-2.88	12433.5
HLA A*0211	1:87-95	9	LAGDAAAAA	1.17	-0.30	-3.76	0.87	-2.88	5688.8
HLA A*0202	1:58-66	9	GVEHAVVTA	1.37	-0.33	-3.92	1.04	-2.88	8369.6
HLA A*0250	1:58-66	9	GVEHAVVTA	1.37	-0.33	-3.93	1.04	-2.89	8438.4
HLA A*2602	1:66-74	9	AEGVEELGR	1.14	0.58	-4.61	1.72	-2.89	40710.7
HLA A*2601	1:92-100	9	AAAATYGVV	1.09	0.30	-4.28	1.39	-2.89	18912.8
HLA B*4001	1:92-100	9	AAAATYGVV	1.09	0.30	-4.28	1.39	-2.89	18978.8
HLA B*4403	1:15-23	9	AAVEALTAR	0.88	0.79	-4.56	1.67	-2.89	36124.1
HLA A*2603	1:66-74	9	AEGVEELGR	1.14	0.58	-4.61	1.72	-2.89	41045.7
HLA A*3201	1:66-74	9	AEGVEELGR	1.14	0.58	-4.61	1.72	-2.89	41053.7
HLA A*0201	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.11	1.22	-2.89	12902.5
HLA B*1502	1:15-23	9	AAVEALTAR	0.88	0.79	-4.56	1.67	-2.89	36188.6
HLA B*1502	1:66-74	9	AEGVEELGR	1.14	0.58	-4.62	1.72	-2.89	41226.2
HLA A*0216	1:61-69	9	HAVVTAEGV	1.02	0.08	-3.99	1.10	-2.89	9826.1
HLA A*3002	1:31-39	9	AAPVITAVV	1.00	0.24	-4.14	1.24	-2.89	13684.9
HLA B*5101	1:31-39	9	AAPVITAVV	1.00	0.24	-4.14	1.24	-2.90	13714.9
HLA B*4501	1:40-48	9	PPAADPVSL	1.65	0.10	-4.65	1.76	-2.90	44975.6
HLA A*3201	1:79-87	9	VGESGASYL	1.43	0.25	-4.58	1.68	-2.90	37848.7
HLA B*2705	1:3-11	9	LRVVPEGLA	1.05	-0.10	-3.85	0.95	-2.90	7028.7
HLA A*3001	1:9-17	9	GLAAASAAV	1.01	0.00	-3.91	1.01	-2.90	8103.3
HLA A*2902	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.16	1.26	-2.90	14390.7
HLA A*2603	1:79-87	9	VGESGASYL	1.43	0.25	-4.58	1.68	-2.90	37971.6
HLA A*6901	1:8-16	9	EGLAAASAA	0.96	-0.49	-3.36	0.46	-2.90	2305.1
HLA A*2402	1:15-23	9	AAVEALTAR	0.88	0.79	-4.57	1.67	-2.90	36922.9
HLA A*0219	1:19-27	9	ALTARLAAA	1.01	-0.25	-3.66	0.76	-2.90	4596.4
HLA B*4403	1:40-48	9	PPAADPVSL	1.65	0.10	-4.66	1.76	-2.90	45503.9
HLA B*3501	1:25-33	9	AAAHASAAP	0.72	0.16	-3.78	0.88	-2.90	6008.2

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*5801	1:54-62	9	FSAQGVEHA	1.07	-0.26	-3.71	0.81	-2.90	5186.1
HLA A*3001	1:30-38	9	SAAPVITAV	0.96	0.26	-4.12	1.21	-2.90	13091.2
HLA B*1502	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.04	1.13	-2.90	10926.5
HLA A*6801	1:40-48	9	PPAADPVSL	1.65	0.10	-4.66	1.76	-2.90	45718.9
HLA B*5801	1:30-38	9	SAAPVITAV	0.96	0.26	-4.12	1.21	-2.90	13123.2
HLA B*3501	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.00	1.10	-2.91	10099.9
HLA A*6802	1:28-36	9	HASAAPVIT	1.18	-0.26	-3.83	0.92	-2.91	6684.1
HLA B*4002	1:15-23	9	AAVEALTAR	0.88	0.79	-4.58	1.67	-2.91	37741.2
HLA B*1501	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.00	1.09	-2.91	10026.0
HLA A*3001	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.13	1.22	-2.91	13435.0
HLA B*5401	1:18-26	9	EALTARLAA	1.39	-0.27	-4.03	1.12	-2.91	10761.2
HLA A*0206	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-3.69	0.77	-2.91	4856.7
HLA B*4002	1:69-77	9	VEELGRAGV	1.03	0.03	-3.97	1.06	-2.91	9339.2
HLA A*3201	1:30-38	9	SAAPVITAV	0.96	0.26	-4.13	1.21	-2.91	13421.9
HLA A*0216	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.18	1.26	-2.92	14966.8
HLA B*1501	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.14	1.22	-2.92	13679.4
HLA A*6802	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.11	1.19	-2.92	12806.5
HLA B*0702	1:31-39	9	AAPVITAVV	1.00	0.24	-4.16	1.24	-2.92	14461.7
HLA A*0201	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.00	1.08	-2.92	9994.8
HLA B*4001	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.22	1.30	-2.92	16668.9
HLA B*0801	1:30-38	9	SAAPVITAV	0.96	0.26	-4.13	1.21	-2.92	13612.2
HLA A*6801	1:79-87	9	VGESGASYL	1.43	0.25	-4.60	1.68	-2.92	39986.7
HLA A*0219	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.02	1.10	-2.92	10490.4
HLA B*1501	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.00	1.08	-2.92	10063.3
HLA A*0101	1:92-100	9	AAAATYGVV	1.09	0.30	-4.31	1.39	-2.92	20498.4
HLA B*0801	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.05	1.13	-2.92	11209.9
HLA B*1801	1:80-88	9	GESGASYLA	1.31	-0.35	-3.88	0.96	-2.92	7599.6
HLA A*0211	1:48-56	9	LQTAAGFSA	1.01	-0.19	-3.74	0.82	-2.92	5524.4
HLA B*1503	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.20	1.28	-2.92	15960.8
HLA A*0202	1:13-21	9	ASAAVEALT	0.86	-0.15	-3.63	0.70	-2.93	4270.1
HLA A*3002	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.23	1.30	-2.93	16931.4
HLA B*7301	1:79-87	9	VGESGASYL	1.43	0.25	-4.61	1.68	-2.93	40732.3
HLA A*6802	1:87-95	9	LAGDAAAAA	1.17	-0.30	-3.80	0.87	-2.93	6353.4
HLA B*1501	1:31-39	9	AAPVITAVV	1.00	0.24	-4.17	1.24	-2.93	14867.2
HLA A*3301	1:79-87	9	VGESGASYL	1.43	0.25	-4.62	1.68	-2.94	41606.2
HLA B*7301	1:15-23	9	AAVEALTAR	0.88	0.79	-4.61	1.67	-2.94	40528.7
HLA A*0212	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.07	1.13	-2.94	11882.8
HLA A*0216	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.02	1.08	-2.94	10546.4
HLA A*3201	1:9-17	9	GLAAASAAV	1.01	0.00	-3.95	1.01	-2.94	8985.2
HLA A*2603	1:27-35	9	AHASAAPVI	1.32	0.37	-4.63	1.69	-2.94	42912.6
HLA A*3101	1:31-39	9	AAPVITAVV	1.00	0.24	-4.19	1.24	-2.95	15397.1
HLA B*4002	1:79-87	9	VGESGASYL	1.43	0.25	-4.63	1.68	-2.95	42382.5
HLA B*5401	1:30-38	9	SAAPVITAV	0.96	0.26	-4.16	1.21	-2.95	14557.1
HLA A*0301	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.21	1.26	-2.95	16202.1
HLA B*3501	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.08	1.13	-2.95	12143.5
HLA B*3501	1:31-39	9	AAPVITAVV	1.00	0.24	-4.19	1.24	-2.95	15558.7
HLA B*5101	1:30-38	9	SAAPVITAV	0.96	0.26	-4.16	1.21	-2.95	14585.8
HLA B*4403	1:79-87	9	VGESGASYL	1.43	0.25	-4.63	1.68	-2.95	42893.8
HLA A*0206	1:69-77	9	VEELGRAGV	1.03	0.03	-4.01	1.06	-2.95	10217.5

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*3301	1:27-35	9	AHASAAPVI	1.32	0.37	-4.64	1.69	-2.95	43969.7
HLA A*3001	1:28-36	9	HASAAPVIT	1.18	-0.26	-3.87	0.92	-2.95	7472.1
HLA A*6801	1:27-35	9	AHASAAPVI	1.32	0.37	-4.65	1.69	-2.96	44177.1
HLA A*0301	1:92-100	9	AAAATYGVV	1.09	0.30	-4.35	1.39	-2.96	22144.7
HLA A*0216	1:35-43	9	ITAVVPPAA	1.01	-0.20	-3.76	0.81	-2.96	5770.8
HLA B*3501	1:38-46	9	VVPPAADPV	0.76	0.28	-4.00	1.04	-2.96	10006.5
HLA B*1509	1:92-100	9	AAAATYGVV	1.09	0.30	-4.35	1.39	-2.96	22298.8
HLA A*0212	1:48-56	9	LQTAAGFSA	1.01	-0.19	-3.78	0.82	-2.96	6007.5
HLA B*5701	1:92-100	9	AAAATYGVV	1.09	0.30	-4.35	1.39	-2.96	22511.0
HLA B*1517	1:31-39	9	AAPVITAVV	1.00	0.24	-4.20	1.24	-2.96	16031.6
HLA B*0801	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.18	1.22	-2.96	15207.4
HLA B*5801	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.24	1.28	-2.96	17507.7
HLA A*3101	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.27	1.30	-2.97	18555.9
HLA B*4501	1:79-87	9	VGESGASYL	1.43	0.25	-4.65	1.68	-2.97	44439.6
HLA B*5401	1:35-43	9	ITAVVPPAA	1.01	-0.20	-3.77	0.81	-2.97	5935.4
HLA A*3101	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.08	1.11	-2.97	12115.8
HLA A*6802	1:50-58	9	TAAGFSAQG	0.80	-0.61	-3.16	0.19	-2.97	1447.0
HLA A*2403	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.27	1.30	-2.97	18760.1
HLA A*0203	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.06	1.09	-2.97	11561.4
HLA B*5401	1:91-99	9	AAAAATYGV	1.05	0.17	-4.19	1.22	-2.97	15387.3
HLA A*3101	1:20-28	9	LTARLAAAH	1.06	-0.16	-3.86	0.89	-2.97	7292.6
HLA A*1101	1:92-100	9	AAAATYGVV	1.09	0.30	-4.36	1.39	-2.97	22999.3
HLA A*0201	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.25	1.28	-2.97	17809.1
HLA B*4001	1:17-25	9	VEALTARLA	1.29	-0.19	-4.07	1.10	-2.97	11863.3
HLA A*2501	1:30-38	9	SAAPVITAV	0.96	0.26	-4.19	1.21	-2.97	15417.0
HLA A*2902	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.11	1.13	-2.97	12859.4
HLA A*2403	1:31-39	9	AAPVITAVV	1.00	0.24	-4.22	1.24	-2.98	16507.0
HLA A*0216	1:54-62	9	FSAQGVEHA	1.07	-0.26	-3.79	0.81	-2.98	6130.8
HLA B*1502	1:92-100	9	AAAATYGVV	1.09	0.30	-4.37	1.39	-2.98	23310.8
HLA A*2403	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.02	1.04	-2.98	10434.2
HLA A*2601	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-3.75	0.77	-2.98	5665.5
HLA B*5801	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.08	1.10	-2.98	12017.4
HLA B*4801	1:92-100	9	AAAATYGVV	1.09	0.30	-4.37	1.39	-2.98	23558.9
HLA B*2705	1:92-100	9	AAAATYGVV	1.09	0.30	-4.37	1.39	-2.98	23563.4
HLA A*3001	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.08	1.10	-2.98	12105.1
HLA A*0211	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.26	1.28	-2.98	18331.1
HLA A*8001	1:92-100	9	AAAATYGVV	1.09	0.30	-4.38	1.39	-2.99	23772.4
HLA A*0201	1:71-79	9	ELGRAGVGV	1.09	-0.09	-3.98	1.00	-2.99	9652.4
HLA A*2402	1:92-100	9	AAAATYGVV	1.09	0.30	-4.38	1.39	-2.99	23796.3
HLA B*5801	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.25	1.26	-2.99	17776.2
HLA B*4402	1:92-100	9	AAAATYGVV	1.09	0.30	-4.38	1.39	-2.99	23960.8
HLA A*0301	1:20-28	9	LTARLAAAH	1.06	-0.16	-3.88	0.89	-2.99	7612.2
HLA B*3901	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.09	1.10	-2.99	12348.8
HLA A*2902	1:92-100	9	AAAATYGVV	1.09	0.30	-4.38	1.39	-2.99	24116.6
HLA A*0216	1:76-84	9	GVGVGESGA	1.07	-0.25	-3.81	0.81	-2.99	6436.2
HLA A*2902	1:20-28	9	LTARLAAAH	1.06	-0.16	-3.89	0.89	-2.99	7679.4
HLA A*3002	1:30-38	9	SAAPVITAV	0.96	0.26	-4.21	1.21	-3.00	16170.8
HLA B*5101	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.10	1.10	-3.00	12446.0
HLA A*2603	1:71-79	9	ELGRAGVGV	1.09	-0.09	-3.99	1.00	-3.00	9859.4

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*0202	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.13	1.13	-3.00	13590.9
HLA B*0801	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.30	1.30	-3.00	20012.6
HLA A*1101	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.26	1.26	-3.00	18191.2
HLA A*0250	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.28	1.28	-3.00	19026.4
HLA A*0201	1:35-43	9	ITAVVPPAA	1.01	-0.20	-3.81	0.81	-3.00	6419.9
HLA A*6802	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.26	1.26	-3.00	18386.5
HLA B*3501	1:57-65	9	QGVEHAVVT	1.29	-0.32	-3.98	0.98	-3.00	9577.0
HLA B*4601	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.23	1.22	-3.01	16813.5
HLA A*2403	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.23	1.22	-3.01	16814.2
HLA B*1517	1:10-18	9	LAAASAAVE	1.14	-0.66	-3.49	0.48	-3.01	3094.4
HLA B*3501	1:32-40	9	APVITAVVP	0.92	0.08	-4.00	0.99	-3.01	10024.1
HLA B*0801	1:31-39	9	AAPVITAVV	1.00	0.24	-4.25	1.24	-3.01	17824.5
HLA A*3101	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.23	1.22	-3.01	16898.6
HLA A*1101	1:91-99	9	AAAAATYGV	1.05	0.17	-4.23	1.22	-3.01	16849.1
HLA B*4402	1:69-77	9	VEELGRAGV	1.03	0.03	-4.07	1.06	-3.01	11702.0
HLA B*1509	1:30-38	9	SAAPVITAV	0.96	0.26	-4.22	1.21	-3.01	16772.4
HLA B*1517	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.13	1.11	-3.01	13379.3
HLA B*4801	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.31	1.30	-3.01	20631.1
HLA A*6901	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.11	1.09	-3.01	12775.8
HLA B*3501	1:26-34	9	AAHASAAPV	0.61	0.30	-3.93	0.91	-3.01	8455.5
HLA B*1517	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.10	1.08	-3.02	12509.6
HLA B*4402	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.32	1.30	-3.02	20886.9
HLA A*2501	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.03	1.01	-3.02	10692.4
HLA A*3002	1:35-43	9	ITAVVPPAA	1.01	-0.20	-3.82	0.81	-3.02	6670.4
HLA A*6901	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.32	1.30	-3.02	21026.2
HLA A*6901	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.21	1.19	-3.02	16284.9
HLA A*3101	1:91-99	9	AAAAATYGV	1.05	0.17	-4.24	1.22	-3.02	17266.3
HLA B*1501	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.24	1.22	-3.02	17365.2
HLA A*2403	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.28	1.26	-3.02	19108.5
HLA B*1517	1:42-50	9	AADPVSLQT	1.20	-0.36	-3.87	0.84	-3.02	7337.6
HLA A*8001	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.28	1.26	-3.02	19219.0
HLA A*3002	1:9-17	9	GLAAASAAV	1.01	0.00	-4.04	1.01	-3.02	10841.9
HLA A*0211	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.11	1.08	-3.02	12758.7
HLA B*4501	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.30	1.28	-3.03	20120.1
HLA B*2705	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.33	1.30	-3.03	21267.9
HLA B*0702	1:18-26	9	EALTARLAA	1.39	-0.27	-4.15	1.12	-3.03	14087.0
HLA B*0802	1:92-100	9	AAAATYGVV	1.09	0.30	-4.42	1.39	-3.03	26281.2
HLA A*2902	1:91-99	9	AAAAATYGV	1.05	0.17	-4.25	1.22	-3.03	17652.7
HLA B*4501	1:70-78	9	EELGRAGVG	0.91	-0.72	-3.21	0.18	-3.03	1632.0
HLA A*0101	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.31	1.28	-3.03	20520.1
HLA A*0206	1:42-50	9	AADPVSLQT	1.20	-0.36	-3.88	0.84	-3.04	7599.3
HLA A*0201	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.14	1.10	-3.04	13714.4
HLA B*0803	1:92-100	9	AAAATYGVV	1.09	0.30	-4.43	1.39	-3.04	26776.0
HLA A*2501	1:92-100	9	AAAATYGVV	1.09	0.30	-4.43	1.39	-3.04	26948.3
HLA A*0211	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.08	1.04	-3.04	12053.6
HLA B*5301	1:92-100	9	AAAATYGVV	1.09	0.30	-4.43	1.39	-3.04	27051.8
HLA B*0702	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.23	1.19	-3.04	17139.3
HLA B*1502	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.35	1.30	-3.04	22173.0
HLA A*0206	1:18-26	9	EALTARLAA	1.39	-0.27	-4.16	1.12	-3.04	14587.1

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*2705	1:48-56	9	LQTAAGFSA	1.01	-0.19	-3.86	0.82	-3.05	7312.1
HLA B*4501	1:18-26	9	EALTARLAA	1.39	-0.27	-4.17	1.12	-3.05	14654.6
HLA A*0212	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.33	1.28	-3.05	21151.8
HLA B*1517	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-3.82	0.77	-3.05	6641.3
HLA B*4002	1:59-67	9	VEHAVVTAE	0.87	-0.71	-3.20	0.16	-3.05	1594.7
HLA B*1501	1:19-27	9	ALTARLAAA	1.01	-0.25	-3.81	0.76	-3.05	6453.4
HLA B*1517	1:24-32	9	LAAAHASAA	0.90	-0.14	-3.80	0.75	-3.05	6349.3
HLA B*5101	1:91-99	9	AAAAATYGV	1.05	0.17	-4.27	1.22	-3.05	18442.5
HLA B*5801	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.35	1.30	-3.05	22539.5
HLA A*0201	1:54-62	9	FSAQGVEHA	1.07	-0.26	-3.86	0.81	-3.05	7321.5
HLA B*5301	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.33	1.28	-3.06	21608.0
HLA A*0301	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.36	1.30	-3.06	22877.9
HLA A*0101	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.36	1.30	-3.06	22922.6
HLA B*2705	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.17	1.11	-3.06	14881.9
HLA A*0216	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.10	1.04	-3.06	12559.9
HLA B*4402	1:91-99	9	AAAAATYGV	1.05	0.17	-4.28	1.22	-3.06	18892.0
HLA A*2602	1:54-62	9	FSAQGVEHA	1.07	-0.26	-3.87	0.81	-3.06	7448.8
HLA B*5701	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.32	1.26	-3.06	20927.1
HLA A*2402	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.36	1.30	-3.06	23080.9
HLA A*3101	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.10	1.04	-3.06	12638.8
HLA B*1517	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.28	1.22	-3.06	19059.3
HLA B*4601	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.34	1.28	-3.06	21875.3
HLA B*5301	1:32-40	9	APVITAVVP	0.92	0.08	-4.05	0.99	-3.06	11344.9
HLA B*5701	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.34	1.28	-3.06	21897.2
HLA B*2705	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.32	1.26	-3.06	21020.8
HLA B*0801	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.32	1.26	-3.06	21104.3
HLA A*0301	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.34	1.28	-3.06	22042.0
HLA B*0801	1:91-99	9	AAAAATYGV	1.05	0.17	-4.28	1.22	-3.07	19124.0
HLA A*0219	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.34	1.28	-3.07	22093.9
HLA B*0702	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.35	1.28	-3.07	22147.7
HLA B*1503	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.29	1.22	-3.07	19318.5
HLA A*2902	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.35	1.28	-3.07	22188.1
HLA B*1801	1:92-100	9	AAAATYGVV	1.09	0.30	-4.46	1.39	-3.07	28707.5
HLA A*0211	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.26	1.19	-3.07	18210.9
HLA B*5801	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.29	1.22	-3.07	19405.5
HLA A*2602	1:92-100	9	AAAATYGVV	1.09	0.30	-4.46	1.39	-3.07	28785.5
HLA A*3201	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.11	1.04	-3.07	12884.9
HLA B*1503	1:54-62	9	FSAQGVEHA	1.07	-0.26	-3.88	0.81	-3.07	7622.5
HLA B*4001	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.29	1.22	-3.07	19462.1
HLA A*2602	1:62-70	9	AVVTAEGVE	1.05	-0.53	-3.59	0.52	-3.07	3902.5
HLA B*5401	1:31-39	9	AAPVITAVV	1.00	0.24	-4.32	1.24	-3.07	20704.7
HLA A*0219	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.33	1.26	-3.07	21587.2
HLA B*5701	1:91-99	9	AAAAATYGV	1.05	0.17	-4.29	1.22	-3.07	19517.6
HLA A*2403	1:30-38	9	SAAPVITAV	0.96	0.26	-4.29	1.21	-3.08	19464.5
HLA B*4001	1:91-99	9	AAAAATYGV	1.05	0.17	-4.29	1.22	-3.08	19594.8
HLA B*1501	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.09	1.01	-3.08	12194.5
HLA B*4501	1:48-56	9	LQTAAGFSA	1.01	-0.19	-3.90	0.82	-3.08	7859.5
HLA B*5401	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.16	1.08	-3.08	14365.2
HLA A*1101	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.13	1.06	-3.08	13611.9

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*1501	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.08	1.00	-3.08	11903.6
HLA A*8001	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.38	1.30	-3.08	24010.0
HLA A*1101	1:30-38	9	SAAPVITAV	0.96	0.26	-4.29	1.21	-3.08	19576.0
HLA B*5801	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.14	1.06	-3.08	13673.3
HLA B*4601	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.38	1.30	-3.08	24092.6
HLA A*0206	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.06	0.98	-3.08	11378.3
HLA A*1101	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.36	1.28	-3.08	22832.2
HLA B*1509	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.30	1.22	-3.08	19919.4
HLA B*0801	1:9-17	9	GLAAASAAV	1.01	0.00	-4.09	1.01	-3.08	12351.0
HLA B*4002	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.38	1.30	-3.08	24200.1
HLA B*0702	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.17	1.09	-3.08	14909.9
HLA A*3101	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.34	1.26	-3.08	21963.0
HLA A*2601	1:91-99	9	AAAAATYGV	1.05	0.17	-4.30	1.22	-3.08	19856.8
HLA B*5401	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.17	1.09	-3.08	14931.4
HLA B*3901	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.36	1.28	-3.08	22990.3
HLA A*2501	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.30	1.22	-3.08	20038.4
HLA A*2403	1:91-99	9	AAAAATYGV	1.05	0.17	-4.30	1.22	-3.08	19928.2
HLA A*8001	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.36	1.28	-3.08	23023.0
HLA A*0101	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.34	1.26	-3.08	22102.5
HLA B*0802	1:91-99	9	AAAAATYGV	1.05	0.17	-4.30	1.22	-3.08	19976.1
HLA A*3002	1:20-28	9	LTARLAAAH	1.06	-0.16	-3.98	0.89	-3.08	9466.4
HLA B*5401	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.21	1.13	-3.08	16304.1
HLA A*0211	1:42-50	9	AADPVSLQT	1.20	-0.36	-3.93	0.84	-3.09	8510.1
HLA A*6901	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.22	1.13	-3.09	16688.2
HLA A*2601	1:31-39	9	AAPVITAVV	1.00	0.24	-4.33	1.24	-3.09	21382.6
HLA A*1101	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.28	1.19	-3.09	19100.2
HLA B*1502	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.31	1.22	-3.09	20348.0
HLA B*5701	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.39	1.30	-3.09	24687.1
HLA B*4801	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.35	1.26	-3.09	22399.1
HLA B*5401	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.31	1.22	-3.09	20377.4
HLA A*3201	1:38-46	9	VVPPAADPV	0.76	0.28	-4.13	1.04	-3.09	13591.4
HLA B*0801	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.18	1.09	-3.09	15259.8
HLA A*1101	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.31	1.22	-3.09	20434.4
HLA B*1502	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.09	1.00	-3.09	12306.7
HLA A*2601	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.40	1.30	-3.09	24852.2
HLA A*2301	1:92-100	9	AAAATYGVV	1.09	0.30	-4.48	1.39	-3.09	30399.7
HLA A*3001	1:25-33	9	AAAHASAAP	0.72	0.16	-3.97	0.88	-3.09	9323.7
HLA B*5801	1:1-9	9	MTLRVVPEG	0.78	-0.59	-3.28	0.19	-3.09	1907.6
HLA A*2601	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.22	1.13	-3.09	16669.3
HLA B*0702	1:38-46	9	VVPPAADPV	0.76	0.28	-4.14	1.04	-3.09	13701.9
HLA B*0702	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.40	1.30	-3.10	24982.0
HLA A*2601	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.37	1.28	-3.10	23646.3
HLA A*2602	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.22	1.13	-3.10	16705.9
HLA A*3002	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.36	1.26	-3.10	22679.3
HLA A*2403	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.38	1.28	-3.10	23736.3
HLA A*6802	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.40	1.30	-3.10	25092.9
HLA A*6802	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.14	1.04	-3.10	13715.5
HLA B*5101	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.38	1.28	-3.10	23758.7
HLA B*3901	1:31-39	9	AAPVITAVV	1.00	0.24	-4.34	1.24	-3.10	21864.8

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*1509	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.29	1.19	-3.10	19479.9
HLA B*4002	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.29	1.19	-3.10	19499.0
HLA A*0101	1:91-99	9	AAAAATYGV	1.05	0.17	-4.32	1.22	-3.10	20677.6
HLA B*1503	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.05	0.95	-3.10	11193.5
HLA B*1503	1:20-28	9	LTARLAAAH	1.06	-0.16	-3.99	0.89	-3.10	9815.3
HLA A*0101	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.32	1.22	-3.10	20900.0
HLA B*4601	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.36	1.26	-3.10	23021.3
HLA B*5801	1:31-39	9	AAPVITAVV	1.00	0.24	-4.34	1.24	-3.10	22121.3
HLA B*4402	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.32	1.22	-3.10	21046.7
HLA A*0201	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.14	1.04	-3.10	13905.9
HLA B*3501	1:9-17	9	GLAAASAAV	1.01	0.00	-4.11	1.01	-3.10	13021.8
HLA B*4601	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.18	1.08	-3.10	15295.4
HLA B*4501	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.22	1.11	-3.10	16539.4
HLA B*4402	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.38	1.28	-3.10	24143.6
HLA B*1503	1:35-43	9	ITAVVPPAA	1.01	-0.20	-3.91	0.81	-3.11	8132.9
HLA A*2601	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.37	1.26	-3.11	23196.7
HLA B*0801	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.33	1.22	-3.11	21178.0
HLA A*3101	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.24	1.13	-3.11	17410.6
HLA A*0219	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.19	1.08	-3.11	15407.8
HLA B*1502	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.22	1.11	-3.11	16673.1
HLA B*5101	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.33	1.22	-3.11	21273.7
HLA A*0250	1:76-84	9	GVGVGESGA	1.07	-0.25	-3.92	0.81	-3.11	8370.1
HLA B*4001	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.33	1.22	-3.11	21332.4
HLA B*4001	1:30-38	9	SAAPVITAV	0.96	0.26	-4.32	1.21	-3.11	21006.3
HLA B*4001	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.37	1.26	-3.11	23426.6
HLA B*3501	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.41	1.30	-3.11	25838.8
HLA A*0101	1:31-39	9	AAPVITAVV	1.00	0.24	-4.35	1.24	-3.11	22545.0
HLA B*3501	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.33	1.22	-3.11	21446.8
HLA B*3901	1:32-40	9	APVITAVVP	0.92	0.08	-4.10	0.99	-3.11	12725.3
HLA B*1517	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.41	1.30	-3.11	25969.9
HLA A*6801	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.39	1.28	-3.11	24642.4
HLA A*8001	1:91-99	9	AAAAATYGV	1.05	0.17	-4.33	1.22	-3.11	21361.1
HLA B*3901	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.03	0.92	-3.11	10785.5
HLA B*3901	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.37	1.26	-3.11	23678.8
HLA A*2402	1:31-39	9	AAPVITAVV	1.00	0.24	-4.36	1.24	-3.11	22718.5
HLA A*0301	1:30-38	9	SAAPVITAV	0.96	0.26	-4.33	1.21	-3.11	21303.6
HLA B*5801	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.34	1.22	-3.11	21637.1
HLA B*1501	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.21	1.10	-3.12	16381.6
HLA A*0301	1:31-39	9	AAPVITAVV	1.00	0.24	-4.36	1.24	-3.12	22785.1
HLA B*5401	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.40	1.28	-3.12	24840.1
HLA B*4601	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.24	1.13	-3.12	17551.2
HLA A*3001	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.24	1.13	-3.12	17555.5
HLA A*0101	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.31	1.19	-3.12	20347.6
HLA B*1501	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.16	1.04	-3.12	14372.9
HLA B*1801	1:30-38	9	SAAPVITAV	0.96	0.26	-4.33	1.21	-3.12	21444.0
HLA A*0101	1:30-38	9	SAAPVITAV	0.96	0.26	-4.33	1.21	-3.12	21466.0
HLA A*0101	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.34	1.22	-3.12	21825.6
HLA A*0301	1:91-99	9	AAAAATYGV	1.05	0.17	-4.34	1.22	-3.12	21677.5
HLA B*5701	1:30-38	9	SAAPVITAV	0.96	0.26	-4.33	1.21	-3.12	21557.2

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*3001	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.13	1.01	-3.12	13500.6
HLA A*0206	1:80-88	9	GESGASYLA	1.31	-0.35	-4.08	0.96	-3.12	12003.6
HLA A*0219	1:87-95	9	LAGDAAAAA	1.17	-0.30	-3.99	0.87	-3.12	9874.5
HLA B*0802	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.42	1.30	-3.12	26545.4
HLA A*2602	1:33-41	9	PVITAVVPP	0.62	-0.01	-3.74	0.62	-3.12	5462.3
HLA B*4501	1:30-38	9	SAAPVITAV	0.96	0.26	-4.34	1.21	-3.12	21652.9
HLA B*5701	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.34	1.22	-3.12	21916.6
HLA B*0802	1:31-39	9	AAPVITAVV	1.00	0.24	-4.36	1.24	-3.12	23138.4
HLA B*1503	1:93-101	9	AAATYGVVG	1.16	-0.45	-3.84	0.72	-3.12	6887.5
HLA A*3101	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.40	1.28	-3.12	25180.1
HLA B*4801	1:9-17	9	GLAAASAAV	1.01	0.00	-4.13	1.01	-3.12	13618.2
HLA B*1501	1:93-101	9	AAATYGVVG	1.16	-0.45	-3.84	0.72	-3.12	6899.5
HLA B*4001	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.40	1.28	-3.12	25264.6
HLA A*0206	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.22	1.09	-3.12	16461.5
HLA A*3001	1:38-46	9	VVPPAADPV	0.76	0.28	-4.17	1.04	-3.12	14675.4
HLA A*0250	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.26	1.13	-3.12	18175.4
HLA A*2602	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.18	1.06	-3.13	15209.9
HLA A*6802	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.26	1.13	-3.13	18246.3
HLA B*4601	1:91-99	9	AAAAATYGV	1.05	0.17	-4.34	1.22	-3.13	22017.8
HLA B*5701	1:31-39	9	AAPVITAVV	1.00	0.24	-4.37	1.24	-3.13	23408.9
HLA A*0212	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.32	1.19	-3.13	20847.7
HLA A*2902	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.43	1.30	-3.13	27010.7
HLA A*0203	1:76-84	9	GVGVGESGA	1.07	-0.25	-3.94	0.81	-3.13	8791.4
HLA A*3201	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.43	1.30	-3.13	27018.4
HLA B*4001	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.32	1.19	-3.13	20971.3
HLA A*2501	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.26	1.13	-3.13	18140.4
HLA A*2601	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.35	1.22	-3.13	22392.5
HLA B*3801	1:92-100	9	AAAATYGVV	1.09	0.30	-4.52	1.39	-3.13	33212.7
HLA B*1502	1:30-38	9	SAAPVITAV	0.96	0.26	-4.35	1.21	-3.13	22227.7
HLA B*4801	1:31-39	9	AAPVITAVV	1.00	0.24	-4.38	1.24	-3.13	23746.7
HLA B*4801	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.35	1.22	-3.13	22504.7
HLA B*0801	1:26-34	9	AAHASAAPV	0.61	0.30	-4.05	0.91	-3.13	11124.0
HLA B*1517	1:54-62	9	FSAQGVEHA	1.07	-0.26	-3.95	0.81	-3.13	8824.1
HLA B*5301	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.23	1.10	-3.14	17166.7
HLA A*3001	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.24	1.11	-3.14	17414.1
HLA A*2602	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.40	1.26	-3.14	24910.6
HLA B*0702	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.36	1.22	-3.14	22762.3
HLA A*0301	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.36	1.22	-3.14	22766.6
HLA B*1502	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.18	1.04	-3.14	15045.4
HLA B*4402	1:31-39	9	AAPVITAVV	1.00	0.24	-4.38	1.24	-3.14	23951.1
HLA B*1503	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.14	1.00	-3.14	13657.0
HLA A*1101	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.44	1.30	-3.14	27537.5
HLA B*2705	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.36	1.22	-3.14	22720.8
HLA B*4001	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.24	1.10	-3.14	17264.7
HLA A*0201	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.27	1.13	-3.14	18750.3
HLA B*4801	1:30-38	9	SAAPVITAV	0.96	0.26	-4.35	1.21	-3.14	22518.0
HLA B*5801	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.33	1.19	-3.14	21398.6
HLA B*1501	1:38-46	9	VVPPAADPV	0.76	0.28	-4.18	1.04	-3.14	15223.0
HLA B*1509	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.42	1.28	-3.14	26243.6

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*3501	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.26	1.11	-3.14	18037.5
HLA B*4001	1:31-39	9	AAPVITAVV	1.00	0.24	-4.38	1.24	-3.14	24220.0
HLA B*7301	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.44	1.30	-3.14	27837.6
HLA A*3201	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.36	1.22	-3.14	23040.6
HLA A*0201	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.33	1.19	-3.14	21576.3
HLA A*0203	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.28	1.13	-3.14	18973.8
HLA A*2501	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.45	1.30	-3.14	27923.4
HLA B*2705	1:91-99	9	AAAAATYGV	1.05	0.17	-4.36	1.22	-3.14	22892.2
HLA A*3201	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.34	1.19	-3.14	21629.5
HLA A*0301	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.36	1.22	-3.14	23038.3
HLA B*4601	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.36	1.22	-3.14	23139.9
HLA B*4402	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.25	1.11	-3.14	17766.3
HLA B*0702	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.15	1.01	-3.14	14285.5
HLA A*3101	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.37	1.22	-3.15	23210.1
HLA A*3002	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.34	1.19	-3.15	21722.3
HLA A*0301	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.34	1.19	-3.15	21734.0
HLA B*4801	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.42	1.28	-3.15	26603.7
HLA A*6802	1:13-21	9	ASAAVEALT	0.86	-0.15	-3.85	0.70	-3.15	7103.1
HLA A*2301	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.45	1.30	-3.15	28142.7
HLA A*2902	1:30-38	9	SAAPVITAV	0.96	0.26	-4.36	1.21	-3.15	23012.7
HLA B*2705	1:73-81	9	GRAGVGVGE	1.10	-0.64	-3.61	0.46	-3.15	4087.4
HLA A*3002	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.28	1.13	-3.15	18882.1
HLA A*2902	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.37	1.22	-3.15	23298.0
HLA B*5101	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.37	1.22	-3.15	23335.9
HLA B*4402	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.34	1.19	-3.15	21920.1
HLA B*1801	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.37	1.22	-3.15	23338.6
HLA B*1801	1:44-52	9	DPVSLQTAA	1.05	-0.40	-3.80	0.65	-3.15	6240.1
HLA B*2705	1:31-39	9	AAPVITAVV	1.00	0.24	-4.39	1.24	-3.15	24663.9
HLA B*5701	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.37	1.22	-3.15	23464.7
HLA A*3002	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.43	1.28	-3.15	26826.6
HLA B*5701	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.25	1.10	-3.15	17765.5
HLA B*1501	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.29	1.13	-3.15	19283.8
HLA A*0203	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.26	1.11	-3.15	18052.8
HLA B*5101	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.45	1.30	-3.15	28479.9
HLA A*3001	1:48-56	9	LQTAAGFSA	1.01	-0.19	-3.97	0.82	-3.15	9385.2
HLA A*2602	1:91-99	9	AAAAATYGV	1.05	0.17	-4.37	1.22	-3.15	23429.3
HLA B*1501	1:18-26	9	EALTARLAA	1.39	-0.27	-4.27	1.12	-3.15	18796.7
HLA A*0216	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.21	1.06	-3.15	16235.3
HLA B*1801	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.46	1.30	-3.15	28593.9
HLA A*3201	1:92-100	9	AAAATYGVV	1.09	0.30	-4.54	1.39	-3.15	34965.4
HLA A*3201	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.05	0.89	-3.15	11120.2
HLA A*2501	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.41	1.26	-3.15	25999.3
HLA A*2902	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-3.93	0.77	-3.15	8505.9
HLA A*8001	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.38	1.22	-3.15	23729.9
HLA B*2705	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.43	1.28	-3.16	27132.8
HLA B*4601	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.35	1.19	-3.16	22225.2
HLA B*1501	1:34-42	9	VITAVVPPA	1.03	-0.23	-3.96	0.81	-3.16	9156.7
HLA B*5701	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.25	1.09	-3.16	17694.8
HLA A*2601	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.38	1.22	-3.16	23780.9

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*0802	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.37	1.22	-3.16	23712.6
HLA A*0219	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.29	1.13	-3.16	19550.4
HLA B*4801	1:91-99	9	AAAAATYGV	1.05	0.17	-4.37	1.22	-3.16	23584.2
HLA B*5801	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.27	1.11	-3.16	18687.1
HLA B*1503	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-3.93	0.77	-3.16	8557.6
HLA A*0250	1:69-77	9	VEELGRAGV	1.03	0.03	-4.22	1.06	-3.16	16435.9
HLA A*6801	1:91-99	9	AAAAATYGV	1.05	0.17	-4.37	1.22	-3.16	23678.3
HLA B*1502	1:26-34	9	AAHASAAPV	0.61	0.30	-4.07	0.91	-3.16	11796.7
HLA A*3101	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.35	1.19	-3.16	22431.3
HLA A*0203	1:18-26	9	EALTARLAA	1.39	-0.27	-4.28	1.12	-3.16	19058.5
HLA B*4402	1:30-38	9	SAAPVITAV	0.96	0.26	-4.37	1.21	-3.16	23648.2
HLA A*2501	1:31-39	9	AAPVITAVV	1.00	0.24	-4.40	1.24	-3.16	25257.6
HLA B*1801	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.42	1.26	-3.16	26343.9
HLA A*0216	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.35	1.19	-3.16	22507.2
HLA A*0203	1:17-25	9	VEALTARLA	1.29	-0.19	-4.26	1.10	-3.16	18314.4
HLA B*5301	1:91-99	9	AAAAATYGV	1.05	0.17	-4.38	1.22	-3.16	23841.6
HLA B*5801	1:35-43	9	ITAVVPPAA	1.01	-0.20	-3.97	0.81	-3.16	9253.8
HLA A*8001	1:31-39	9	AAPVITAVV	1.00	0.24	-4.40	1.24	-3.16	25350.6
HLA A*6801	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.29	1.13	-3.16	19472.2
HLA B*0803	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.47	1.30	-3.16	29246.7
HLA B*4402	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.42	1.26	-3.16	26533.3
HLA A*3001	1:17-25	9	VEALTARLA	1.29	-0.19	-4.27	1.10	-3.16	18447.2
HLA B*5301	1:30-38	9	SAAPVITAV	0.96	0.26	-4.38	1.21	-3.16	23873.1
HLA A*3201	1:26-34	9	AAHASAAPV	0.61	0.30	-4.08	0.91	-3.16	11943.2
HLA A*6801	1:92-100	9	AAAATYGVV	1.09	0.30	-4.55	1.39	-3.16	35855.2
HLA A*3001	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.04	0.87	-3.17	10940.3
HLA A*1101	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.06	0.89	-3.17	11416.2
HLA A*0212	1:76-84	9	GVGVGESGA	1.07	-0.25	-3.98	0.81	-3.17	9599.1
HLA A*2403	1:38-46	9	VVPPAADPV	0.76	0.28	-4.21	1.04	-3.17	16205.3
HLA B*4801	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.30	1.13	-3.17	20090.3
HLA A*2403	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.36	1.19	-3.17	22893.5
HLA B*3901	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.28	1.11	-3.17	19210.3
HLA B*3501	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.18	1.01	-3.17	15102.5
HLA A*0301	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.23	1.06	-3.17	16818.5
HLA B*4801	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.36	1.19	-3.17	22970.3
HLA A*2403	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.39	1.22	-3.17	24561.4
HLA B*0802	1:30-38	9	SAAPVITAV	0.96	0.26	-4.38	1.21	-3.17	24185.0
HLA B*2705	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.30	1.13	-3.17	19865.9
HLA A*3201	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.45	1.28	-3.17	28137.0
HLA B*1801	1:18-26	9	EALTARLAA	1.39	-0.27	-4.29	1.12	-3.17	19571.0
HLA B*4801	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.29	1.11	-3.17	19317.1
HLA A*2601	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.27	1.10	-3.17	18648.5
HLA A*1101	1:31-39	9	AAPVITAVV	1.00	0.24	-4.41	1.24	-3.17	25917.6
HLA B*3501	1:8-16	9	EGLAAASAA	0.96	-0.49	-3.64	0.46	-3.17	4323.5
HLA A*6801	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.25	1.08	-3.17	17905.6
HLA A*0250	1:54-62	9	FSAQGVEHA	1.07	-0.26	-3.98	0.81	-3.17	9642.6
HLA B*2705	1:30-38	9	SAAPVITAV	0.96	0.26	-4.39	1.21	-3.17	24348.8
HLA B*3901	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.31	1.13	-3.17	20315.4
HLA A*8001	1:30-38	9	SAAPVITAV	0.96	0.26	-4.39	1.21	-3.17	24375.6

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*0702	1:32-40	9	APVITAVVP	0.92	0.08	-4.17	0.99	-3.17	14668.0
HLA B*1502	1:91-99	9	AAAAATYGV	1.05	0.17	-4.39	1.22	-3.17	24539.4
HLA B*4601	1:26-34	9	AAHASAAPV	0.61	0.30	-4.09	0.91	-3.17	12199.8
HLA B*4002	1:92-100	9	AAAATYGVV	1.09	0.30	-4.56	1.39	-3.17	36690.1
HLA A*8001	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.39	1.22	-3.18	24760.3
HLA B*0802	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.45	1.28	-3.18	28458.2
HLA B*4501	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.31	1.13	-3.18	20472.4
HLA A*2902	1:31-39	9	AAPVITAVV	1.00	0.24	-4.42	1.24	-3.18	26294.9
HLA B*5701	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.29	1.11	-3.18	19659.3
HLA B*5401	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.44	1.26	-3.18	27497.3
HLA B*1509	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.31	1.13	-3.18	20270.3
HLA A*0301	1:9-17	9	GLAAASAAV	1.01	0.00	-4.19	1.01	-3.18	15521.9
HLA B*4402	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.40	1.22	-3.18	25046.8
HLA B*1801	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.46	1.28	-3.18	28779.6
HLA B*4501	1:59-67	9	VEHAVVTAE	0.87	-0.71	-3.34	0.16	-3.18	2167.4
HLA B*3501	1:10-18	9	LAAASAAVE	1.14	-0.66	-3.67	0.48	-3.18	4625.0
HLA B*1503	1:38-46	9	VVPPAADPV	0.76	0.28	-4.22	1.04	-3.18	16759.3
HLA A*0301	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.31	1.13	-3.18	20402.7
HLA A*3201	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.31	1.13	-3.18	20440.0
HLA B*5101	1:38-46	9	VVPPAADPV	0.76	0.28	-4.23	1.04	-3.18	16821.8
HLA A*2902	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.40	1.22	-3.18	25371.0
HLA B*0801	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.32	1.13	-3.18	20840.5
HLA B*5301	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.40	1.22	-3.18	25320.5
HLA A*0101	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.31	1.13	-3.19	20593.3
HLA A*2501	1:91-99	9	AAAAATYGV	1.05	0.17	-4.40	1.22	-3.19	25272.8
HLA A*3002	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.41	1.22	-3.19	25616.4
HLA A*2902	1:9-17	9	GLAAASAAV	1.01	0.00	-4.20	1.01	-3.19	15833.9
HLA A*2602	1:30-38	9	SAAPVITAV	0.96	0.26	-4.40	1.21	-3.19	25270.7
HLA B*4501	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.29	1.11	-3.19	19691.2
HLA B*1517	1:35-43	9	ITAVVPPAA	1.01	-0.20	-3.99	0.81	-3.19	9878.9
HLA B*3801	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.45	1.26	-3.19	28215.9
HLA A*2501	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.47	1.28	-3.19	29446.9
HLA B*1509	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.29	1.10	-3.19	19539.7
HLA B*3901	1:18-26	9	EALTARLAA	1.39	-0.27	-4.31	1.12	-3.19	20521.3
HLA A*0219	1:26-34	9	AAHASAAPV	0.61	0.30	-4.10	0.91	-3.19	12716.5
HLA A*2403	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.31	1.11	-3.19	20303.2
HLA B*3501	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.29	1.09	-3.19	19276.9
HLA B*1801	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.33	1.13	-3.19	21280.1
HLA B*7301	1:92-100	9	AAAATYGVV	1.09	0.30	-4.58	1.39	-3.19	38294.0
HLA A*0219	1:18-26	9	EALTARLAA	1.39	-0.27	-4.31	1.12	-3.19	20653.6
HLA A*2602	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.39	1.19	-3.19	24330.8
HLA A*0212	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.07	0.87	-3.19	11692.1
HLA A*0101	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.09	0.89	-3.20	12201.7
HLA A*0206	1:17-25	9	VEALTARLA	1.29	-0.19	-4.30	1.10	-3.20	19814.5
HLA A*3001	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.24	1.04	-3.20	17321.4
HLA B*1509	1:31-39	9	AAPVITAVV	1.00	0.24	-4.44	1.24	-3.20	27627.4
HLA A*0203	1:69-77	9	VEELGRAGV	1.03	0.03	-4.26	1.06	-3.20	18085.3
HLA B*0801	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.39	1.19	-3.20	24640.9
HLA B*7301	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.39	1.19	-3.20	24642.5

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*1509	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.34	1.13	-3.20	21630.8
HLA B*4403	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.50	1.30	-3.20	31850.0
HLA A*2603	1:91-99	9	AAAAATYGV	1.05	0.17	-4.42	1.22	-3.20	26196.7
HLA B*0803	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.48	1.28	-3.20	30267.9
HLA B*2705	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.42	1.22	-3.20	26538.9
HLA A*0202	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-3.98	0.77	-3.20	9516.7
HLA B*4801	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.42	1.22	-3.20	26557.3
HLA B*0802	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.46	1.26	-3.20	29137.3
HLA A*2601	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.40	1.19	-3.21	24945.1
HLA A*1101	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.43	1.22	-3.21	26694.0
HLA B*2705	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.40	1.19	-3.21	25004.7
HLA A*3001	1:69-77	9	VEELGRAGV	1.03	0.03	-4.27	1.06	-3.21	18419.3
HLA A*0219	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.40	1.19	-3.21	25090.4
HLA A*2403	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.34	1.13	-3.21	21683.9
HLA B*1801	1:59-67	9	VEHAVVTAE	0.87	-0.71	-3.36	0.16	-3.21	2312.1
HLA B*1509	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.47	1.26	-3.21	29520.8
HLA B*5701	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.40	1.19	-3.21	25231.5
HLA B*5101	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.47	1.26	-3.21	29581.4
HLA A*0211	1:1-9	9	MTLRVVPEG	0.78	-0.59	-3.40	0.19	-3.21	2504.3
HLA A*6801	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.31	1.10	-3.21	20484.6
HLA B*1503	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.35	1.13	-3.21	22253.2
HLA B*1503	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.25	1.04	-3.21	17972.4
HLA B*0702	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.35	1.13	-3.21	22351.2
HLA A*2902	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.33	1.11	-3.22	21376.6
HLA B*4403	1:92-100	9	AAAATYGVV	1.09	0.30	-4.61	1.39	-3.22	40326.6
HLA A*3101	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.32	1.10	-3.22	20761.4
HLA B*1517	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.35	1.13	-3.22	22165.8
HLA A*2603	1:92-100	9	AAAATYGVV	1.09	0.30	-4.61	1.39	-3.22	40618.9
HLA B*1801	1:91-99	9	AAAAATYGV	1.05	0.17	-4.44	1.22	-3.22	27252.8
HLA B*1801	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.41	1.19	-3.22	25765.3
HLA B*3801	1:30-38	9	SAAPVITAV	0.96	0.26	-4.43	1.21	-3.22	27138.2
HLA B*5401	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.23	1.01	-3.22	17025.8
HLA B*0802	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.44	1.22	-3.22	27628.1
HLA B*1501	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.26	1.04	-3.22	18276.4
HLA A*3001	1:24-32	9	LAAAHASAA	0.90	-0.14	-3.98	0.75	-3.22	9462.9
HLA B*1503	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.33	1.11	-3.22	21255.3
HLA B*1503	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.14	0.92	-3.22	13845.1
HLA B*5801	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.36	1.13	-3.22	22775.9
HLA B*1501	1:17-25	9	VEALTARLA	1.29	-0.19	-4.32	1.10	-3.22	21134.6
HLA A*3301	1:92-100	9	AAAATYGVV	1.09	0.30	-4.61	1.39	-3.22	41003.5
HLA A*0206	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.33	1.11	-3.22	21326.6
HLA B*0702	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.10	0.87	-3.22	12508.8
HLA A*8001	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.42	1.19	-3.22	26066.5
HLA A*0101	1:18-26	9	EALTARLAA	1.39	-0.27	-4.35	1.12	-3.22	22138.6
HLA B*5801	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.31	1.08	-3.23	20245.1
HLA A*3001	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.12	0.89	-3.23	13096.4
HLA B*0803	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.44	1.22	-3.23	27844.3
HLA B*5801	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.35	1.13	-3.23	22586.8
HLA A*0301	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.36	1.13	-3.23	22977.3

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*2601	1:9-17	9	GLAAASAAV	1.01	0.00	-4.24	1.01	-3.23	17297.7
HLA B*0803	1:91-99	9	AAAAATYGV	1.05	0.17	-4.44	1.22	-3.23	27749.3
HLA A*2602	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.45	1.22	-3.23	27910.7
HLA A*3002	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.24	1.01	-3.23	17280.1
HLA A*3101	1:18-26	9	EALTARLAA	1.39	-0.27	-4.35	1.12	-3.23	22292.4
HLA A*2402	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.51	1.28	-3.23	32077.8
HLA B*3901	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.45	1.22	-3.23	28080.5
HLA A*2902	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.42	1.19	-3.23	26319.9
HLA B*3801	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.53	1.30	-3.23	34044.8
HLA A*1101	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.35	1.11	-3.23	22161.1
HLA B*3501	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.29	1.06	-3.23	19400.6
HLA B*5301	1:31-39	9	AAPVITAVV	1.00	0.24	-4.47	1.24	-3.23	29728.6
HLA A*2601	1:18-26	9	EALTARLAA	1.39	-0.27	-4.35	1.12	-3.23	22468.8
HLA B*3501	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.01	0.77	-3.23	10141.4
HLA A*2603	1:18-26	9	EALTARLAA	1.39	-0.27	-4.35	1.12	-3.23	22478.9
HLA B*0803	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.49	1.26	-3.23	31014.8
HLA B*1502	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.49	1.26	-3.23	31053.1
HLA B*0803	1:31-39	9	AAPVITAVV	1.00	0.24	-4.47	1.24	-3.23	29816.4
HLA A*6901	1:1-9	9	MTLRVVPEG	0.78	-0.59	-3.42	0.19	-3.23	2626.3
HLA A*6901	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.27	1.04	-3.23	18738.6
HLA A*0301	1:18-26	9	EALTARLAA	1.39	-0.27	-4.35	1.12	-3.23	22555.9
HLA B*0802	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.42	1.19	-3.23	26587.2
HLA A*0212	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.29	1.06	-3.23	19502.7
HLA A*0301	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.27	1.04	-3.23	18801.8
HLA A*3201	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.23	1.00	-3.23	17066.4
HLA B*4601	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.13	0.89	-3.23	13366.4
HLA B*1801	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.36	1.13	-3.24	23078.5
HLA B*1502	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.34	1.10	-3.24	21646.1
HLA B*4601	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.34	1.10	-3.24	21651.4
HLA A*2602	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.54	1.30	-3.24	34584.6
HLA A*3101	1:26-34	9	AAHASAAPV	0.61	0.30	-4.15	0.91	-3.24	14089.2
HLA B*4001	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.37	1.13	-3.24	23507.2
HLA B*5801	1:18-26	9	EALTARLAA	1.39	-0.27	-4.36	1.12	-3.24	22752.1
HLA B*1517	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.11	0.87	-3.24	12886.0
HLA B*5401	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.05	0.81	-3.24	11192.3
HLA A*0203	1:80-88	9	GESGASYLA	1.31	-0.35	-4.20	0.96	-3.24	15697.6
HLA A*2501	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.43	1.19	-3.24	26866.7
HLA A*2403	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.32	1.08	-3.24	20842.7
HLA A*2301	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.37	1.13	-3.24	23602.0
HLA B*4001	1:18-26	9	EALTARLAA	1.39	-0.27	-4.36	1.12	-3.24	22844.6
HLA B*5101	1:18-26	9	EALTARLAA	1.39	-0.27	-4.36	1.12	-3.24	22849.0
HLA B*0803	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.46	1.22	-3.24	28777.9
HLA A*2601	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.13	0.89	-3.24	13503.5
HLA B*3501	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.28	1.04	-3.24	19050.3
HLA A*6801	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.46	1.22	-3.24	28725.7
HLA A*3101	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.33	1.09	-3.24	21495.1
HLA A*2301	1:31-39	9	AAPVITAVV	1.00	0.24	-4.48	1.24	-3.24	30379.1
HLA A*0101	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.30	1.06	-3.24	19833.1
HLA A*2301	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.50	1.26	-3.24	31699.3

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*0801	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.32	1.08	-3.24	21016.1
HLA B*4001	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.36	1.11	-3.24	22724.7
HLA B*1517	1:18-26	9	EALTARLAA	1.39	-0.27	-4.36	1.12	-3.24	23033.0
HLA B*1502	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.06	0.82	-3.24	11516.5
HLA B*1509	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.46	1.22	-3.24	29019.6
HLA A*6901	1:17-25	9	VEALTARLA	1.29	-0.19	-4.34	1.10	-3.24	22098.9
HLA A*8001	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.36	1.11	-3.24	22764.4
HLA A*0250	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.06	0.82	-3.24	11526.0
HLA B*0803	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.36	1.11	-3.24	22772.7
HLA B*5401	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.34	1.10	-3.24	22056.1
HLA A*2501	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.47	1.22	-3.24	29177.4
HLA A*8001	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.37	1.13	-3.24	23563.2
HLA A*3101	1:9-17	9	GLAAASAAV	1.01	0.00	-4.26	1.01	-3.25	18031.1
HLA B*4801	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.37	1.13	-3.25	23577.1
HLA A*0212	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.33	1.08	-3.25	21211.9
HLA B*1503	1:17-25	9	VEALTARLA	1.29	-0.19	-4.35	1.10	-3.25	22269.6
HLA B*4403	1:69-77	9	VEELGRAGV	1.03	0.03	-4.30	1.06	-3.25	20123.6
HLA B*1801	1:31-39	9	AAPVITAVV	1.00	0.24	-4.49	1.24	-3.25	30811.1
HLA B*4002	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.07	0.82	-3.25	11635.7
HLA B*5101	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.44	1.19	-3.25	27427.2
HLA A*0202	1:25-33	9	AAAHASAAP	0.72	0.16	-4.12	0.88	-3.25	13274.0
HLA B*4001	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.37	1.13	-3.25	23684.5
HLA B*5401	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.55	1.30	-3.25	35481.8
HLA B*4601	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.38	1.13	-3.25	24113.6
HLA B*3801	1:91-99	9	AAAAATYGV	1.05	0.17	-4.46	1.22	-3.25	29088.5
HLA A*0301	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.34	1.09	-3.25	21875.8
HLA A*0219	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.05	0.81	-3.25	11301.7
HLA B*0803	1:30-38	9	SAAPVITAV	0.96	0.26	-4.46	1.21	-3.25	28965.0
HLA B*5801	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.35	1.11	-3.25	22590.2
HLA B*1501	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.35	1.11	-3.25	22599.0
HLA A*0201	1:18-26	9	EALTARLAA	1.39	-0.27	-4.37	1.12	-3.25	23411.9
HLA A*2501	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.38	1.13	-3.25	24225.0
HLA A*0101	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.36	1.11	-3.25	23152.4
HLA A*0101	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.39	1.13	-3.25	24295.1
HLA B*1503	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.34	1.09	-3.25	22052.5
HLA B*3801	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.53	1.28	-3.25	33872.8
HLA B*4402	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.33	1.08	-3.25	21539.7
HLA A*2402	1:91-99	9	AAAAATYGV	1.05	0.17	-4.47	1.22	-3.25	29463.2
HLA A*0101	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.35	1.10	-3.25	22541.6
HLA B*1503	1:32-40	9	APVITAVVP	0.92	0.08	-4.25	0.99	-3.25	17670.6
HLA A*2301	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.47	1.22	-3.25	29722.9
HLA B*1502	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.45	1.19	-3.26	27994.5
HLA A*6801	1:18-26	9	EALTARLAA	1.39	-0.27	-4.38	1.12	-3.26	23782.2
HLA B*1509	1:17-25	9	VEALTARLA	1.29	-0.19	-4.36	1.10	-3.26	22786.7
HLA A*3301	1:30-38	9	SAAPVITAV	0.96	0.26	-4.47	1.21	-3.26	29533.9
HLA B*3901	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.45	1.19	-3.26	28060.9
HLA A*2403	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.36	1.10	-3.26	22710.9
HLA B*4402	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.39	1.13	-3.26	24650.4
HLA B*1502	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.48	1.22	-3.26	30046.8

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*3501	1:39-47	9	VPPAADPVS	0.96	-1.07	-3.15	-0.11	-3.26	1398.5
HLA B*4402	1:18-26	9	EALTARLAA	1.39	-0.27	-4.38	1.12	-3.26	23915.5
HLA B*1517	1:9-17	9	GLAAASAAV	1.01	0.00	-4.27	1.01	-3.26	18589.1
HLA A*0101	1:17-25	9	VEALTARLA	1.29	-0.19	-4.36	1.10	-3.26	22921.3
HLA B*5801	1:17-25	9	VEALTARLA	1.29	-0.19	-4.36	1.10	-3.26	22922.1
HLA A*3301	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.48	1.22	-3.26	30004.1
HLA A*2301	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.54	1.28	-3.26	34444.6
HLA A*0301	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.34	1.08	-3.26	21856.4
HLA B*1509	1:91-99	9	AAAAATYGV	1.05	0.17	-4.47	1.22	-3.26	29851.1
HLA A*8001	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.39	1.13	-3.26	24754.4
HLA A*3101	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.32	1.06	-3.26	20760.5
HLA A*6801	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.07	0.81	-3.26	11633.1
HLA B*5801	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.35	1.09	-3.26	22532.5
HLA A*0301	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.36	1.10	-3.26	22928.4
HLA A*2501	1:18-26	9	EALTARLAA	1.39	-0.27	-4.38	1.12	-3.26	24090.1
HLA A*2403	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.37	1.11	-3.26	23282.3
HLA A*3001	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.04	0.77	-3.26	10887.8
HLA B*3801	1:31-39	9	AAPVITAVV	1.00	0.24	-4.50	1.24	-3.26	31948.2
HLA A*0301	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.37	1.11	-3.26	23322.9
HLA A*2601	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.40	1.13	-3.26	24983.4
HLA A*3001	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.26	1.00	-3.26	18247.8
HLA A*2402	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.40	1.13	-3.26	24997.2
HLA A*0301	1:17-25	9	VEALTARLA	1.29	-0.19	-4.37	1.10	-3.26	23182.1
HLA A*2403	1:18-26	9	EALTARLAA	1.39	-0.27	-4.38	1.12	-3.26	24256.3
HLA B*4601	1:38-46	9	VVPPAADPV	0.76	0.28	-4.31	1.04	-3.26	20262.4
HLA B*2705	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.36	1.10	-3.27	23152.3
HLA B*4801	1:26-34	9	AAHASAAPV	0.61	0.30	-4.18	0.91	-3.27	15075.2
HLA B*4601	1:18-26	9	EALTARLAA	1.39	-0.27	-4.39	1.12	-3.27	24363.2
HLA B*7301	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.54	1.28	-3.27	35058.0
HLA A*2602	1:31-39	9	AAPVITAVV	1.00	0.24	-4.51	1.24	-3.27	32260.9
HLA A*2603	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.28	1.01	-3.27	18953.8
HLA B*1502	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.55	1.28	-3.27	35173.1
HLA A*0211	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.02	0.75	-3.27	10526.8
HLA A*2402	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.49	1.22	-3.27	30697.7
HLA A*2602	1:18-26	9	EALTARLAA	1.39	-0.27	-4.39	1.12	-3.27	24488.7
HLA A*2601	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.38	1.11	-3.27	24181.5
HLA A*2501	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.38	1.11	-3.27	24183.2
HLA B*2705	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.40	1.13	-3.27	25327.1
HLA B*0801	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.37	1.10	-3.27	23369.5
HLA A*1101	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.35	1.08	-3.27	22401.3
HLA A*2402	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.53	1.26	-3.27	33887.0
HLA B*5701	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.33	1.06	-3.27	21260.6
HLA A*2301	1:91-99	9	AAAAATYGV	1.05	0.17	-4.49	1.22	-3.27	30707.5
HLA B*0801	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.27	1.00	-3.27	18599.7
HLA A*0101	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.38	1.11	-3.27	23801.0
HLA B*4001	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.35	1.08	-3.27	22542.9
HLA B*5701	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.40	1.13	-3.27	25114.1
HLA A*0203	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.05	0.77	-3.27	11170.2
HLA B*4402	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.37	1.10	-3.27	23598.7

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*5401	1:17-25	9	VEALTARLA	1.29	-0.19	-4.38	1.10	-3.27	23751.5
HLA A*0201	1:17-25	9	VEALTARLA	1.29	-0.19	-4.38	1.10	-3.27	23765.6
HLA A*0101	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.36	1.08	-3.27	22654.6
HLA A*6901	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.38	1.11	-3.27	23971.2
HLA B*3801	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.49	1.22	-3.27	31152.4
HLA B*4402	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.33	1.06	-3.28	21474.1
HLA B*4402	1:7-15	9	PEGLAAASA	1.26	-0.55	-3.98	0.71	-3.28	9644.9
HLA A*2902	1:18-26	9	EALTARLAA	1.39	-0.27	-4.40	1.12	-3.28	24887.2
HLA A*2402	1:30-38	9	SAAPVITAV	0.96	0.26	-4.49	1.21	-3.28	30929.7
HLA A*3101	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.40	1.13	-3.28	25367.7
HLA A*0203	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.20	0.92	-3.28	15697.1
HLA A*0250	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.33	1.06	-3.28	21574.7
HLA B*3901	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.36	1.08	-3.28	22851.3
HLA A*3002	1:38-46	9	VVPPAADPV	0.76	0.28	-4.32	1.04	-3.28	20917.9
HLA A*0212	1:18-26	9	EALTARLAA	1.39	-0.27	-4.40	1.12	-3.28	25063.6
HLA B*0801	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.38	1.11	-3.28	24206.5
HLA B*4501	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.54	1.26	-3.28	34628.8
HLA A*6901	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.12	0.84	-3.28	13311.9
HLA B*5701	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.42	1.13	-3.28	26003.8
HLA A*3101	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.36	1.08	-3.28	22983.2
HLA B*5301	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.58	1.30	-3.28	38322.8
HLA A*0216	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.39	1.11	-3.28	24331.8
HLA A*0101	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.37	1.09	-3.28	23617.9
HLA A*1101	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.32	1.04	-3.28	20972.9
HLA B*5401	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.34	1.06	-3.28	21800.8
HLA A*0201	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.39	1.11	-3.28	24374.8
HLA B*4601	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.40	1.11	-3.28	24920.2
HLA A*0219	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.34	1.06	-3.28	21831.9
HLA A*0216	1:69-77	9	VEELGRAGV	1.03	0.03	-4.34	1.06	-3.28	21878.1
HLA B*5701	1:18-26	9	EALTARLAA	1.39	-0.27	-4.40	1.12	-3.28	25286.6
HLA A*0212	1:69-77	9	VEELGRAGV	1.03	0.03	-4.34	1.06	-3.28	21896.3
HLA B*1501	1:80-88	9	GESGASYLA	1.31	-0.35	-4.24	0.96	-3.28	17432.5
HLA A*3101	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.39	1.11	-3.28	24468.0
HLA A*0216	1:18-26	9	EALTARLAA	1.39	-0.27	-4.40	1.12	-3.28	25350.7
HLA A*6901	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.20	0.92	-3.28	15949.2
HLA A*8001	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.38	1.10	-3.28	24179.4
HLA A*3201	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.42	1.13	-3.28	26239.7
HLA B*4801	1:18-26	9	EALTARLAA	1.39	-0.27	-4.41	1.12	-3.28	25424.0
HLA B*1801	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.40	1.11	-3.29	25126.5
HLA A*2601	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.39	1.11	-3.29	24651.3
HLA A*2601	1:17-25	9	VEALTARLA	1.29	-0.19	-4.39	1.10	-3.29	24463.2
HLA A*2601	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.38	1.09	-3.29	23923.1
HLA A*2301	1:30-38	9	SAAPVITAV	0.96	0.26	-4.50	1.21	-3.29	31694.5
HLA B*1502	1:31-39	9	AAPVITAVV	1.00	0.24	-4.53	1.24	-3.29	33842.6
HLA B*4601	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.16	0.87	-3.29	14498.8
HLA B*1801	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.51	1.22	-3.29	32312.4
HLA B*1501	1:72-80	9	LGRAGVGVG	0.85	-0.77	-3.37	0.08	-3.29	2324.9
HLA B*1801	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.00	0.71	-3.29	9965.4
HLA A*8001	1:17-25	9	VEALTARLA	1.29	-0.19	-4.39	1.10	-3.29	24635.6

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*3501	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.33	1.04	-3.29	21371.6
HLA B*0702	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.35	1.06	-3.29	22222.0
HLA A*1101	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.42	1.13	-3.29	26147.8
HLA B*5801	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.21	0.92	-3.29	16180.8
HLA B*3901	1:69-77	9	VEELGRAGV	1.03	0.03	-4.35	1.06	-3.29	22288.3
HLA B*0801	1:17-25	9	VEALTARLA	1.29	-0.19	-4.39	1.10	-3.29	24689.4
HLA B*1502	1:38-46	9	VVPPAADPV	0.76	0.28	-4.33	1.04	-3.29	21523.6
HLA B*5101	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.37	1.08	-3.29	23552.2
HLA A*0201	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.38	1.09	-3.29	24184.7
HLA A*3001	1:80-88	9	GESGASYLA	1.31	-0.35	-4.25	0.96	-3.29	17782.3
HLA B*2705	1:18-26	9	EALTARLAA	1.39	-0.27	-4.41	1.12	-3.29	25835.4
HLA B*5701	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.37	1.08	-3.29	23588.2
HLA B*5301	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.55	1.26	-3.29	35719.5
HLA B*4601	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.40	1.11	-3.29	25049.1
HLA B*1517	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.21	0.92	-3.29	16309.8
HLA B*2705	1:17-25	9	VEALTARLA	1.29	-0.19	-4.40	1.10	-3.29	24877.0
HLA A*0219	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.33	1.04	-3.29	21598.7
HLA B*5801	1:38-46	9	VVPPAADPV	0.76	0.28	-4.34	1.04	-3.30	21738.1
HLA A*0301	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.34	1.04	-3.30	21647.1
HLA B*0702	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.34	1.04	-3.30	21663.9
HLA A*6901	1:44-52	9	DPVSLQTAA	1.05	-0.40	-3.94	0.65	-3.30	8746.7
HLA B*5701	1:17-25	9	VEALTARLA	1.29	-0.19	-4.40	1.10	-3.30	25023.5
HLA A*2902	1:80-88	9	GESGASYLA	1.31	-0.35	-4.26	0.96	-3.30	17992.3
HLA A*0216	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.14	0.84	-3.30	13829.8
HLA B*5801	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.34	1.04	-3.30	21756.0
HLA A*6901	1:69-77	9	VEELGRAGV	1.03	0.03	-4.36	1.06	-3.30	22654.9
HLA B*0702	1:17-25	9	VEALTARLA	1.29	-0.19	-4.40	1.10	-3.30	25097.8
HLA B*4601	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.39	1.09	-3.30	24558.8
HLA B*1517	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.43	1.13	-3.30	27092.9
HLA B*1517	1:38-46	9	VVPPAADPV	0.76	0.28	-4.34	1.04	-3.30	21895.1
HLA B*4601	1:17-25	9	VEALTARLA	1.29	-0.19	-4.40	1.10	-3.30	25120.4
HLA A*0211	1:18-26	9	EALTARLAA	1.39	-0.27	-4.42	1.12	-3.30	26222.6
HLA A*3101	1:17-25	9	VEALTARLA	1.29	-0.19	-4.40	1.10	-3.30	25122.4
HLA A*2601	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.31	1.01	-3.30	20344.1
HLA A*2601	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.38	1.08	-3.30	23943.0
HLA B*4001	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.36	1.06	-3.30	22673.7
HLA B*5101	1:32-40	9	APVITAVVP	0.92	0.08	-4.29	0.99	-3.30	19594.8
HLA B*1801	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.12	0.82	-3.30	13135.0
HLA B*4402	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.43	1.13	-3.30	26726.1
HLA A*8001	1:18-26	9	EALTARLAA	1.39	-0.27	-4.42	1.12	-3.30	26351.3
HLA B*0803	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.49	1.19	-3.30	31049.4
HLA B*5401	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.52	1.22	-3.30	33195.3
HLA A*0202	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.22	0.92	-3.30	16591.5
HLA A*6802	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.02	0.72	-3.30	10410.6
HLA A*2301	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.52	1.22	-3.30	33272.1
HLA B*0801	1:69-77	9	VEELGRAGV	1.03	0.03	-4.36	1.06	-3.30	22877.7
HLA A*0219	1:69-77	9	VEELGRAGV	1.03	0.03	-4.36	1.06	-3.30	22883.8
HLA A*6802	1:25-33	9	AAAHASAAP	0.72	0.16	-4.18	0.88	-3.30	15075.0
HLA B*7301	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.56	1.26	-3.30	36502.2

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*0101	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.15	0.84	-3.30	14016.9
HLA B*4801	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.40	1.10	-3.30	25226.7
HLA B*4001	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.39	1.09	-3.30	24811.0
HLA B*0803	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.43	1.13	-3.30	26922.5
HLA B*0802	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.40	1.10	-3.30	25238.8
HLA A*3001	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.28	0.98	-3.30	19024.0
HLA B*1501	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.11	0.81	-3.30	12829.0
HLA B*3901	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.36	1.06	-3.30	22905.8
HLA A*2402	1:38-46	9	VVPPAADPV	0.76	0.28	-4.35	1.04	-3.30	22161.3
HLA B*5801	1:69-77	9	VEELGRAGV	1.03	0.03	-4.36	1.06	-3.30	22966.8
HLA A*6802	1:17-25	9	VEALTARLA	1.29	-0.19	-4.41	1.10	-3.30	25435.6
HLA A*0216	1:80-88	9	GESGASYLA	1.31	-0.35	-4.26	0.96	-3.30	18304.3
HLA A*3001	1:32-40	9	APVITAVVP	0.92	0.08	-4.30	0.99	-3.30	19845.5
HLA A*2602	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.40	1.10	-3.31	25374.3
HLA A*2603	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.57	1.26	-3.31	36797.4
HLA B*5101	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.40	1.09	-3.31	24993.6
HLA A*0201	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.18	0.87	-3.31	15105.6
HLA A*0212	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.41	1.11	-3.31	25783.3
HLA A*6802	1:69-77	9	VEELGRAGV	1.03	0.03	-4.36	1.06	-3.31	23118.7
HLA B*1503	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.07	0.76	-3.31	11706.3
HLA B*5701	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.41	1.11	-3.31	25804.7
HLA A*6801	1:31-39	9	AAPVITAVV	1.00	0.24	-4.55	1.24	-3.31	35394.9
HLA B*4501	1:31-39	9	AAPVITAVV	1.00	0.24	-4.55	1.24	-3.31	35400.7
HLA A*2601	1:38-46	9	VVPPAADPV	0.76	0.28	-4.35	1.04	-3.31	22356.0
HLA A*0212	1:17-25	9	VEALTARLA	1.29	-0.19	-4.41	1.10	-3.31	25693.9
HLA B*4601	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.32	1.01	-3.31	20839.2
HLA A*6801	1:10-18	9	LAAASAAVE	1.14	-0.66	-3.79	0.48	-3.31	6193.8
HLA B*3801	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.53	1.22	-3.31	33825.6
HLA A*2602	1:38-46	9	VVPPAADPV	0.76	0.28	-4.35	1.04	-3.31	22453.7
HLA A*3101	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.35	1.04	-3.31	22370.7
HLA B*4402	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.40	1.09	-3.31	25225.4
HLA A*2902	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.41	1.10	-3.31	25651.0
HLA B*4601	1:9-17	9	GLAAASAAV	1.01	0.00	-4.32	1.01	-3.31	20940.6
HLA A*0301	1:69-77	9	VEELGRAGV	1.03	0.03	-4.37	1.06	-3.31	23314.8
HLA B*4601	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.37	1.06	-3.31	23284.7
HLA A*6901	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.29	0.98	-3.31	19353.9
HLA B*4402	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.43	1.11	-3.31	26614.7
HLA B*2705	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.39	1.08	-3.31	24624.8
HLA A*2603	1:31-39	9	AAPVITAVV	1.00	0.24	-4.55	1.24	-3.31	35713.5
HLA B*5401	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.45	1.13	-3.31	27889.6
HLA A*0219	1:80-88	9	GESGASYLA	1.31	-0.35	-4.27	0.96	-3.31	18606.1
HLA B*4001	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.35	1.04	-3.31	22470.5
HLA A*2603	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.61	1.30	-3.31	41116.2
HLA B*4403	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.53	1.22	-3.31	34059.4
HLA A*2902	1:17-25	9	VEALTARLA	1.29	-0.19	-4.41	1.10	-3.31	25987.8
HLA A*0219	1:17-25	9	VEALTARLA	1.29	-0.19	-4.41	1.10	-3.31	25990.2
HLA B*5801	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.35	1.04	-3.31	22546.2
HLA A*6802	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.42	1.11	-3.31	26219.9
HLA B*1501	1:69-77	9	VEELGRAGV	1.03	0.03	-4.37	1.06	-3.31	23511.0

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*2705	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.37	1.06	-3.31	23469.3
HLA A*2402	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.43	1.11	-3.31	26819.0
HLA B*4801	1:80-88	9	GESGASYLA	1.31	-0.35	-4.27	0.96	-3.31	18724.4
HLA A*0216	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.41	1.09	-3.31	25497.2
HLA A*1101	1:18-26	9	EALTARLAA	1.39	-0.27	-4.43	1.12	-3.31	27221.6
HLA A*2602	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.59	1.28	-3.31	39195.1
HLA B*1517	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.36	1.04	-3.32	22664.0
HLA A*0212	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.41	1.09	-3.32	25558.2
HLA B*5301	1:18-26	9	EALTARLAA	1.39	-0.27	-4.44	1.12	-3.32	27293.4
HLA A*3301	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.45	1.13	-3.32	28205.2
HLA A*0202	1:17-25	9	VEALTARLA	1.29	-0.19	-4.42	1.10	-3.32	26148.6
HLA B*0702	1:69-77	9	VEELGRAGV	1.03	0.03	-4.37	1.06	-3.32	23618.3
HLA A*6901	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.03	0.72	-3.32	10766.8
HLA A*2602	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.45	1.13	-3.32	28226.2
HLA A*0216	1:17-25	9	VEALTARLA	1.29	-0.19	-4.42	1.10	-3.32	26187.5
HLA B*4002	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.58	1.26	-3.32	37708.7
HLA B*0801	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.36	1.04	-3.32	22720.5
HLA A*6802	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.08	0.76	-3.32	11979.5
HLA B*5701	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.24	0.92	-3.32	17184.3
HLA A*0101	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.13	0.81	-3.32	13435.0
HLA B*0802	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.41	1.09	-3.32	25627.2
HLA A*0202	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.42	1.11	-3.32	26464.3
HLA B*1502	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.09	0.77	-3.32	12369.2
HLA A*3101	1:69-77	9	VEELGRAGV	1.03	0.03	-4.38	1.06	-3.32	23737.2
HLA B*0802	1:18-26	9	EALTARLAA	1.39	-0.27	-4.44	1.12	-3.32	27438.9
HLA B*4001	1:38-46	9	VVPPAADPV	0.76	0.28	-4.36	1.04	-3.32	22913.0
HLA B*0801	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.38	1.06	-3.32	23725.8
HLA A*0101	1:69-77	9	VEELGRAGV	1.03	0.03	-4.38	1.06	-3.32	23789.0
HLA A*0301	1:38-46	9	VVPPAADPV	0.76	0.28	-4.36	1.04	-3.32	22957.2
HLA B*0802	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.45	1.13	-3.32	28464.8
HLA A*2402	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.54	1.22	-3.32	34742.3
HLA B*4403	1:91-99	9	AAAAATYGV	1.05	0.17	-4.54	1.22	-3.32	34448.3
HLA A*0101	1:38-46	9	VVPPAADPV	0.76	0.28	-4.36	1.04	-3.32	23126.4
HLA A*2501	1:38-46	9	VVPPAADPV	0.76	0.28	-4.36	1.04	-3.32	23127.0
HLA B*4601	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.36	1.04	-3.32	23030.1
HLA B*4801	1:17-25	9	VEALTARLA	1.29	-0.19	-4.42	1.10	-3.32	26536.6
HLA A*8001	1:69-77	9	VEELGRAGV	1.03	0.03	-4.38	1.06	-3.32	23970.5
HLA A*2902	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.40	1.08	-3.32	25296.9
HLA A*1101	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.46	1.13	-3.32	28638.1
HLA B*0802	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.45	1.13	-3.32	28161.4
HLA B*0803	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.41	1.09	-3.32	25974.6
HLA B*1503	1:69-77	9	VEELGRAGV	1.03	0.03	-4.38	1.06	-3.32	24002.3
HLA A*3301	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.63	1.30	-3.32	42256.8
HLA A*2601	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.38	1.06	-3.32	24008.5
HLA B*2705	1:9-17	9	GLAAASAAV	1.01	0.00	-4.33	1.01	-3.32	21607.5
HLA B*4001	1:9-17	9	GLAAASAAV	1.01	0.00	-4.33	1.01	-3.32	21608.6
HLA B*4001	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.43	1.11	-3.32	26845.2
HLA B*5801	1:9-17	9	GLAAASAAV	1.01	0.00	-4.34	1.01	-3.32	21635.1
HLA A*2603	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.54	1.22	-3.32	34911.3

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*0802	1:69-77	9	VEELGRAGV	1.03	0.03	-4.38	1.06	-3.32	24102.6
HLA B*5301	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.55	1.22	-3.32	35080.6
HLA A*6802	1:44-52	9	DPVSLQTAA	1.05	-0.40	-3.97	0.65	-3.33	9342.4
HLA A*6802	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.14	0.82	-3.33	13935.4
HLA B*1509	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.44	1.11	-3.33	27530.4
HLA A*0219	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.42	1.09	-3.33	26156.3
HLA A*0201	1:69-77	9	VEELGRAGV	1.03	0.03	-4.38	1.06	-3.33	24163.1
HLA B*4002	1:31-39	9	AAPVITAVV	1.00	0.24	-4.57	1.24	-3.33	36993.2
HLA B*1517	1:25-33	9	AAAHASAAP	0.72	0.16	-4.20	0.88	-3.33	15940.8
HLA A*0212	1:80-88	9	GESGASYLA	1.31	-0.35	-4.28	0.96	-3.33	19273.8
HLA A*2601	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.32	1.00	-3.33	21117.9
HLA B*1801	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.42	1.09	-3.33	26255.6
HLA A*3301	1:18-26	9	EALTARLAA	1.39	-0.27	-4.45	1.12	-3.33	28046.0
HLA A*2403	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.38	1.06	-3.33	24260.8
HLA A*3002	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.41	1.08	-3.33	25661.4
HLA B*0802	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.44	1.11	-3.33	27758.8
HLA A*2403	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.34	1.01	-3.33	21832.2
HLA B*4001	1:26-34	9	AAHASAAPV	0.61	0.30	-4.24	0.91	-3.33	17440.6
HLA A*0211	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.43	1.11	-3.33	27187.6
HLA B*7301	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.46	1.13	-3.33	29105.5
HLA A*3002	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.03	0.70	-3.33	10818.4
HLA A*3201	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.43	1.10	-3.33	26863.6
HLA A*6801	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.25	0.92	-3.33	17729.1
HLA B*1501	1:10-18	9	LAAASAAVE	1.14	-0.66	-3.81	0.48	-3.33	6511.3
HLA A*0101	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.37	1.04	-3.33	23482.1
HLA A*3001	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.28	0.95	-3.33	19058.4
HLA A*2403	1:17-25	9	VEALTARLA	1.29	-0.19	-4.43	1.10	-3.33	27075.9
HLA B*2705	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.42	1.09	-3.33	26500.0
HLA B*4402	1:9-17	9	GLAAASAAV	1.01	0.00	-4.34	1.01	-3.33	22007.4
HLA B*4801	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.44	1.11	-3.33	27338.9
HLA B*7301	1:31-39	9	AAPVITAVV	1.00	0.24	-4.57	1.24	-3.33	37477.9
HLA A*0211	1:69-77	9	VEELGRAGV	1.03	0.03	-4.39	1.06	-3.33	24529.9
HLA A*2501	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.43	1.10	-3.33	27032.9
HLA B*0702	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.43	1.10	-3.33	27049.1
HLA A*3002	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.39	1.06	-3.33	24527.9
HLA A*0301	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.34	1.01	-3.33	22035.8
HLA A*0101	1:9-17	9	GLAAASAAV	1.01	0.00	-4.34	1.01	-3.33	22092.4
HLA B*4001	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.37	1.04	-3.33	23628.3
HLA B*1509	1:69-77	9	VEELGRAGV	1.03	0.03	-4.39	1.06	-3.33	24636.5
HLA B*5701	1:38-46	9	VVPPAADPV	0.76	0.28	-4.38	1.04	-3.33	23780.8
HLA A*6901	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.37	1.04	-3.33	23686.0
HLA A*0219	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.44	1.11	-3.33	27507.5
HLA A*0203	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.05	0.71	-3.33	11182.5
HLA A*2601	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.37	1.04	-3.33	23690.0
HLA A*2601	1:69-77	9	VEELGRAGV	1.03	0.03	-4.39	1.06	-3.33	24670.6
HLA A*0219	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.15	0.82	-3.33	14248.9
HLA B*4403	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.61	1.28	-3.33	41054.2
HLA A*8001	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.23	0.89	-3.34	16843.7
HLA A*2403	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.43	1.09	-3.34	26749.6

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*3002	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.38	1.04	-3.34	23749.7
HLA B*3501	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.05	0.72	-3.34	11256.2
HLA B*4402	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.38	1.04	-3.34	23780.0
HLA B*0702	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.10	0.76	-3.34	12543.2
HLA B*0801	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.35	1.01	-3.34	22221.4
HLA A*8001	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.44	1.11	-3.34	27660.0
HLA A*6802	1:8-16	9	EGLAAASAA	0.96	-0.49	-3.80	0.46	-3.34	6321.2
HLA A*2602	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.56	1.22	-3.34	36099.6
HLA A*2902	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.39	1.06	-3.34	24771.7
HLA B*4801	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.42	1.08	-3.34	26186.1
HLA B*4001	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.16	0.82	-3.34	14332.6
HLA B*0702	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.38	1.04	-3.34	23870.4
HLA A*2902	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.38	1.04	-3.34	23898.7
HLA B*3501	1:17-25	9	VEALTARLA	1.29	-0.19	-4.44	1.10	-3.34	27569.1
HLA A*0101	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.34	1.00	-3.34	21716.0
HLA B*4601	1:69-77	9	VEELGRAGV	1.03	0.03	-4.40	1.06	-3.34	24907.8
HLA A*0101	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.14	0.81	-3.34	13932.3
HLA A*3002	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.44	1.10	-3.34	27434.3
HLA A*8001	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.43	1.09	-3.34	26982.2
HLA B*4801	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.43	1.09	-3.34	26996.3
HLA B*5101	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.44	1.11	-3.34	27825.4
HLA B*1501	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.32	0.98	-3.34	20687.0
HLA B*4001	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.34	1.00	-3.34	21770.0
HLA A*2601	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.38	1.04	-3.34	24024.3
HLA B*0803	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.48	1.13	-3.34	29878.3
HLA A*6802	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.23	0.89	-3.34	17065.9
HLA A*3101	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.35	1.01	-3.34	22457.6
HLA B*5301	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.26	0.92	-3.34	18212.2
HLA A*0216	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.22	0.87	-3.34	16418.3
HLA A*2902	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.43	1.09	-3.34	27201.6
HLA B*1517	1:17-25	9	VEALTARLA	1.29	-0.19	-4.45	1.10	-3.34	27878.4
HLA B*5801	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.19	0.84	-3.34	15415.5
HLA A*2902	1:38-46	9	VVPPAADPV	0.76	0.28	-4.39	1.04	-3.34	24322.0
HLA A*0206	1:25-33	9	AAAHASAAP	0.72	0.16	-4.22	0.88	-3.34	16598.9
HLA A*6802	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.32	0.98	-3.34	20915.5
HLA A*8001	1:38-46	9	VVPPAADPV	0.76	0.28	-4.39	1.04	-3.34	24346.3
HLA B*3501	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.19	0.84	-3.34	15433.2
HLA B*5801	1:26-34	9	AAHASAAPV	0.61	0.30	-4.26	0.91	-3.34	18081.5
HLA A*3301	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.62	1.28	-3.35	42033.8
HLA B*4801	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.40	1.06	-3.35	25249.8
HLA B*4002	1:91-99	9	AAAAATYGV	1.05	0.17	-4.56	1.22	-3.35	36497.9
HLA A*0101	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.36	1.01	-3.35	22717.5
HLA B*5401	1:38-46	9	VVPPAADPV	0.76	0.28	-4.39	1.04	-3.35	24468.8
HLA A*0301	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.34	1.00	-3.35	22111.1
HLA B*5801	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.36	1.01	-3.35	22747.2
HLA B*5101	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.47	1.13	-3.35	29804.5
HLA A*0101	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.39	1.04	-3.35	24391.3
HLA B*5101	1:17-25	9	VEALTARLA	1.29	-0.19	-4.45	1.10	-3.35	28126.5
HLA B*4002	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.63	1.28	-3.35	42320.6

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*2603	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.45	1.10	-3.35	28035.4
HLA B*0702	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.45	1.11	-3.35	28425.4
HLA B*3901	1:17-25	9	VEALTARLA	1.29	-0.19	-4.45	1.10	-3.35	28211.6
HLA B*1801	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.45	1.10	-3.35	28061.6
HLA A*6901	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.24	0.89	-3.35	17399.0
HLA B*1517	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.45	1.11	-3.35	28470.7
HLA B*4801	1:38-46	9	VVPPAADPV	0.76	0.28	-4.39	1.04	-3.35	24630.8
HLA B*0801	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.33	0.98	-3.35	21186.8
HLA A*2602	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.35	1.00	-3.35	22284.2
HLA B*0803	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.45	1.10	-3.35	28152.6
HLA A*0203	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.33	0.98	-3.35	21221.4
HLA A*8001	1:9-17	9	GLAAASAAV	1.01	0.00	-4.36	1.01	-3.35	22978.5
HLA A*6801	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.61	1.26	-3.35	40789.4
HLA A*2301	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.54	1.19	-3.35	34839.5
HLA A*2501	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.24	0.89	-3.35	17464.2
HLA B*7301	1:18-26	9	EALTARLAA	1.39	-0.27	-4.47	1.12	-3.35	29605.2
HLA B*3501	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.46	1.11	-3.35	28586.1
HLA B*5801	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.35	1.00	-3.35	22346.1
HLA B*4601	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.39	1.04	-3.35	24656.8
HLA B*7301	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.57	1.22	-3.35	37202.2
HLA A*1101	1:17-25	9	VEALTARLA	1.29	-0.19	-4.45	1.10	-3.35	28441.9
HLA B*0803	1:69-77	9	VEELGRAGV	1.03	0.03	-4.41	1.06	-3.35	25725.1
HLA A*3301	1:31-39	9	AAPVITAVV	1.00	0.24	-4.59	1.24	-3.35	39354.6
HLA A*0203	1:25-33	9	AAAHASAAP	0.72	0.16	-4.23	0.88	-3.35	16948.4
HLA B*5101	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.49	1.13	-3.35	30786.5
HLA B*4801	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.39	1.04	-3.35	24772.5
HLA B*5701	1:69-77	9	VEELGRAGV	1.03	0.03	-4.41	1.06	-3.35	25791.3
HLA B*1801	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.36	1.01	-3.35	23151.8
HLA A*1101	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.46	1.11	-3.36	28940.3
HLA A*0201	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.40	1.04	-3.36	24928.7
HLA A*0206	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.17	0.81	-3.36	14837.6
HLA A*3301	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.62	1.26	-3.36	41377.5
HLA A*2501	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.46	1.11	-3.36	28971.3
HLA B*0802	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.44	1.08	-3.36	27394.6
HLA B*5701	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.40	1.04	-3.36	24952.8
HLA B*7301	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.48	1.13	-3.36	30524.1
HLA A*2501	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.36	1.00	-3.36	22677.7
HLA B*5101	1:26-34	9	AAHASAAPV	0.61	0.30	-4.27	0.91	-3.36	18621.6
HLA B*5701	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.40	1.04	-3.36	25042.2
HLA A*6801	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.17	0.81	-3.36	14808.1
HLA B*4002	1:30-38	9	SAAPVITAV	0.96	0.26	-4.57	1.21	-3.36	37368.2
HLA A*8001	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.44	1.08	-3.36	27541.9
HLA B*4801	1:69-77	9	VEELGRAGV	1.03	0.03	-4.42	1.06	-3.36	26128.0
HLA A*0250	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.55	1.19	-3.36	35563.7
HLA B*5401	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.47	1.11	-3.36	29841.0
HLA B*4002	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.58	1.22	-3.36	37933.2
HLA B*7301	1:17-25	9	VEALTARLA	1.29	-0.19	-4.46	1.10	-3.36	29036.1
HLA B*7301	1:30-38	9	SAAPVITAV	0.96	0.26	-4.58	1.21	-3.36	37625.8
HLA B*0801	1:32-40	9	APVITAVVP	0.92	0.08	-4.36	0.99	-3.36	22649.5

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*8001	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.40	1.04	-3.36	25268.5
HLA A*2403	1:69-77	9	VEELGRAGV	1.03	0.03	-4.42	1.06	-3.36	26323.0
HLA B*0803	1:18-26	9	EALTARLAA	1.39	-0.27	-4.48	1.12	-3.36	30429.8
HLA A*2902	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.47	1.11	-3.36	29397.3
HLA A*0211	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.18	0.81	-3.36	15073.7
HLA B*4601	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.34	0.98	-3.36	21868.1
HLA A*0212	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.40	1.04	-3.36	25338.2
HLA A*2501	1:17-25	9	VEALTARLA	1.29	-0.19	-4.47	1.10	-3.36	29207.2
HLA A*6901	1:32-40	9	APVITAVVP	0.92	0.08	-4.36	0.99	-3.36	22737.7
HLA A*6802	1:80-88	9	GESGASYLA	1.31	-0.35	-4.32	0.96	-3.36	21029.3
HLA B*0803	1:17-25	9	VEALTARLA	1.29	-0.19	-4.47	1.10	-3.36	29290.9
HLA B*2705	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.41	1.04	-3.37	25427.1
HLA A*2403	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.41	1.04	-3.37	25421.1
HLA A*3002	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.17	0.81	-3.37	14842.0
HLA A*6801	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.46	1.09	-3.37	28683.9
HLA B*0801	1:38-46	9	VVPPAADPV	0.76	0.28	-4.41	1.04	-3.37	25568.7
HLA B*3801	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.56	1.19	-3.37	36068.0
HLA A*2501	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.46	1.09	-3.37	28704.7
HLA B*1501	1:32-40	9	APVITAVVP	0.92	0.08	-4.36	0.99	-3.37	22843.5
HLA B*2705	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.47	1.11	-3.37	29589.5
HLA B*5801	1:32-40	9	APVITAVVP	0.92	0.08	-4.36	0.99	-3.37	22852.7
HLA A*0202	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.46	1.09	-3.37	28737.0
HLA B*4403	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.56	1.19	-3.37	36124.6
HLA B*1503	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.41	1.04	-3.37	25528.1
HLA B*3501	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.17	0.81	-3.37	14893.5
HLA B*5801	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.34	0.98	-3.37	22097.4
HLA B*1503	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.17	0.81	-3.37	14937.4
HLA B*3901	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.34	0.98	-3.37	22116.1
HLA B*4801	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.19	0.82	-3.37	15394.6
HLA A*6801	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.56	1.19	-3.37	36357.0
HLA A*0201	1:80-88	9	GESGASYLA	1.31	-0.35	-4.33	0.96	-3.37	21264.3
HLA B*7301	1:91-99	9	AAAAATYGV	1.05	0.17	-4.59	1.22	-3.37	38494.0
HLA B*7301	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.59	1.22	-3.37	38873.9
HLA A*3002	1:69-77	9	VEELGRAGV	1.03	0.03	-4.43	1.06	-3.37	26757.7
HLA A*2501	1:69-77	9	VEELGRAGV	1.03	0.03	-4.43	1.06	-3.37	26759.2
HLA A*3301	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.46	1.09	-3.37	28982.6
HLA B*5701	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.26	0.89	-3.37	18273.5
HLA A*0250	1:18-26	9	EALTARLAA	1.39	-0.27	-4.49	1.12	-3.37	30966.5
HLA A*3101	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.37	1.00	-3.37	23373.0
HLA A*8001	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.43	1.06	-3.37	26754.3
HLA B*3501	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.37	1.00	-3.37	23405.4
HLA A*0203	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.41	1.04	-3.37	25828.0
HLA A*2403	1:9-17	9	GLAAASAAV	1.01	0.00	-4.38	1.01	-3.37	24151.4
HLA B*1517	1:69-77	9	VEELGRAGV	1.03	0.03	-4.43	1.06	-3.37	26908.1
HLA A*0301	1:32-40	9	APVITAVVP	0.92	0.08	-4.37	0.99	-3.37	23189.3
HLA B*3501	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.19	0.82	-3.37	15541.2
HLA A*0211	1:17-25	9	VEALTARLA	1.29	-0.19	-4.47	1.10	-3.37	29808.5
HLA B*3901	1:38-46	9	VVPPAADPV	0.76	0.28	-4.41	1.04	-3.37	25984.0
HLA A*6801	1:56-64	9	AQGVEHAVV	1.12	0.18	-4.68	1.30	-3.37	47386.1

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*2902	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.38	1.01	-3.37	24182.3
HLA A*2603	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.59	1.22	-3.37	39265.3
HLA B*5701	1:26-34	9	AAHASAAPV	0.61	0.30	-4.29	0.91	-3.37	19335.6
HLA A*2603	1:14-22	9	SAAVEALTA	1.39	-0.11	-4.65	1.28	-3.37	44964.6
HLA B*3901	1:80-88	9	GESGASYLA	1.31	-0.35	-4.33	0.96	-3.37	21534.8
HLA B*2705	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.41	1.04	-3.37	25989.3
HLA B*0801	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.42	1.04	-3.38	26030.1
HLA A*2902	1:69-77	9	VEELGRAGV	1.03	0.03	-4.43	1.06	-3.38	27106.1
HLA B*4001	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.39	1.01	-3.38	24331.6
HLA B*5101	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.43	1.06	-3.38	27110.9
HLA B*0803	1:9-17	9	GLAAASAAV	1.01	0.00	-4.39	1.01	-3.38	24406.0
HLA B*5401	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.30	0.92	-3.38	19750.4
HLA A*2602	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.49	1.11	-3.38	31032.6
HLA B*4403	1:30-38	9	SAAPVITAV	0.96	0.26	-4.59	1.21	-3.38	39017.8
HLA B*2705	1:26-34	9	AAHASAAPV	0.61	0.30	-4.29	0.91	-3.38	19507.3
HLA A*1101	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.47	1.09	-3.38	29499.9
HLA A*1101	1:9-17	9	GLAAASAAV	1.01	0.00	-4.39	1.01	-3.38	24491.8
HLA B*5101	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.49	1.11	-3.38	31106.2
HLA A*3201	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.18	0.81	-3.38	15275.8
HLA B*4402	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.42	1.04	-3.38	26241.2
HLA B*4403	1:4-12	9	RVVPEGLAA	1.27	-0.01	-4.64	1.26	-3.38	43558.2
HLA B*3801	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.48	1.10	-3.38	30079.5
HLA B*4801	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.42	1.04	-3.38	26261.8
HLA B*0802	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.38	1.00	-3.38	23868.9
HLA A*2501	1:9-17	9	GLAAASAAV	1.01	0.00	-4.39	1.01	-3.38	24629.4
HLA B*3901	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.47	1.09	-3.38	29701.0
HLA A*3101	1:38-46	9	VVPPAADPV	0.76	0.28	-4.42	1.04	-3.38	26476.9
HLA B*2705	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.38	1.00	-3.38	23930.0
HLA B*0802	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.44	1.06	-3.38	27449.0
HLA B*2705	1:38-46	9	VVPPAADPV	0.76	0.28	-4.42	1.04	-3.38	26599.0
HLA B*5701	1:9-17	9	GLAAASAAV	1.01	0.00	-4.39	1.01	-3.38	24791.9
HLA A*1101	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.42	1.04	-3.38	26515.8
HLA B*1501	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.30	0.92	-3.38	20062.0
HLA A*3301	1:91-99	9	AAAAATYGV	1.05	0.17	-4.60	1.22	-3.38	39810.7
HLA A*0301	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.36	0.98	-3.38	22937.5
HLA A*1101	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.48	1.10	-3.38	30446.9
HLA B*3801	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.52	1.13	-3.39	33111.2
HLA B*1801	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.44	1.06	-3.39	27691.1
HLA A*1101	1:69-77	9	VEELGRAGV	1.03	0.03	-4.44	1.06	-3.39	27754.6
HLA A*8001	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.38	1.00	-3.39	24202.3
HLA B*0702	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.28	0.89	-3.39	18930.8
HLA B*1503	1:22-30	9	ARLAAAHAS	1.08	-0.81	-3.66	0.27	-3.39	4545.4
HLA B*0802	1:17-25	9	VEALTARLA	1.29	-0.19	-4.49	1.10	-3.39	30772.6
HLA B*2705	1:69-77	9	VEELGRAGV	1.03	0.03	-4.44	1.06	-3.39	27796.3
HLA B*5801	1:80-88	9	GESGASYLA	1.31	-0.35	-4.34	0.96	-3.39	22123.1
HLA A*2301	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.50	1.11	-3.39	31724.2
HLA B*1517	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.40	1.01	-3.39	24964.2
HLA A*0101	1:32-40	9	APVITAVVP	0.92	0.08	-4.38	0.99	-3.39	23991.8
HLA B*1517	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.09	0.70	-3.39	12360.4

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*1517	1:32-40	9	APVITAVVP	0.92	0.08	-4.38	0.99	-3.39	24023.9
HLA A*0250	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.49	1.11	-3.39	31128.8
HLA A*0212	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.19	0.81	-3.39	15606.0
HLA B*0802	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.49	1.11	-3.39	31150.7
HLA A*2501	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.45	1.06	-3.39	27868.0
HLA B*4002	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.61	1.22	-3.39	40617.8
HLA A*2402	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.58	1.19	-3.39	38012.3
HLA B*1801	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.47	1.08	-3.39	29475.3
HLA A*3002	1:26-34	9	AAHASAAPV	0.61	0.30	-4.30	0.91	-3.39	20011.2
HLA B*4403	1:31-39	9	AAPVITAVV	1.00	0.24	-4.63	1.24	-3.39	42757.6
HLA A*6801	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.61	1.22	-3.39	40674.8
HLA B*3801	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.52	1.13	-3.39	32877.5
HLA B*5801	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.09	0.70	-3.39	12430.5
HLA A*3101	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.31	0.92	-3.39	20345.3
HLA B*5101	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.40	1.01	-3.39	25138.1
HLA A*2603	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.58	1.19	-3.39	38179.4
HLA A*1101	1:38-46	9	VVPPAADPV	0.76	0.28	-4.43	1.04	-3.39	27112.4
HLA B*5301	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.47	1.08	-3.39	29699.7
HLA B*5401	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.20	0.81	-3.39	15791.9
HLA A*0211	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.48	1.09	-3.39	30517.2
HLA B*3901	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.50	1.11	-3.39	31466.7
HLA B*1509	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.50	1.11	-3.39	31477.5
HLA B*3901	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.43	1.04	-3.39	27104.8
HLA B*5301	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.58	1.19	-3.39	38439.3
HLA B*3501	1:69-77	9	VEELGRAGV	1.03	0.03	-4.45	1.06	-3.39	28284.2
HLA B*3501	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.20	0.81	-3.39	15852.6
HLA A*0250	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.15	0.75	-3.39	14075.6
HLA B*4601	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.39	1.00	-3.39	24676.4
HLA A*2301	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.49	1.10	-3.39	31179.5
HLA A*2403	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.39	1.00	-3.39	24700.2
HLA B*1509	1:9-17	9	GLAAASAAV	1.01	0.00	-4.41	1.01	-3.40	25467.1
HLA A*3001	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.21	0.81	-3.40	16227.9
HLA B*0803	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.50	1.11	-3.40	31701.0
HLA A*0201	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.37	0.98	-3.40	23583.0
HLA B*3801	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.51	1.11	-3.40	32435.5
HLA B*1509	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.45	1.06	-3.40	28393.3
HLA A*1101	1:26-34	9	AAHASAAPV	0.61	0.30	-4.31	0.91	-3.40	20368.6
HLA B*4403	1:55-63	9	SAQGVEHAV	1.10	0.12	-4.62	1.22	-3.40	41245.2
HLA B*1509	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.48	1.08	-3.40	30059.5
HLA A*0216	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.44	1.04	-3.40	27394.6
HLA B*0702	1:25-33	9	AAAHASAAP	0.72	0.16	-4.27	0.88	-3.40	18774.5
HLA B*4001	1:32-40	9	APVITAVVP	0.92	0.08	-4.39	0.99	-3.40	24569.3
HLA B*5101	1:69-77	9	VEELGRAGV	1.03	0.03	-4.46	1.06	-3.40	28555.5
HLA A*2403	1:32-40	9	APVITAVVP	0.92	0.08	-4.39	0.99	-3.40	24607.6
HLA A*3101	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.17	0.77	-3.40	14922.3
HLA A*3101	1:32-40	9	APVITAVVP	0.92	0.08	-4.39	0.99	-3.40	24658.9
HLA A*3002	1:18-26	9	EALTARLAA	1.39	-0.27	-4.52	1.12	-3.40	33079.7
HLA A*0219	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.44	1.04	-3.40	27506.4
HLA B*4501	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.53	1.13	-3.40	33615.1

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*2705	1:80-88	9	GESGASYLA	1.31	-0.35	-4.36	0.96	-3.40	22834.8
HLA A*0203	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.35	0.95	-3.40	22378.1
HLA B*0802	1:9-17	9	GLAAASAAV	1.01	0.00	-4.41	1.01	-3.40	25791.0
HLA A*0201	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.24	0.84	-3.40	17567.7
HLA A*3201	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.48	1.08	-3.40	30308.1
HLA A*0101	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.38	0.98	-3.40	23830.7
HLA A*2601	1:32-40	9	APVITAVVP	0.92	0.08	-4.39	0.99	-3.40	24761.5
HLA A*0202	1:18-26	9	EALTARLAA	1.39	-0.27	-4.52	1.12	-3.40	33216.8
HLA B*1509	1:18-26	9	EALTARLAA	1.39	-0.27	-4.52	1.12	-3.40	33222.6
HLA A*2603	1:30-38	9	SAAPVITAV	0.96	0.26	-4.61	1.21	-3.40	41201.4
HLA A*6802	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.44	1.04	-3.40	27659.2
HLA B*0802	1:38-46	9	VVPPAADPV	0.76	0.28	-4.44	1.04	-3.40	27779.8
HLA A*2301	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.53	1.13	-3.40	33827.4
HLA A*2501	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.48	1.08	-3.40	30402.5
HLA B*5801	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.35	0.95	-3.40	22472.0
HLA B*5401	1:6-14	9	VPEGLAAAS	1.10	-1.12	-3.38	-0.03	-3.40	2376.8
HLA B*4801	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.41	1.01	-3.40	25859.7
HLA B*5701	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.40	1.00	-3.40	25185.4
HLA A*0301	1:80-88	9	GESGASYLA	1.31	-0.35	-4.36	0.96	-3.40	22992.8
HLA A*8001	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.44	1.04	-3.40	27764.2
HLA B*1503	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.38	0.98	-3.40	23991.0
HLA B*4402	1:38-46	9	VVPPAADPV	0.76	0.28	-4.45	1.04	-3.40	27912.5
HLA B*4801	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.38	0.98	-3.40	23994.0
HLA A*8001	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.41	1.01	-3.40	25950.1
HLA A*0301	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.17	0.76	-3.40	14664.2
HLA A*0219	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.22	0.81	-3.40	16569.1
HLA B*1502	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.42	1.01	-3.40	26009.0
HLA B*1509	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.50	1.09	-3.41	31431.7
HLA B*1503	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.28	0.87	-3.41	18985.1
HLA A*0201	1:32-40	9	APVITAVVP	0.92	0.08	-4.40	0.99	-3.41	25037.6
HLA B*1509	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.32	0.92	-3.41	21112.2
HLA B*1517	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.38	0.98	-3.41	24126.4
HLA B*5701	1:32-40	9	APVITAVVP	0.92	0.08	-4.40	0.99	-3.41	25096.1
HLA B*3901	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.45	1.04	-3.41	28001.0
HLA B*0702	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.41	1.00	-3.41	25416.3
HLA A*6901	1:80-88	9	GESGASYLA	1.31	-0.35	-4.37	0.96	-3.41	23204.7
HLA B*1517	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.12	0.72	-3.41	13274.2
HLA A*3001	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.25	0.84	-3.41	17852.5
HLA A*3301	1:51-59	9	AAGFSAQGV	1.07	0.15	-4.63	1.22	-3.41	42472.4
HLA B*1509	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.45	1.04	-3.41	28062.4
HLA A*0301	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.33	0.92	-3.41	21226.0
HLA B*1503	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.42	1.01	-3.41	26228.0
HLA B*1801	1:38-46	9	VVPPAADPV	0.76	0.28	-4.45	1.04	-3.41	28237.5
HLA B*5101	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.28	0.87	-3.41	19139.1
HLA A*3201	1:18-26	9	EALTARLAA	1.39	-0.27	-4.53	1.12	-3.41	33905.3
HLA B*4601	1:32-40	9	APVITAVVP	0.92	0.08	-4.40	0.99	-3.41	25290.0
HLA B*0803	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.49	1.08	-3.41	30970.9
HLA A*0211	1:80-88	9	GESGASYLA	1.31	-0.35	-4.37	0.96	-3.41	23379.5
HLA A*0301	1:26-34	9	AAHASAAPV	0.61	0.30	-4.32	0.91	-3.41	21062.5

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*0250	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.50	1.09	-3.41	31856.9
HLA B*4501	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.50	1.09	-3.41	31858.3
HLA A*2601	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.39	0.98	-3.41	24411.8
HLA A*0101	1:80-88	9	GESGASYLA	1.31	-0.35	-4.37	0.96	-3.41	23464.4
HLA A*0101	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.36	0.95	-3.41	22981.3
HLA B*5701	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.42	1.01	-3.41	26442.7
HLA B*0802	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.45	1.04	-3.41	28333.6
HLA B*1801	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.52	1.11	-3.41	32969.2
HLA A*3201	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.42	1.01	-3.41	26512.5
HLA A*2902	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.41	1.00	-3.41	25787.0
HLA A*2501	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.45	1.04	-3.41	28414.7
HLA A*0212	1:32-40	9	APVITAVVP	0.92	0.08	-4.41	0.99	-3.41	25500.6
HLA B*1801	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.45	1.04	-3.41	28434.2
HLA A*6901	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.36	0.95	-3.41	23084.0
HLA B*1517	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.45	1.04	-3.41	28491.8
HLA B*0801	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.29	0.87	-3.42	19412.2
HLA B*4002	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.53	1.11	-3.42	33888.4
HLA B*4402	1:32-40	9	APVITAVVP	0.92	0.08	-4.41	0.99	-3.42	25615.4
HLA B*4001	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.39	0.98	-3.42	24680.6
HLA A*2601	1:26-34	9	AAHASAAPV	0.61	0.30	-4.33	0.91	-3.42	21315.6
HLA B*0803	1:38-46	9	VVPPAADPV	0.76	0.28	-4.46	1.04	-3.42	28747.0
HLA A*2402	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.54	1.13	-3.42	35059.2
HLA A*0301	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.37	0.95	-3.42	23274.2
HLA A*6801	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.53	1.11	-3.42	34052.9
HLA A*3301	1:84-92	9	ASYLAGDAA	1.27	-0.08	-4.61	1.19	-3.42	40632.4
HLA A*3002	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.51	1.09	-3.42	32327.2
HLA B*0802	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.46	1.04	-3.42	28713.1
HLA B*4801	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.34	0.92	-3.42	21705.7
HLA A*2301	1:18-26	9	EALTARLAA	1.39	-0.27	-4.54	1.12	-3.42	34556.8
HLA B*1801	1:9-17	9	GLAAASAAV	1.01	0.00	-4.43	1.01	-3.42	26858.5
HLA A*3101	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.18	0.76	-3.42	15167.1
HLA A*2603	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.31	0.89	-3.42	20449.2
HLA A*0201	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.34	0.92	-3.42	21794.1
HLA A*2603	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.55	1.13	-3.42	35840.2
HLA A*2603	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.48	1.06	-3.42	29969.7
HLA B*0801	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.31	0.89	-3.42	20479.3
HLA A*2301	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.53	1.11	-3.42	33549.9
HLA B*5101	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.46	1.04	-3.42	28895.1
HLA B*4402	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.42	1.00	-3.42	26236.3
HLA A*6802	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.37	0.95	-3.42	23477.2
HLA B*4402	1:26-34	9	AAHASAAPV	0.61	0.30	-4.33	0.91	-3.42	21595.6
HLA B*5101	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.34	0.92	-3.42	21916.8
HLA A*2403	1:80-88	9	GESGASYLA	1.31	-0.35	-4.38	0.96	-3.42	24032.2
HLA B*3801	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.50	1.08	-3.42	31859.3
HLA B*0803	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.48	1.06	-3.42	30149.8
HLA A*3301	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.55	1.13	-3.42	35475.1
HLA A*2601	1:80-88	9	GESGASYLA	1.31	-0.35	-4.38	0.96	-3.42	24073.2
HLA A*6801	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.48	1.06	-3.42	30196.8
HLA B*3801	1:18-26	9	EALTARLAA	1.39	-0.27	-4.54	1.12	-3.42	34971.6

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*3101	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.40	0.98	-3.42	25125.1
HLA A*1101	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.43	1.01	-3.42	27175.7
HLA B*1801	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.47	1.04	-3.43	29213.7
HLA B*1509	1:38-46	9	VVPPAADPV	0.76	0.28	-4.47	1.04	-3.43	29353.1
HLA B*7301	1:73-81	9	GRAGVGVGE	1.10	-0.64	-3.89	0.46	-3.43	7739.9
HLA B*5401	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.53	1.11	-3.43	33989.4
HLA B*5401	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.47	1.04	-3.43	29266.0
HLA A*0212	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.40	0.98	-3.43	25339.4
HLA A*0301	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.23	0.81	-3.43	17115.8
HLA B*5301	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.56	1.13	-3.43	35892.8
HLA B*1801	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.43	1.00	-3.43	26671.9
HLA A*6802	1:32-40	9	APVITAVVP	0.92	0.08	-4.42	0.99	-3.43	26361.8
HLA A*3001	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.14	0.72	-3.43	13936.8
HLA A*0101	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.35	0.92	-3.43	22268.5
HLA A*0202	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.41	0.98	-3.43	25451.4
HLA B*0803	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.47	1.04	-3.43	29506.7
HLA B*5701	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.41	0.98	-3.43	25489.2
HLA A*0203	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.13	0.70	-3.43	13637.6
HLA A*2301	1:38-46	9	VVPPAADPV	0.76	0.28	-4.47	1.04	-3.43	29664.7
HLA B*3801	1:69-77	9	VEELGRAGV	1.03	0.03	-4.49	1.06	-3.43	30743.7
HLA B*0803	1:26-34	9	AAHASAAPV	0.61	0.30	-4.34	0.91	-3.43	22024.6
HLA B*5401	1:25-33	9	AAAHASAAP	0.72	0.16	-4.31	0.88	-3.43	20282.9
HLA B*4002	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.57	1.13	-3.43	36796.8
HLA B*0801	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.35	0.92	-3.43	22389.8
HLA B*5101	1:9-17	9	GLAAASAAV	1.01	0.00	-4.44	1.01	-3.43	27708.8
HLA B*2705	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.44	1.01	-3.43	27666.7
HLA B*1502	1:69-77	9	VEELGRAGV	1.03	0.03	-4.49	1.06	-3.43	30928.4
HLA B*3801	1:17-25	9	VEALTARLA	1.29	-0.19	-4.53	1.10	-3.43	34244.1
HLA B*1502	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.49	1.06	-3.43	30916.0
HLA A*0202	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.47	1.04	-3.43	29766.0
HLA B*4402	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.44	1.01	-3.43	27773.6
HLA A*3101	1:80-88	9	GESGASYLA	1.31	-0.35	-4.39	0.96	-3.43	24666.2
HLA A*0202	1:69-77	9	VEELGRAGV	1.03	0.03	-4.49	1.06	-3.43	31032.9
HLA B*4801	1:32-40	9	APVITAVVP	0.92	0.08	-4.43	0.99	-3.43	26761.2
HLA B*4002	1:18-26	9	EALTARLAA	1.39	-0.27	-4.56	1.12	-3.44	35938.9
HLA A*1101	1:80-88	9	GESGASYLA	1.31	-0.35	-4.39	0.96	-3.44	24757.7
HLA B*7301	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.55	1.11	-3.44	35481.8
HLA B*4801	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.43	1.00	-3.44	27129.3
HLA B*0702	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.24	0.81	-3.44	17409.8
HLA A*3001	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.14	0.70	-3.44	13838.8
HLA A*6901	1:25-33	9	AAAHASAAP	0.72	0.16	-4.31	0.88	-3.44	20542.6
HLA B*7301	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.53	1.09	-3.44	33787.4
HLA A*0203	1:32-40	9	APVITAVVP	0.92	0.08	-4.43	0.99	-3.44	26913.7
HLA B*5801	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.31	0.87	-3.44	20435.2
HLA A*3002	1:17-25	9	VEALTARLA	1.29	-0.19	-4.54	1.10	-3.44	34612.9
HLA B*4001	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.36	0.92	-3.44	22714.5
HLA A*0101	1:26-34	9	AAHASAAPV	0.61	0.30	-4.35	0.91	-3.44	22423.9
HLA A*0219	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.42	0.98	-3.44	26009.0
HLA A*2602	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.53	1.09	-3.44	33947.3

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*0201	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.25	0.81	-3.44	17939.8
HLA A*3101	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.24	0.81	-3.44	17577.1
HLA A*2603	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.57	1.13	-3.44	36861.0
HLA A*2402	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.54	1.10	-3.44	34560.7
HLA A*2403	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.42	0.98	-3.44	26054.9
HLA A*0201	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.19	0.75	-3.44	15628.9
HLA A*2301	1:17-25	9	VEALTARLA	1.29	-0.19	-4.54	1.10	-3.44	34838.1
HLA A*0301	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.25	0.81	-3.44	17619.2
HLA A*0201	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.39	0.95	-3.44	24582.4
HLA B*2705	1:32-40	9	APVITAVVP	0.92	0.08	-4.43	0.99	-3.44	27191.7
HLA A*0219	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.25	0.81	-3.44	17921.9
HLA B*0702	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.09	0.65	-3.44	12219.6
HLA B*5101	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.44	1.00	-3.44	27553.5
HLA B*4601	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.25	0.81	-3.44	17683.0
HLA A*3101	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.26	0.82	-3.44	18269.4
HLA A*6801	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.01	0.57	-3.44	10258.6
HLA A*2402	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.55	1.11	-3.44	35319.8
HLA A*2601	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.39	0.95	-3.44	24685.6
HLA B*0702	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.36	0.92	-3.44	23043.1
HLA A*2902	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.29	0.84	-3.44	19407.9
HLA B*1801	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.34	0.89	-3.44	21656.4
HLA B*7301	1:80-88	9	GESGASYLA	1.31	-0.35	-4.40	0.96	-3.44	25310.5
HLA B*1501	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.26	0.81	-3.44	18188.0
HLA B*5401	1:9-17	9	GLAAASAAV	1.01	0.00	-4.46	1.01	-3.45	28590.3
HLA A*2301	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.54	1.09	-3.45	34474.8
HLA B*0702	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.42	0.98	-3.45	26417.9
HLA B*4002	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.50	1.06	-3.45	31848.0
HLA B*1502	1:18-26	9	EALTARLAA	1.39	-0.27	-4.57	1.12	-3.45	36907.5
HLA A*2402	1:17-25	9	VEALTARLA	1.29	-0.19	-4.55	1.10	-3.45	35359.5
HLA B*4002	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.57	1.13	-3.45	37564.0
HLA B*1501	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.40	0.95	-3.45	24944.9
HLA B*5701	1:80-88	9	GESGASYLA	1.31	-0.35	-4.41	0.96	-3.45	25470.3
HLA A*2403	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.37	0.92	-3.45	23255.6
HLA B*4801	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.40	0.95	-3.45	24964.3
HLA B*2705	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.37	0.92	-3.45	23301.7
HLA B*3801	1:38-46	9	VVPPAADPV	0.76	0.28	-4.49	1.04	-3.45	30963.3
HLA A*0203	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.34	0.89	-3.45	21893.9
HLA B*0801	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.40	0.95	-3.45	25038.6
HLA A*3101	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.40	0.95	-3.45	25039.8
HLA A*2301	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.53	1.08	-3.45	33892.3
HLA B*1509	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.45	1.00	-3.45	28022.1
HLA A*2403	1:26-34	9	AAHASAAPV	0.61	0.30	-4.36	0.91	-3.45	23020.3
HLA B*3501	1:80-88	9	GESGASYLA	1.31	-0.35	-4.41	0.96	-3.45	25605.7
HLA A*2402	1:18-26	9	EALTARLAA	1.39	-0.27	-4.57	1.12	-3.45	37221.9
HLA B*1801	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.43	0.98	-3.45	26722.2
HLA B*3901	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.46	1.01	-3.45	28889.0
HLA A*0219	1:32-40	9	APVITAVVP	0.92	0.08	-4.44	0.99	-3.45	27766.4
HLA B*1517	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.45	1.00	-3.45	28102.7
HLA A*0211	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.43	0.98	-3.45	26747.5

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*4601	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.37	0.92	-3.45	23426.6
HLA B*5301	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.59	1.13	-3.45	38538.0
HLA A*0202	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.34	0.89	-3.45	22029.1
HLA B*4403	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.56	1.11	-3.45	36049.1
HLA B*1801	1:32-40	9	APVITAVVP	0.92	0.08	-4.44	0.99	-3.45	27842.1
HLA B*4601	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.40	0.95	-3.45	25198.2
HLA B*0802	1:26-34	9	AAHASAAPV	0.61	0.30	-4.36	0.91	-3.45	23170.2
HLA A*3001	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.26	0.81	-3.45	18376.2
HLA B*1509	1:26-34	9	AAHASAAPV	0.61	0.30	-4.37	0.91	-3.45	23181.4
HLA B*3801	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.56	1.11	-3.45	36139.5
HLA B*0803	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.49	1.04	-3.45	31124.6
HLA B*0702	1:80-88	9	GESGASYLA	1.31	-0.35	-4.41	0.96	-3.45	25786.0
HLA B*0801	1:80-88	9	GESGASYLA	1.31	-0.35	-4.41	0.96	-3.45	25828.6
HLA A*2501	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.49	1.04	-3.45	31240.0
HLA A*0206	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.37	0.92	-3.45	23628.7
HLA B*4601	1:80-88	9	GESGASYLA	1.31	-0.35	-4.41	0.96	-3.45	25896.1
HLA B*3901	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.45	1.00	-3.46	28400.9
HLA B*5401	1:26-34	9	AAHASAAPV	0.61	0.30	-4.37	0.91	-3.46	23339.9
HLA A*0219	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.37	0.92	-3.46	23696.9
HLA A*3301	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.57	1.11	-3.46	37329.4
HLA A*8001	1:32-40	9	APVITAVVP	0.92	0.08	-4.45	0.99	-3.46	28229.3
HLA A*2603	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.57	1.11	-3.46	37497.2
HLA B*5101	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.50	1.04	-3.46	31619.1
HLA B*4402	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.44	0.98	-3.46	27296.4
HLA A*0203	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.30	0.84	-3.46	20136.6
HLA B*3501	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.27	0.81	-3.46	18701.6
HLA A*6802	1:90-98	9	DAAAAATYG	0.74	-0.73	-3.47	0.01	-3.46	2950.5
HLA B*5301	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.55	1.09	-3.46	35691.3
HLA B*5401	1:69-77	9	VEELGRAGV	1.03	0.03	-4.52	1.06	-3.46	32976.9
HLA A*2902	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.44	0.98	-3.46	27369.9
HLA B*4403	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.54	1.08	-3.46	34816.8
HLA B*4501	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.50	1.04	-3.46	31698.3
HLA B*5101	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.41	0.95	-3.46	25743.2
HLA B*4402	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.41	0.95	-3.46	25753.2
HLA B*2705	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.44	0.98	-3.46	27452.3
HLA A*0250	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.31	0.84	-3.46	20246.2
HLA A*6901	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.28	0.82	-3.46	19129.5
HLA B*3801	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.55	1.09	-3.46	35891.5
HLA B*7301	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.57	1.11	-3.46	36995.1
HLA A*2902	1:32-40	9	APVITAVVP	0.92	0.08	-4.46	0.99	-3.46	28593.1
HLA B*5701	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.41	0.95	-3.46	25876.8
HLA B*3801	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.50	1.04	-3.46	31935.6
HLA B*4501	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.56	1.10	-3.46	36616.7
HLA B*4001	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.41	0.95	-3.46	25939.3
HLA A*2601	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.38	0.92	-3.47	24196.7
HLA B*0801	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.27	0.81	-3.47	18671.0
HLA A*0301	1:25-33	9	AAAHASAAP	0.72	0.16	-4.34	0.88	-3.47	21944.4
HLA A*2602	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.55	1.08	-3.47	35160.6
HLA A*0212	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.28	0.81	-3.47	18941.0

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*1101	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.44	0.98	-3.47	27739.4
HLA B*7301	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.55	1.08	-3.47	35280.4
HLA B*0702	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.42	0.95	-3.47	26097.3
HLA A*0250	1:17-25	9	VEALTARLA	1.29	-0.19	-4.57	1.10	-3.47	37069.4
HLA A*2902	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.27	0.81	-3.47	18735.8
HLA A*0216	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.44	0.98	-3.47	27829.7
HLA B*3801	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.51	1.04	-3.47	32320.9
HLA B*5101	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.45	0.98	-3.47	27910.4
HLA A*2501	1:80-88	9	GESGASYLA	1.31	-0.35	-4.43	0.96	-3.47	26796.0
HLA A*2402	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.53	1.06	-3.47	33644.9
HLA B*1502	1:17-25	9	VEALTARLA	1.29	-0.19	-4.57	1.10	-3.47	37326.0
HLA B*3801	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.53	1.06	-3.47	33680.4
HLA A*0101	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.34	0.87	-3.47	22074.8
HLA A*8001	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.42	0.95	-3.47	26329.0
HLA B*5801	1:25-33	9	AAAHASAAP	0.72	0.16	-4.35	0.88	-3.47	22244.3
HLA B*3901	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.29	0.82	-3.47	19505.2
HLA A*0206	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.42	0.95	-3.47	26337.2
HLA B*0802	1:32-40	9	APVITAVVP	0.92	0.08	-4.46	0.99	-3.47	29115.2
HLA A*2902	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.42	0.95	-3.47	26363.2
HLA B*4601	1:25-33	9	AAAHASAAP	0.72	0.16	-4.35	0.88	-3.47	22270.8
HLA A*2301	1:69-77	9	VEELGRAGV	1.03	0.03	-4.53	1.06	-3.47	33827.3
HLA B*5401	1:80-88	9	GESGASYLA	1.31	-0.35	-4.43	0.96	-3.47	26930.0
HLA A*2402	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.55	1.08	-3.47	35698.6
HLA A*8001	1:80-88	9	GESGASYLA	1.31	-0.35	-4.43	0.96	-3.47	26933.8
HLA A*3002	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.58	1.11	-3.47	37802.1
HLA A*2402	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.51	1.04	-3.47	32665.3
HLA B*4403	1:18-26	9	EALTARLAA	1.39	-0.27	-4.59	1.12	-3.47	39319.7
HLA A*8001	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.45	0.98	-3.47	28242.1
HLA A*1101	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.47	1.00	-3.48	29723.3
HLA B*0803	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.49	1.01	-3.48	30570.9
HLA A*2301	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.52	1.04	-3.48	32772.0
HLA A*0212	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.42	0.95	-3.48	26599.6
HLA B*0802	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.49	1.01	-3.48	30607.9
HLA A*2301	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.52	1.04	-3.48	32816.6
HLA A*8001	1:26-34	9	AAHASAAPV	0.61	0.30	-4.39	0.91	-3.48	24495.8
HLA A*2403	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.43	0.95	-3.48	26677.7
HLA B*4402	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.30	0.82	-3.48	19765.2
HLA B*1502	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.57	1.09	-3.48	37081.2
HLA A*2902	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.29	0.81	-3.48	19457.1
HLA B*1502	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.58	1.11	-3.48	38289.9
HLA A*2402	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.57	1.09	-3.48	37156.9
HLA A*1101	1:32-40	9	APVITAVVP	0.92	0.08	-4.47	0.99	-3.48	29606.0
HLA B*1503	1:80-88	9	GESGASYLA	1.31	-0.35	-4.44	0.96	-3.48	27350.3
HLA A*1101	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.25	0.77	-3.48	17928.7
HLA B*1509	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.43	0.95	-3.48	26846.8
HLA A*2403	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.37	0.89	-3.48	23492.3
HLA A*3201	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.29	0.81	-3.48	19304.5
HLA B*0702	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.26	0.77	-3.48	17994.2
HLA B*4601	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.23	0.75	-3.48	17168.2

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*2705	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.37	0.89	-3.48	23553.1
HLA A*0212	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.40	0.92	-3.48	25087.4
HLA A*3002	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.52	1.04	-3.48	33189.0
HLA A*0250	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.29	0.81	-3.48	19323.2
HLA A*0211	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.52	1.04	-3.48	33224.2
HLA B*3801	1:32-40	9	APVITAVVP	0.92	0.08	-4.47	0.99	-3.48	29830.9
HLA B*0803	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.48	1.00	-3.48	30192.2
HLA A*2601	1:25-33	9	AAAHASAAP	0.72	0.16	-4.36	0.88	-3.48	22834.6
HLA A*0301	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.36	0.87	-3.48	22689.5
HLA B*7301	1:69-77	9	VEELGRAGV	1.03	0.03	-4.54	1.06	-3.48	34708.1
HLA A*0216	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.40	0.92	-3.48	25218.3
HLA A*3002	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.48	1.00	-3.48	30344.6
HLA B*1502	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.56	1.08	-3.48	36718.9
HLA A*2301	1:9-17	9	GLAAASAAV	1.01	0.00	-4.50	1.01	-3.48	31261.4
HLA B*0801	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.13	0.65	-3.48	13476.9
HLA A*6801	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.62	1.13	-3.48	41588.2
HLA B*5801	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.24	0.75	-3.48	17330.7
HLA B*7301	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.58	1.10	-3.48	38359.3
HLA A*0202	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.33	0.84	-3.48	21330.7
HLA A*0301	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.33	0.84	-3.48	21333.1
HLA A*3301	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.58	1.10	-3.49	38402.5
HLA A*3101	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.29	0.81	-3.49	19508.4
HLA B*1509	1:32-40	9	APVITAVVP	0.92	0.08	-4.48	0.99	-3.49	30060.2
HLA A*0219	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.33	0.84	-3.49	21408.8
HLA A*2301	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.54	1.06	-3.49	34932.5
HLA B*0801	1:25-33	9	AAAHASAAP	0.72	0.16	-4.36	0.88	-3.49	23057.4
HLA B*5301	1:17-25	9	VEALTARLA	1.29	-0.19	-4.59	1.10	-3.49	38771.2
HLA A*6801	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.24	0.75	-3.49	17443.9
HLA B*3901	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.26	0.77	-3.49	18292.6
HLA B*1509	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.53	1.04	-3.49	33699.4
HLA B*7301	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.54	1.06	-3.49	35027.3
HLA B*5301	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.60	1.11	-3.49	40032.5
HLA A*1101	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.30	0.81	-3.49	19730.2
HLA A*0301	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.26	0.77	-3.49	18368.0
HLA B*5301	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.55	1.06	-3.49	35196.7
HLA B*5801	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.30	0.81	-3.49	19758.4
HLA B*5101	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.24	0.75	-3.49	17578.6
HLA A*0216	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.44	0.95	-3.49	27563.0
HLA A*0212	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.38	0.89	-3.49	24162.8
HLA A*2403	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.34	0.84	-3.49	21686.9
HLA B*0802	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.47	0.98	-3.49	29425.3
HLA A*2602	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.60	1.11	-3.49	39659.0
HLA A*3201	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.60	1.11	-3.49	39682.2
HLA A*0216	1:32-40	9	APVITAVVP	0.92	0.08	-4.49	0.99	-3.49	30672.8
HLA A*2501	1:32-40	9	APVITAVVP	0.92	0.08	-4.49	0.99	-3.49	30673.4
HLA B*4403	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.20	0.71	-3.49	15966.3
HLA B*1509	1:60-68	9	EHAVVTAEG	0.69	-0.66	-3.52	0.02	-3.49	3286.7
HLA A*0201	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.39	0.89	-3.49	24323.3
HLA B*4001	1:25-33	9	AAAHASAAP	0.72	0.16	-4.37	0.88	-3.49	23489.0

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*3901	1:25-33	9	AAAHASAAP	0.72	0.16	-4.37	0.88	-3.49	23490.1
HLA A*2902	1:26-34	9	AAHASAAPV	0.61	0.30	-4.41	0.91	-3.50	25583.7
HLA B*0801	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.31	0.82	-3.50	20637.0
HLA B*4403	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.60	1.10	-3.50	39386.2
HLA B*5301	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.60	1.11	-3.50	39929.2
HLA A*0219	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.45	0.95	-3.50	27911.5
HLA A*2402	1:9-17	9	GLAAASAAV	1.01	0.00	-4.51	1.01	-3.50	32197.9
HLA A*6801	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.54	1.04	-3.50	34457.3
HLA B*4403	1:85-93	9	SYLAGDAAA	1.15	-0.02	-4.63	1.13	-3.50	42870.0
HLA A*2501	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.47	0.98	-3.50	29787.2
HLA A*0206	1:32-40	9	APVITAVVP	0.92	0.08	-4.49	0.99	-3.50	30976.8
HLA A*6901	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.26	0.76	-3.50	18229.9
HLA B*4402	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.42	0.92	-3.50	26166.2
HLA B*4801	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.39	0.89	-3.50	24573.7
HLA A*0206	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.54	1.04	-3.50	34643.8
HLA B*3801	1:9-17	9	GLAAASAAV	1.01	0.00	-4.51	1.01	-3.50	32391.3
HLA A*2603	1:38-46	9	VVPPAADPV	0.76	0.28	-4.54	1.04	-3.50	34818.7
HLA A*0101	1:25-33	9	AAAHASAAP	0.72	0.16	-4.38	0.88	-3.50	23772.4
HLA A*3301	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.51	1.01	-3.50	32392.2
HLA B*5401	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.39	0.89	-3.50	24644.8
HLA A*2501	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.31	0.81	-3.50	20208.1
HLA B*4002	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.58	1.08	-3.50	38129.1
HLA B*3501	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.45	0.95	-3.50	28203.9
HLA B*1502	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.26	0.76	-3.50	18324.4
HLA B*3901	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.39	0.89	-3.50	24697.3
HLA B*7301	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.51	1.01	-3.50	32477.3
HLA A*2301	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.50	1.00	-3.50	31594.0
HLA A*2602	1:26-34	9	AAHASAAPV	0.61	0.30	-4.42	0.91	-3.50	26015.2
HLA B*5701	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.35	0.84	-3.50	22237.0
HLA B*0802	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.42	0.92	-3.50	26423.3
HLA B*1509	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.39	0.89	-3.50	24816.7
HLA B*5301	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.54	1.04	-3.50	35010.6
HLA A*2601	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.38	0.87	-3.50	23859.1
HLA B*4601	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.32	0.81	-3.50	20723.5
HLA B*4402	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.38	0.87	-3.50	23877.2
HLA B*1509	1:80-88	9	GESGASYLA	1.31	-0.35	-4.46	0.96	-3.51	29087.8
HLA A*3101	1:25-33	9	AAAHASAAP	0.72	0.16	-4.38	0.88	-3.51	24069.3
HLA B*0802	1:80-88	9	GESGASYLA	1.31	-0.35	-4.46	0.96	-3.51	29102.2
HLA B*0803	1:80-88	9	GESGASYLA	1.31	-0.35	-4.46	0.96	-3.51	29109.1
HLA B*1517	1:80-88	9	GESGASYLA	1.31	-0.35	-4.46	0.96	-3.51	29118.1
HLA A*3201	1:17-25	9	VEALTARLA	1.29	-0.19	-4.61	1.10	-3.51	40561.9
HLA A*3101	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.38	0.87	-3.51	23961.0
HLA A*3201	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.28	0.77	-3.51	19108.5
HLA B*1517	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.46	0.95	-3.51	28574.4
HLA B*0801	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.31	0.81	-3.51	20513.1
HLA A*0201	1:25-33	9	AAAHASAAP	0.72	0.16	-4.38	0.88	-3.51	24190.9
HLA B*0801	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.32	0.81	-3.51	20867.2
HLA A*2403	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.38	0.87	-3.51	24036.0
HLA B*4402	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.40	0.89	-3.51	25071.6

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*2902	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.43	0.92	-3.51	26700.3
HLA B*4001	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.40	0.89	-3.51	25078.8
HLA A*2402	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.55	1.04	-3.51	35322.5
HLA A*3001	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.22	0.71	-3.51	16697.8
HLA A*2602	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.31	0.81	-3.51	20638.9
HLA B*4403	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.57	1.06	-3.51	36773.6
HLA B*0803	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.49	0.98	-3.51	30587.7
HLA B*1509	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.52	1.01	-3.51	33073.9
HLA B*4002	1:61-69	9	HAVVTAEGV	1.02	0.08	-4.61	1.10	-3.51	40652.8
HLA A*1101	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.43	0.92	-3.51	26828.6
HLA A*6801	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.22	0.70	-3.51	16413.3
HLA A*2602	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.23	0.72	-3.51	16866.8
HLA B*4501	1:9-17	9	GLAAASAAV	1.01	0.00	-4.52	1.01	-3.51	33251.4
HLA B*1801	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.38	0.87	-3.51	24217.4
HLA B*0801	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.29	0.77	-3.51	19327.0
HLA B*5401	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.55	1.04	-3.51	35624.1
HLA A*6801	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.55	1.04	-3.51	35628.6
HLA B*3801	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.51	1.00	-3.51	32384.3
HLA B*0802	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.40	0.89	-3.51	25334.9
HLA A*2501	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.32	0.81	-3.51	21096.6
HLA A*1101	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.46	0.95	-3.51	28997.3
HLA A*2603	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.62	1.11	-3.51	41544.8
HLA A*1101	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.32	0.81	-3.51	20832.7
HLA B*0803	1:32-40	9	APVITAVVP	0.92	0.08	-4.51	0.99	-3.51	32124.5
HLA B*0702	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.32	0.81	-3.51	20902.1
HLA A*2602	1:17-25	9	VEALTARLA	1.29	-0.19	-4.62	1.10	-3.51	41321.3
HLA A*2403	1:25-33	9	AAAHASAAP	0.72	0.16	-4.39	0.88	-3.51	24576.2
HLA A*0206	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.23	0.72	-3.51	17013.2
HLA A*0202	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.33	0.81	-3.51	21358.1
HLA A*0212	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.27	0.75	-3.52	18631.8
HLA A*2902	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.39	0.87	-3.52	24497.9
HLA A*0101	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.34	0.82	-3.52	21648.0
HLA B*2705	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.33	0.81	-3.52	21304.0
HLA A*2403	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.34	0.82	-3.52	21662.6
HLA B*5101	1:80-88	9	GESGASYLA	1.31	-0.35	-4.48	0.96	-3.52	29865.0
HLA A*0211	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.44	0.92	-3.52	27267.9
HLA A*8001	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.44	0.92	-3.52	27305.4
HLA B*1801	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.44	0.92	-3.52	27349.6
HLA A*2402	1:69-77	9	VEELGRAGV	1.03	0.03	-4.58	1.06	-3.52	37675.9
HLA B*4801	1:25-33	9	AAAHASAAP	0.72	0.16	-4.39	0.88	-3.52	24810.3
HLA B*3801	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.53	1.01	-3.52	33792.3
HLA A*2603	1:26-34	9	AAHASAAPV	0.61	0.30	-4.43	0.91	-3.52	27009.6
HLA A*2301	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.53	1.01	-3.52	33821.6
HLA B*5701	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.39	0.87	-3.52	24675.1
HLA A*2603	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.61	1.09	-3.52	40883.7
HLA A*0212	1:25-33	9	AAAHASAAP	0.72	0.16	-4.40	0.88	-3.52	24900.5
HLA A*2402	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.52	1.00	-3.52	32997.1
HLA B*1502	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.56	1.04	-3.52	36381.8
HLA B*5801	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.34	0.82	-3.52	21872.8

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*0219	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.28	0.75	-3.52	18845.4
HLA B*5701	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.33	0.81	-3.52	21188.4
HLA A*2402	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.53	1.01	-3.52	33975.4
HLA B*4001	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.39	0.87	-3.52	24791.4
HLA B*4501	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.28	0.76	-3.52	19210.8
HLA B*1501	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.37	0.84	-3.52	23227.8
HLA A*3201	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.56	1.04	-3.52	36557.8
HLA A*6901	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.34	0.81	-3.52	21757.9
HLA B*3901	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.28	0.75	-3.52	18942.4
HLA B*4002	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.62	1.09	-3.52	41239.6
HLA A*2403	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.34	0.81	-3.52	21653.9
HLA A*0301	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.34	0.82	-3.52	22019.2
HLA B*3901	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.47	0.95	-3.52	29734.3
HLA B*4403	1:86-94	9	YLAGDAAAA	1.33	-0.20	-4.65	1.13	-3.52	44799.0
HLA B*0702	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.34	0.82	-3.52	22033.1
HLA A*2601	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.24	0.72	-3.52	17412.4
HLA A*0206	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.42	0.89	-3.52	26069.9
HLA A*2603	1:69-77	9	VEELGRAGV	1.03	0.03	-4.58	1.06	-3.53	38255.3
HLA B*4501	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.52	1.00	-3.53	33376.1
HLA A*3002	1:80-88	9	GESGASYLA	1.31	-0.35	-4.48	0.96	-3.53	30506.4
HLA A*3201	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.62	1.09	-3.53	41503.5
HLA B*5301	1:69-77	9	VEELGRAGV	1.03	0.03	-4.58	1.06	-3.53	38342.3
HLA B*4402	1:25-33	9	AAAHASAAP	0.72	0.16	-4.40	0.88	-3.53	25279.9
HLA B*0702	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.37	0.84	-3.53	23490.5
HLA A*2602	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.33	0.81	-3.53	21474.8
HLA A*2602	1:69-77	9	VEELGRAGV	1.03	0.03	-4.58	1.06	-3.53	38411.5
HLA A*3002	1:25-33	9	AAAHASAAP	0.72	0.16	-4.40	0.88	-3.53	25320.1
HLA B*5301	1:38-46	9	VVPPAADPV	0.76	0.28	-4.57	1.04	-3.53	37109.1
HLA A*0250	1:80-88	9	GESGASYLA	1.31	-0.35	-4.49	0.96	-3.53	30606.5
HLA B*4601	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.37	0.84	-3.53	23545.0
HLA A*2602	1:9-17	9	GLAAASAAV	1.01	0.00	-4.54	1.01	-3.53	34656.7
HLA A*3101	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.37	0.84	-3.53	23611.0
HLA B*1502	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.42	0.89	-3.53	26358.3
HLA B*5401	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.53	1.00	-3.53	33733.1
HLA A*6802	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.37	0.84	-3.53	23675.6
HLA A*0301	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.35	0.81	-3.53	22143.0
HLA A*3301	1:17-25	9	VEALTARLA	1.29	-0.19	-4.63	1.10	-3.53	42870.4
HLA B*1801	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.31	0.77	-3.53	20215.5
HLA A*0219	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.42	0.89	-3.53	26466.6
HLA A*6801	1:38-46	9	VVPPAADPV	0.76	0.28	-4.57	1.04	-3.53	37485.0
HLA A*3201	1:69-77	9	VEELGRAGV	1.03	0.03	-4.59	1.06	-3.53	38867.6
HLA A*0101	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.31	0.77	-3.53	20281.1
HLA B*1509	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.34	0.81	-3.53	21778.3
HLA A*0250	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.57	1.04	-3.53	37427.5
HLA A*2501	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.45	0.92	-3.53	28350.7
HLA B*1509	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.35	0.81	-3.53	22176.7
HLA B*4801	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.41	0.87	-3.53	25564.0
HLA B*5801	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.35	0.81	-3.53	22367.9
HLA B*0802	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.48	0.95	-3.54	30506.9

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*1801	1:26-34	9	AAHASAAPV	0.61	0.30	-4.45	0.91	-3.54	28037.5
HLA A*2601	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.35	0.81	-3.54	22245.4
HLA B*4001	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.38	0.84	-3.54	23973.2
HLA A*2601	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.34	0.81	-3.54	21958.7
HLA B*5701	1:25-33	9	AAAHASAAP	0.72	0.16	-4.41	0.88	-3.54	25833.0
HLA A*0206	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.24	0.70	-3.54	17430.9
HLA A*3301	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.62	1.08	-3.54	41442.2
HLA A*0211	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.49	0.95	-3.54	30626.7
HLA A*3301	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.64	1.11	-3.54	43890.1
HLA A*2902	1:25-33	9	AAAHASAAP	0.72	0.16	-4.41	0.88	-3.54	25928.9
HLA A*8001	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.38	0.84	-3.54	24133.3
HLA A*3002	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.36	0.82	-3.54	22794.3
HLA A*0211	1:32-40	9	APVITAVVP	0.92	0.08	-4.53	0.99	-3.54	34035.4
HLA A*2501	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.49	0.95	-3.54	30813.1
HLA A*3002	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.30	0.76	-3.54	20019.0
HLA A*2601	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.38	0.84	-3.54	24233.1
HLA A*2603	1:17-25	9	VEALTARLA	1.29	-0.19	-4.64	1.10	-3.54	43932.3
HLA A*0101	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.35	0.81	-3.54	22300.7
HLA A*0301	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.30	0.75	-3.54	19831.5
HLA A*2602	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.58	1.04	-3.54	38304.0
HLA B*7301	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.36	0.82	-3.54	23045.3
HLA B*4002	1:9-17	9	GLAAASAAV	1.01	0.00	-4.56	1.01	-3.54	35894.2
HLA B*3801	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.52	0.98	-3.54	33171.2
HLA B*5301	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.58	1.04	-3.54	38428.9
HLA A*8001	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.32	0.77	-3.54	20859.8
HLA B*7301	1:38-46	9	VVPPAADPV	0.76	0.28	-4.59	1.04	-3.54	38617.5
HLA B*0803	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.49	0.95	-3.54	31209.7
HLA A*3301	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.59	1.04	-3.55	38491.3
HLA A*6801	1:17-25	9	VEALTARLA	1.29	-0.19	-4.65	1.10	-3.55	44350.5
HLA B*7301	1:32-40	9	APVITAVVP	0.92	0.08	-4.54	0.99	-3.55	34514.4
HLA A*0202	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.49	0.95	-3.55	31227.8
HLA B*4601	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.35	0.81	-3.55	22450.6
HLA B*4403	1:23-31	9	RLAAAHASA	1.16	-0.04	-4.66	1.11	-3.55	45784.2
HLA B*7301	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.35	0.81	-3.55	22468.8
HLA B*5301	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.19	0.65	-3.55	15558.9
HLA A*2301	1:32-40	9	APVITAVVP	0.92	0.08	-4.54	0.99	-3.55	34634.1
HLA B*4001	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.26	0.71	-3.55	18020.4
HLA A*2501	1:26-34	9	AAHASAAPV	0.61	0.30	-4.46	0.91	-3.55	28805.0
HLA A*1101	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.37	0.82	-3.55	23257.6
HLA B*1502	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.52	0.98	-3.55	33429.7
HLA A*0219	1:25-33	9	AAAHASAAP	0.72	0.16	-4.42	0.88	-3.55	26550.4
HLA A*8001	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.42	0.87	-3.55	26412.4
HLA A*1101	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.39	0.84	-3.55	24723.7
HLA A*3301	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.32	0.77	-3.55	21129.9
HLA B*5101	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.36	0.81	-3.55	22665.1
HLA A*0301	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.36	0.81	-3.55	23036.8
HLA A*3301	1:69-77	9	VEELGRAGV	1.03	0.03	-4.61	1.06	-3.55	40633.5
HLA B*5301	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.56	1.01	-3.55	36444.0
HLA A*6801	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.55	1.00	-3.55	35476.2

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*4002	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.59	1.04	-3.55	39121.6
HLA B*0801	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.27	0.72	-3.55	18538.5
HLA A*3301	1:29-37	9	ASAAPVITA	1.21	-0.15	-4.61	1.06	-3.55	40666.9
HLA B*5301	1:26-34	9	AAHASAAPV	0.61	0.30	-4.47	0.91	-3.55	29231.9
HLA B*5401	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.53	0.98	-3.55	33910.8
HLA B*0801	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.40	0.84	-3.56	25074.6
HLA B*3901	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.40	0.84	-3.56	25083.0
HLA A*3002	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.37	0.81	-3.56	23474.8
HLA B*7301	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.60	1.04	-3.56	39441.4
HLA A*3002	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.51	0.95	-3.56	32033.2
HLA A*0101	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.31	0.75	-3.56	20462.0
HLA A*3301	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.60	1.04	-3.56	39533.0
HLA A*2902	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.38	0.82	-3.56	23771.8
HLA B*5301	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.37	0.81	-3.56	23393.4
HLA A*3002	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.48	0.92	-3.56	29972.0
HLA A*2902	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.36	0.81	-3.56	23130.2
HLA A*0212	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.40	0.84	-3.56	25262.8
HLA B*0802	1:25-33	9	AAAHASAAP	0.72	0.16	-4.43	0.88	-3.56	27203.8
HLA B*1509	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.54	0.98	-3.56	34284.5
HLA A*2301	1:80-88	9	GESGASYLA	1.31	-0.35	-4.52	0.96	-3.56	32907.4
HLA B*4403	1:21-29	9	TARLAAAHA	1.27	-0.18	-4.65	1.09	-3.56	44820.6
HLA A*0250	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.48	0.92	-3.56	30074.5
HLA B*4402	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.40	0.84	-3.56	25332.3
HLA A*3001	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.18	0.62	-3.56	14977.5
HLA A*2602	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.60	1.04	-3.56	39824.1
HLA B*4001	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.37	0.81	-3.56	23532.6
HLA A*2301	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.54	0.98	-3.56	34418.1
HLA A*8001	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.37	0.81	-3.56	23205.3
HLA B*5101	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.41	0.84	-3.56	25456.5
HLA A*3301	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.45	0.89	-3.56	28415.9
HLA B*4501	1:32-40	9	APVITAVVP	0.92	0.08	-4.56	0.99	-3.56	35916.7
HLA B*1502	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.32	0.75	-3.56	20777.2
HLA A*1101	1:25-33	9	AAAHASAAP	0.72	0.16	-4.44	0.88	-3.56	27521.8
HLA A*0201	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.27	0.70	-3.56	18548.3
HLA A*0101	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.38	0.81	-3.56	23910.7
HLA B*5701	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.38	0.81	-3.56	23739.9
HLA A*6801	1:9-17	9	GLAAASAAV	1.01	0.00	-4.58	1.01	-3.56	37593.7
HLA B*5101	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.38	0.81	-3.56	23777.7
HLA B*5701	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.38	0.82	-3.56	24178.1
HLA B*5801	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.34	0.77	-3.56	21837.5
HLA B*4002	1:26-34	9	AAHASAAPV	0.61	0.30	-4.48	0.91	-3.56	30010.5
HLA A*6802	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.38	0.81	-3.56	23981.5
HLA A*3201	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.33	0.76	-3.57	21243.1
HLA A*6801	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.44	0.87	-3.57	27448.5
HLA A*2601	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.38	0.81	-3.57	24020.2
HLA B*4001	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.38	0.81	-3.57	24023.2
HLA B*2705	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.33	0.76	-3.57	21276.9
HLA A*2602	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.54	0.98	-3.57	34857.0
HLA B*1517	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.39	0.82	-3.57	24299.5

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*4601	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.39	0.82	-3.57	24338.4
HLA A*3301	1:38-46	9	VVPPAADPV	0.76	0.28	-4.61	1.04	-3.57	40711.1
HLA A*0216	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.46	0.89	-3.57	28775.6
HLA B*0802	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.41	0.84	-3.57	25820.9
HLA B*4002	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.28	0.71	-3.57	18914.4
HLA A*0250	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.54	0.98	-3.57	35051.6
HLA B*0801	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.38	0.81	-3.57	24180.1
HLA A*3301	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.57	1.00	-3.57	36929.9
HLA A*2601	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.39	0.82	-3.57	24457.7
HLA A*8001	1:25-33	9	AAAHASAAP	0.72	0.16	-4.45	0.88	-3.57	27903.6
HLA B*0702	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.38	0.81	-3.57	24239.4
HLA A*0203	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.29	0.72	-3.57	19318.3
HLA A*2603	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.61	1.04	-3.57	40742.2
HLA B*4002	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.61	1.04	-3.57	40780.1
HLA A*3101	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.38	0.81	-3.57	24118.0
HLA A*3201	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.49	0.92	-3.57	30964.0
HLA A*2601	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.38	0.81	-3.57	23841.1
HLA A*1101	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.45	0.87	-3.57	27890.2
HLA A*6801	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.58	1.01	-3.57	38244.7
HLA B*4001	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.38	0.81	-3.57	23857.4
HLA A*2902	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.39	0.81	-3.57	24405.3
HLA B*2705	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.38	0.81	-3.57	23953.0
HLA B*5701	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.38	0.81	-3.57	23958.5
HLA B*5301	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.55	0.98	-3.57	35495.8
HLA A*2501	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.45	0.87	-3.57	27986.1
HLA A*3001	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.28	0.71	-3.57	19190.6
HLA A*0216	1:25-33	9	AAAHASAAP	0.72	0.16	-4.45	0.88	-3.57	28220.6
HLA A*6801	1:43-51	9	ADPVSLQTA	1.35	-0.24	-4.68	1.11	-3.57	47860.7
HLA A*0101	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.28	0.70	-3.57	19039.7
HLA B*4402	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.39	0.81	-3.58	24377.4
HLA B*4501	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.62	1.04	-3.58	41276.9
HLA B*4601	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.35	0.77	-3.58	22402.9
HLA B*0803	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.47	0.89	-3.58	29312.5
HLA B*2705	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.42	0.84	-3.58	26298.6
HLA A*2603	1:11-19	9	AAASAAVEA	1.20	-0.12	-4.66	1.08	-3.58	45368.0
HLA A*3002	1:52-60	9	AGFSAQGVE	0.95	-0.62	-3.91	0.33	-3.58	8108.4
HLA B*1801	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.38	0.81	-3.58	24135.6
HLA B*5301	1:9-17	9	GLAAASAAV	1.01	0.00	-4.59	1.01	-3.58	38773.7
HLA B*5101	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.47	0.89	-3.58	29517.7
HLA A*2403	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.38	0.81	-3.58	24259.1
HLA A*3301	1:9-17	9	GLAAASAAV	1.01	0.00	-4.59	1.01	-3.58	38893.9
HLA B*4002	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.59	1.01	-3.58	38831.0
HLA B*1517	1:37-45	9	AVVPPAADP	0.41	0.20	-4.19	0.61	-3.58	15586.7
HLA A*3101	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.29	0.70	-3.58	19275.5
HLA A*3001	1:37-45	9	AVVPPAADP	0.41	0.20	-4.19	0.61	-3.58	15632.0
HLA A*3002	1:32-40	9	APVITAVVP	0.92	0.08	-4.57	0.99	-3.58	37458.2
HLA B*4801	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.42	0.84	-3.58	26599.3
HLA B*3801	1:80-88	9	GESGASYLA	1.31	-0.35	-4.54	0.96	-3.58	34623.9
HLA B*3801	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.47	0.89	-3.58	29672.6

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*0803	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.50	0.92	-3.58	31608.0
HLA A*6802	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.30	0.71	-3.58	19743.9
HLA A*0211	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.47	0.89	-3.58	29696.2
HLA A*2301	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.53	0.95	-3.58	33951.0
HLA A*3002	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.45	0.87	-3.58	28484.1
HLA B*4403	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.62	1.04	-3.58	41899.6
HLA A*3201	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.56	0.98	-3.58	36174.7
HLA B*7301	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.58	1.00	-3.58	38032.2
HLA B*7301	1:53-61	9	GFSAQGVEH	1.21	-0.17	-4.62	1.04	-3.58	41921.4
HLA A*2501	1:25-33	9	AAAHASAAP	0.72	0.16	-4.46	0.88	-3.58	28734.0
HLA B*5701	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.29	0.70	-3.58	19364.2
HLA B*4501	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.56	0.98	-3.58	36219.5
HLA A*2603	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.62	1.04	-3.58	41962.2
HLA B*1801	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.53	0.95	-3.58	34064.3
HLA B*7301	1:9-17	9	GLAAASAAV	1.01	0.00	-4.59	1.01	-3.58	39270.0
HLA A*2402	1:32-40	9	APVITAVVP	0.92	0.08	-4.58	0.99	-3.58	37717.3
HLA B*3801	1:26-34	9	AAHASAAPV	0.61	0.30	-4.50	0.91	-3.58	31353.1
HLA B*1517	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.39	0.81	-3.58	24552.9
HLA A*8001	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.39	0.81	-3.58	24568.4
HLA A*8001	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.40	0.82	-3.58	25347.3
HLA A*3001	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.30	0.72	-3.59	20018.4
HLA B*5101	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.40	0.82	-3.59	25376.1
HLA B*3801	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.53	0.95	-3.59	34272.5
HLA A*2603	1:9-17	9	GLAAASAAV	1.01	0.00	-4.60	1.01	-3.59	39518.7
HLA B*1509	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.36	0.77	-3.59	22955.0
HLA A*2601	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.34	0.75	-3.59	21932.8
HLA B*3901	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.46	0.87	-3.59	28835.9
HLA A*2403	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.40	0.81	-3.59	25229.9
HLA B*2705	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.46	0.87	-3.59	28846.0
HLA B*4002	1:38-46	9	VVPPAADPV	0.76	0.28	-4.63	1.04	-3.59	42582.4
HLA A*1101	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.29	0.70	-3.59	19586.4
HLA A*0202	1:32-40	9	APVITAVVP	0.92	0.08	-4.58	0.99	-3.59	38033.1
HLA B*4001	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.39	0.81	-3.59	24738.5
HLA A*6901	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.29	0.70	-3.59	19610.0
HLA A*2403	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.34	0.75	-3.59	21989.9
HLA B*5101	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.23	0.65	-3.59	17123.5
HLA B*4402	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.39	0.81	-3.59	24737.0
HLA B*5301	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.46	0.87	-3.59	28951.6
HLA A*0216	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.34	0.75	-3.59	22038.1
HLA B*5301	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.43	0.84	-3.59	27116.7
HLA B*2705	1:25-33	9	AAAHASAAP	0.72	0.16	-4.47	0.88	-3.59	29199.8
HLA B*5101	1:25-33	9	AAAHASAAP	0.72	0.16	-4.47	0.88	-3.59	29201.8
HLA B*4601	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.40	0.81	-3.59	25366.2
HLA A*6901	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.30	0.71	-3.59	20120.2
HLA A*2403	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.36	0.77	-3.59	23148.6
HLA B*1501	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.30	0.71	-3.59	20143.0
HLA A*3002	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.57	0.98	-3.59	36868.2
HLA B*4801	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.37	0.77	-3.59	23206.9
HLA B*0802	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.46	0.87	-3.59	29135.1

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*2402	1:80-88	9	GESGASYLA	1.31	-0.35	-4.55	0.96	-3.59	35474.5
HLA B*1801	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.40	0.81	-3.59	24931.2
HLA B*4801	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.35	0.75	-3.59	22192.9
HLA B*1509	1:25-33	9	AAAHASAAP	0.72	0.16	-4.47	0.88	-3.59	29381.5
HLA A*8001	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.41	0.81	-3.59	25525.5
HLA A*3201	1:32-40	9	APVITAVVP	0.92	0.08	-4.59	0.99	-3.59	38511.5
HLA A*2301	1:26-34	9	AAHASAAPV	0.61	0.30	-4.51	0.91	-3.59	32021.6
HLA B*1502	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.51	0.92	-3.59	32510.2
HLA A*2403	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.40	0.81	-3.59	25074.5
HLA A*6801	1:26-34	9	AAHASAAPV	0.61	0.30	-4.51	0.91	-3.59	32140.8
HLA A*2501	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.41	0.82	-3.59	25921.8
HLA A*3002	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.41	0.81	-3.59	25505.2
HLA A*1101	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.36	0.76	-3.60	22763.3
HLA A*3201	1:80-88	9	GESGASYLA	1.31	-0.35	-4.55	0.96	-3.60	35783.1
HLA A*0101	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.36	0.76	-3.60	22774.3
HLA A*0212	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.37	0.77	-3.60	23484.8
HLA B*4001	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.37	0.77	-3.60	23586.7
HLA A*0201	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.37	0.77	-3.60	23601.2
HLA A*0250	1:32-40	9	APVITAVVP	0.92	0.08	-4.59	0.99	-3.60	39036.8
HLA B*1501	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.30	0.70	-3.60	20109.5
HLA B*5301	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.60	1.00	-3.60	39539.4
HLA B*3901	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.31	0.72	-3.60	20647.4
HLA A*0250	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.55	0.95	-3.60	35419.1
HLA B*7301	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.58	0.98	-3.60	37693.2
HLA B*4801	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.41	0.81	-3.60	25458.9
HLA A*2402	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.58	0.98	-3.60	37785.1
HLA B*5301	1:80-88	9	GESGASYLA	1.31	-0.35	-4.56	0.96	-3.60	36257.0
HLA B*5801	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.08	0.48	-3.60	12139.1
HLA A*2902	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.36	0.75	-3.60	22667.3
HLA B*5801	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.36	0.76	-3.60	23086.6
HLA B*3501	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.31	0.70	-3.60	20254.9
HLA B*7301	1:22-30	9	ARLAAAHAS	1.08	-0.81	-3.87	0.27	-3.60	7484.0
HLA A*2902	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.37	0.76	-3.60	23179.5
HLA B*1502	1:32-40	9	APVITAVVP	0.92	0.08	-4.60	0.99	-3.60	39447.1
HLA B*5701	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.42	0.81	-3.60	26198.4
HLA A*3002	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.32	0.71	-3.60	20786.9
HLA A*2602	1:32-40	9	APVITAVVP	0.92	0.08	-4.60	0.99	-3.60	39492.2
HLA A*8001	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.42	0.81	-3.60	26069.3
HLA A*2601	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.37	0.76	-3.60	23263.3
HLA B*3501	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.42	0.81	-3.60	26278.6
HLA B*4801	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.41	0.81	-3.60	25758.0
HLA A*2902	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.32	0.71	-3.61	20859.1
HLA B*0702	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.32	0.72	-3.61	20935.9
HLA B*1502	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.56	0.95	-3.61	35899.8
HLA B*4001	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.36	0.75	-3.61	22938.6
HLA B*1517	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.37	0.76	-3.61	23361.4
HLA B*4403	1:58-66	9	GVEHAVVTA	1.37	-0.33	-4.65	1.04	-3.61	44344.0
HLA B*3901	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.42	0.81	-3.61	26238.4
HLA B*4501	1:38-46	9	VVPPAADPV	0.76	0.28	-4.65	1.04	-3.61	44618.1

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*2301	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.53	0.92	-3.61	33589.8
HLA B*0802	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.42	0.81	-3.61	26315.4
HLA B*4501	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.48	0.87	-3.61	30327.1
HLA B*1502	1:80-88	9	GESGASYLA	1.31	-0.35	-4.57	0.96	-3.61	36932.1
HLA B*3501	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.37	0.76	-3.61	23507.4
HLA B*1503	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.45	0.84	-3.61	28398.7
HLA A*0202	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.32	0.71	-3.61	21059.7
HLA A*3101	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.36	0.75	-3.61	23105.7
HLA B*4601	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.37	0.76	-3.61	23568.8
HLA B*1517	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.43	0.81	-3.61	26630.9
HLA B*5401	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.37	0.76	-3.61	23609.1
HLA A*0216	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.39	0.77	-3.61	24392.7
HLA A*6801	1:69-77	9	VEELGRAGV	1.03	0.03	-4.67	1.06	-3.61	46798.4
HLA B*3501	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.10	0.49	-3.61	12540.2
HLA A*0201	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.33	0.71	-3.61	21238.6
HLA A*3101	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.43	0.81	-3.61	26865.2
HLA A*0203	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.33	0.72	-3.61	21396.0
HLA B*0702	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.43	0.81	-3.62	26721.4
HLA B*4501	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.53	0.92	-3.62	34192.1
HLA B*4801	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.43	0.81	-3.62	26990.1
HLA A*6801	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.59	0.98	-3.62	39247.7
HLA A*3101	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.33	0.72	-3.62	21545.0
HLA A*2402	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.54	0.92	-3.62	34405.3
HLA B*4601	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.33	0.72	-3.62	21576.1
HLA A*0211	1:25-33	9	AAAHASAAP	0.72	0.16	-4.49	0.88	-3.62	31230.2
HLA B*3901	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.42	0.81	-3.62	26525.7
HLA B*1801	1:25-33	9	AAAHASAAP	0.72	0.16	-4.49	0.88	-3.62	31253.7
HLA B*4001	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.38	0.76	-3.62	24040.9
HLA A*0301	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.32	0.70	-3.62	21071.8
HLA A*2403	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.38	0.76	-3.62	24061.1
HLA B*5801	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.34	0.72	-3.62	21646.6
HLA A*2402	1:26-34	9	AAHASAAPV	0.61	0.30	-4.53	0.91	-3.62	34099.2
HLA B*4403	1:38-46	9	VVPPAADPV	0.76	0.28	-4.66	1.04	-3.62	45963.4
HLA B*5301	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.37	0.75	-3.62	23704.2
HLA A*0211	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.40	0.77	-3.62	24849.8
HLA A*0101	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.34	0.72	-3.62	21694.5
HLA B*5401	1:39-47	9	VPPAADPVS	0.96	-1.07	-3.51	-0.11	-3.62	3228.3
HLA B*4402	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.44	0.81	-3.62	27308.6
HLA B*0803	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.44	0.82	-3.62	27639.0
HLA B*4402	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.38	0.75	-3.62	23815.4
HLA B*3801	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.54	0.92	-3.62	34783.3
HLA B*4501	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.63	1.01	-3.62	42947.9
HLA B*4403	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.62	1.00	-3.62	41816.7
HLA B*4801	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.44	0.81	-3.62	27300.8
HLA B*3901	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.43	0.81	-3.62	26952.4
HLA B*0802	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.40	0.77	-3.62	25097.2
HLA A*2603	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.60	0.98	-3.62	39930.2
HLA B*2705	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.43	0.81	-3.63	26944.0
HLA B*0803	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.50	0.87	-3.63	31608.2

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*2501	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.43	0.81	-3.63	27103.0
HLA B*4002	1:71-79	9	ELGRAGVGV	1.09	-0.09	-4.63	1.00	-3.63	42212.7
HLA B*1502	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.44	0.81	-3.63	27500.2
HLA B*4402	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.43	0.81	-3.63	27145.4
HLA A*2403	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.34	0.72	-3.63	22047.8
HLA B*5301	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.58	0.95	-3.63	37927.4
HLA B*4002	1:32-40	9	APVITAVVP	0.92	0.08	-4.62	0.99	-3.63	41997.2
HLA A*2402	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.58	0.95	-3.63	38001.0
HLA A*0219	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.41	0.77	-3.63	25425.3
HLA A*3301	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.55	0.92	-3.63	35538.3
HLA B*0802	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.45	0.82	-3.63	28324.9
HLA A*2402	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.44	0.81	-3.63	27466.7
HLA B*4402	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.41	0.77	-3.63	25617.3
HLA A*2501	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.48	0.84	-3.63	30072.7
HLA A*6802	1:1-9	9	MTLRVVPEG	0.78	-0.59	-3.82	0.19	-3.63	6622.7
HLA A*6801	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.44	0.81	-3.63	27573.9
HLA B*5101	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.44	0.81	-3.63	27591.4
HLA B*4403	1:9-17	9	GLAAASAAV	1.01	0.00	-4.65	1.01	-3.63	44244.3
HLA B*4402	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.40	0.76	-3.64	25003.9
HLA B*5701	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.39	0.75	-3.64	24580.8
HLA B*5801	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.35	0.71	-3.64	22454.5
HLA B*5801	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.35	0.72	-3.64	22566.3
HLA B*1501	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.25	0.62	-3.64	17933.4
HLA A*3201	1:25-33	9	AAAHASAAP	0.72	0.16	-4.51	0.88	-3.64	32689.3
HLA B*1801	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.39	0.75	-3.64	24773.1
HLA B*0803	1:25-33	9	AAAHASAAP	0.72	0.16	-4.52	0.88	-3.64	32798.3
HLA A*2402	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.53	0.89	-3.64	34000.4
HLA A*1101	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.45	0.81	-3.64	28360.3
HLA A*3002	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.49	0.84	-3.64	30572.9
HLA B*1509	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.46	0.82	-3.64	28859.0
HLA B*0802	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.45	0.81	-3.64	27968.4
HLA A*0301	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.36	0.72	-3.64	22769.0
HLA B*4403	1:26-34	9	AAHASAAPV	0.61	0.30	-4.55	0.91	-3.64	35828.4
HLA A*0206	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.13	0.49	-3.64	13406.1
HLA B*4403	1:32-40	9	APVITAVVP	0.92	0.08	-4.63	0.99	-3.64	43127.7
HLA A*0301	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.36	0.71	-3.64	22746.3
HLA B*5701	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.42	0.77	-3.64	26194.6
HLA B*1801	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.46	0.81	-3.64	28568.7
HLA A*0206	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.36	0.72	-3.64	22898.5
HLA B*4501	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.40	0.75	-3.64	25071.8
HLA B*0803	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.41	0.76	-3.65	25585.9
HLA A*2602	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.56	0.92	-3.65	36725.3
HLA A*2501	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.46	0.81	-3.65	28934.7
HLA A*3301	1:32-40	9	APVITAVVP	0.92	0.08	-4.64	0.99	-3.65	43605.1
HLA A*0206	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.36	0.71	-3.65	22958.8
HLA A*2602	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.41	0.76	-3.65	25644.8
HLA B*4002	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.62	0.98	-3.65	42073.8
HLA A*8001	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.41	0.76	-3.65	25682.7
HLA B*1501	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.36	0.71	-3.65	22725.8

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*1501	1:37-45	9	AVVPPAADP	0.41	0.20	-4.26	0.61	-3.65	18243.2
HLA B*7301	1:26-34	9	AAHASAAPV	0.61	0.30	-4.56	0.91	-3.65	36343.8
HLA B*2705	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.46	0.81	-3.65	29049.3
HLA A*1101	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.46	0.81	-3.65	29068.0
HLA A*2602	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.60	0.95	-3.65	39651.9
HLA A*6802	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.36	0.72	-3.65	23150.5
HLA B*0801	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.36	0.71	-3.65	23081.7
HLA B*5801	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.36	0.71	-3.65	22814.8
HLA A*6901	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.37	0.72	-3.65	23211.8
HLA B*1503	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.35	0.70	-3.65	22643.3
HLA B*1509	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.52	0.87	-3.65	33369.2
HLA A*0250	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.43	0.77	-3.65	26650.0
HLA B*5701	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.41	0.76	-3.65	25890.5
HLA A*2301	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.54	0.89	-3.65	34892.3
HLA A*0101	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.37	0.72	-3.65	23335.5
HLA A*0301	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.37	0.72	-3.65	23341.2
HLA B*4501	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.60	0.95	-3.65	39937.6
HLA B*0803	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.46	0.81	-3.65	29123.7
HLA B*0803	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.50	0.84	-3.65	31437.8
HLA B*4403	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.47	0.82	-3.65	29680.6
HLA B*4801	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.42	0.76	-3.65	26068.2
HLA B*1502	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.47	0.81	-3.65	29447.1
HLA A*0203	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.36	0.71	-3.65	23088.2
HLA A*2501	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.42	0.76	-3.65	26094.9
HLA B*4501	1:25-33	9	AAAHASAAP	0.72	0.16	-4.53	0.88	-3.65	33943.3
HLA B*4601	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.37	0.71	-3.65	23396.2
HLA A*3001	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.30	0.65	-3.65	19969.9
HLA A*3301	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.63	0.98	-3.66	42817.6
HLA A*3201	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.50	0.84	-3.66	31575.4
HLA A*0212	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.37	0.71	-3.66	23415.5
HLA A*1101	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.41	0.75	-3.66	25679.6
HLA A*2601	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.36	0.70	-3.66	22927.2
HLA A*2601	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.37	0.72	-3.66	23515.1
HLA B*0802	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.47	0.81	-3.66	29620.3
HLA B*7301	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.47	0.81	-3.66	29418.4
HLA B*4501	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.36	0.70	-3.66	23005.6
HLA B*1509	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.50	0.84	-3.66	31727.8
HLA A*3301	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.46	0.81	-3.66	29010.8
HLA B*4002	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.58	0.92	-3.66	37726.3
HLA B*1503	1:37-45	9	AVVPPAADP	0.41	0.20	-4.27	0.61	-3.66	18682.3
HLA B*1501	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.37	0.72	-3.66	23700.5
HLA B*4403	1:57-65	9	QGVEHAVVT	1.29	-0.32	-4.63	0.98	-3.66	43150.1
HLA A*0301	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.37	0.71	-3.66	23346.9
HLA A*6801	1:32-40	9	APVITAVVP	0.92	0.08	-4.65	0.99	-3.66	44948.3
HLA B*4403	1:5-13	9	VVPEGLAAA	1.10	-0.09	-4.67	1.01	-3.66	46835.1
HLA B*1503	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.31	0.65	-3.66	20320.7
HLA A*0203	1:47-55	9	SLQTAAGFS	1.15	-0.94	-3.87	0.21	-3.66	7461.0
HLA A*2301	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.54	0.87	-3.66	34353.4
HLA B*3501	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.38	0.71	-3.66	23845.1

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*3801	1:25-33	9	AAAHASAAP	0.72	0.16	-4.54	0.88	-3.66	34619.4
HLA A*0201	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.38	0.72	-3.66	23971.4
HLA A*0216	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.37	0.70	-3.66	23361.4
HLA A*0202	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.38	0.72	-3.66	23962.5
HLA B*3801	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.51	0.84	-3.67	32311.9
HLA B*7301	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.58	0.92	-3.67	38386.9
HLA B*1801	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.51	0.84	-3.67	32349.1
HLA B*3901	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.48	0.81	-3.67	30259.2
HLA A*8001	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.42	0.75	-3.67	26335.2
HLA A*0250	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.56	0.89	-3.67	36117.4
HLA A*0101	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.38	0.71	-3.67	23727.7
HLA B*0801	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.38	0.72	-3.67	24142.3
HLA A*3301	1:80-88	9	GESGASYLA	1.31	-0.35	-4.62	0.96	-3.67	42168.4
HLA A*6802	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.28	0.62	-3.67	19169.4
HLA A*6801	1:80-88	9	GESGASYLA	1.31	-0.35	-4.63	0.96	-3.67	42228.4
HLA B*2705	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.44	0.77	-3.67	27669.9
HLA B*2705	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.42	0.75	-3.67	26411.3
HLA A*6901	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.38	0.71	-3.67	23799.4
HLA A*2301	1:25-33	9	AAAHASAAP	0.72	0.16	-4.54	0.88	-3.67	35017.5
HLA A*2603	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.62	0.95	-3.67	41463.5
HLA B*4403	1:59-67	9	VEHAVVTAE	0.87	-0.71	-3.82	0.16	-3.67	6659.8
HLA A*0201	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.39	0.72	-3.67	24266.8
HLA B*3901	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.32	0.65	-3.67	20662.1
HLA B*1503	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.49	0.81	-3.67	30566.1
HLA A*2602	1:80-88	9	GESGASYLA	1.31	-0.35	-4.63	0.96	-3.67	42538.4
HLA B*4001	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.39	0.72	-3.67	24331.1
HLA B*3801	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.54	0.87	-3.67	34960.5
HLA B*1502	1:25-33	9	AAAHASAAP	0.72	0.16	-4.55	0.88	-3.67	35244.6
HLA B*0802	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.48	0.81	-3.67	30004.6
HLA A*0101	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.39	0.71	-3.67	24309.1
HLA A*2601	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.39	0.71	-3.67	24318.0
HLA A*0211	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.38	0.70	-3.67	23793.4
HLA B*3501	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.39	0.72	-3.67	24447.1
HLA B*7301	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.48	0.81	-3.67	30064.2
HLA A*2603	1:32-40	9	APVITAVVP	0.92	0.08	-4.66	0.99	-3.67	46237.5
HLA B*4402	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.39	0.71	-3.67	24365.4
HLA B*0702	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.38	0.70	-3.67	23846.2
HLA A*1101	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.39	0.72	-3.67	24475.7
HLA B*5301	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.56	0.89	-3.67	36718.7
HLA B*4601	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.39	0.72	-3.67	24540.6
HLA A*6801	1:25-33	9	AAAHASAAP	0.72	0.16	-4.55	0.88	-3.67	35473.2
HLA A*6801	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.62	0.95	-3.67	41996.1
HLA B*1502	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.55	0.87	-3.67	35244.2
HLA B*5701	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.39	0.72	-3.68	24593.9
HLA A*3301	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.63	0.95	-3.68	42264.1
HLA B*4001	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.39	0.71	-3.68	24600.5
HLA B*0803	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.48	0.81	-3.68	30387.2
HLA B*4002	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.63	0.95	-3.68	42299.1
HLA B*4001	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.38	0.70	-3.68	24115.7

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*7301	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.55	0.87	-3.68	35550.2
HLA B*5101	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.49	0.81	-3.68	31094.4
HLA A*0216	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.39	0.71	-3.68	24680.6
HLA B*2705	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.39	0.72	-3.68	24779.6
HLA B*0802	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.44	0.76	-3.68	27592.4
HLA B*5401	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.39	0.72	-3.68	24808.7
HLA B*0803	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.45	0.77	-3.68	28455.8
HLA B*5301	1:25-33	9	AAAHASAAP	0.72	0.16	-4.56	0.88	-3.68	35965.7
HLA A*3201	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.63	0.95	-3.68	42762.0
HLA A*0201	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.39	0.71	-3.68	24584.4
HLA B*3901	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.45	0.76	-3.68	27894.7
HLA A*2601	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.39	0.71	-3.68	24695.3
HLA B*4801	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.39	0.70	-3.68	24491.3
HLA B*0801	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.39	0.71	-3.68	24732.8
HLA B*4001	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.40	0.72	-3.68	25163.6
HLA A*2603	1:80-88	9	GESGASYLA	1.31	-0.35	-4.64	0.96	-3.68	43971.3
HLA A*3101	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.40	0.71	-3.68	25060.9
HLA A*2601	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.30	0.62	-3.68	19974.0
HLA A*2603	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.60	0.92	-3.69	40155.1
HLA B*0803	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.44	0.75	-3.69	27524.6
HLA B*1517	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.14	0.45	-3.69	13798.7
HLA A*0219	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.39	0.70	-3.69	24577.0
HLA B*0803	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.50	0.81	-3.69	31696.0
HLA A*3002	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.44	0.75	-3.69	27571.2
HLA A*2902	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.39	0.70	-3.69	24608.7
HLA A*3301	1:26-34	9	AAHASAAPV	0.61	0.30	-4.60	0.91	-3.69	39759.5
HLA B*7301	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.58	0.89	-3.69	37888.9
HLA B*4601	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.39	0.70	-3.69	24671.0
HLA A*2403	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.39	0.70	-3.69	24742.7
HLA B*5701	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.40	0.71	-3.69	25329.7
HLA A*8001	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.39	0.70	-3.69	24804.5
HLA A*0219	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.40	0.71	-3.69	25047.1
HLA B*4501	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.41	0.72	-3.69	25441.5
HLA A*0250	1:25-33	9	AAAHASAAP	0.72	0.16	-4.57	0.88	-3.69	36937.5
HLA B*2705	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.40	0.70	-3.69	24903.3
HLA B*5401	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.54	0.84	-3.69	34364.0
HLA A*0206	1:37-45	9	AVVPPAADP	0.41	0.20	-4.31	0.61	-3.69	20236.1
HLA A*2602	1:25-33	9	AAAHASAAP	0.72	0.16	-4.57	0.88	-3.69	37068.8
HLA B*1502	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.50	0.81	-3.69	31561.9
HLA B*5401	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.47	0.77	-3.69	29390.6
HLA A*2402	1:25-33	9	AAAHASAAP	0.72	0.16	-4.57	0.88	-3.69	37157.9
HLA B*7301	1:25-33	9	AAAHASAAP	0.72	0.16	-4.57	0.88	-3.69	37178.6
HLA A*0301	1:37-45	9	AVVPPAADP	0.41	0.20	-4.31	0.61	-3.69	20309.8
HLA A*2301	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.51	0.82	-3.69	32627.7
HLA A*2402	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.51	0.82	-3.69	32649.4
HLA B*0803	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.50	0.81	-3.70	31655.6
HLA A*0219	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.41	0.72	-3.70	25797.4
HLA B*4403	1:70-78	9	EELGRAGVG	0.91	-0.72	-3.88	0.18	-3.70	7539.6
HLA A*6901	1:37-45	9	AVVPPAADP	0.41	0.20	-4.31	0.61	-3.70	20403.2

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*0206	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.16	0.46	-3.70	14468.6
HLA B*5301	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.52	0.82	-3.70	32800.4
HLA B*4801	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.41	0.71	-3.70	25786.0
HLA A*2301	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.50	0.81	-3.70	31796.1
HLA B*3801	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.50	0.81	-3.70	31822.1
HLA A*2403	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.41	0.72	-3.70	25945.4
HLA A*0212	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.41	0.72	-3.70	25913.4
HLA B*4402	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.41	0.72	-3.70	25919.4
HLA A*3301	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.57	0.87	-3.70	37298.5
HLA A*2301	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.54	0.84	-3.70	34903.4
HLA A*0212	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.41	0.71	-3.70	25582.4
HLA B*5401	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.41	0.71	-3.70	25933.6
HLA A*3001	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.22	0.52	-3.70	16540.1
HLA A*2402	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.57	0.87	-3.70	37525.6
HLA A*3001	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.16	0.45	-3.70	14316.9
HLA B*4501	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.51	0.81	-3.70	32136.3
HLA B*4403	1:3-11	9	LRVVPEGLA	1.05	-0.10	-4.65	0.95	-3.70	44812.8
HLA A*0211	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.42	0.72	-3.70	26248.5
HLA B*1801	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.46	0.76	-3.70	29168.5
HLA A*2602	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.58	0.87	-3.70	37671.6
HLA A*6901	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.32	0.62	-3.70	20826.3
HLA B*3801	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.52	0.82	-3.70	33289.2
HLA B*1509	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.52	0.81	-3.70	33011.4
HLA B*1517	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.42	0.71	-3.70	26192.0
HLA B*3801	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.48	0.77	-3.70	30135.6
HLA A*3201	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.58	0.87	-3.70	37793.1
HLA B*0702	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.41	0.71	-3.70	25905.4
HLA A*0212	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.41	0.70	-3.70	25665.2
HLA B*0802	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.46	0.75	-3.70	28781.8
HLA A*2501	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.42	0.72	-3.70	26370.0
HLA B*5701	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.41	0.71	-3.71	25940.3
HLA B*5101	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.48	0.77	-3.71	30199.9
HLA B*1509	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.51	0.81	-3.71	32449.9
HLA B*0801	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.41	0.70	-3.71	25730.9
HLA B*5701	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.42	0.72	-3.71	26449.3
HLA B*4801	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.42	0.72	-3.71	26420.7
HLA B*1801	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.52	0.81	-3.71	33220.6
HLA A*2301	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.52	0.81	-3.71	33041.4
HLA B*4601	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.42	0.71	-3.71	26160.3
HLA B*4402	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.41	0.70	-3.71	25918.4
HLA B*5801	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.35	0.65	-3.71	22614.2
HLA B*1503	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.32	0.62	-3.71	21134.4
HLA B*4402	1:59-67	9	VEHAVVTAE	0.87	-0.71	-3.86	0.16	-3.71	7320.7
HLA A*0203	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.33	0.62	-3.71	21161.8
HLA A*2501	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.46	0.75	-3.71	29172.1
HLA A*6802	1:37-45	9	AVVPPAADP	0.41	0.20	-4.32	0.61	-3.71	21101.8
HLA A*2602	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.47	0.75	-3.71	29213.7
HLA A*0206	1:1-9	9	MTLRVVPEG	0.78	-0.59	-3.90	0.19	-3.71	7911.7
HLA A*8001	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.42	0.71	-3.71	26370.6

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*4501	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.52	0.81	-3.71	33435.5
HLA A*6901	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.28	0.57	-3.71	19135.3
HLA A*0202	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.43	0.72	-3.71	26908.4
HLA B*3901	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.42	0.70	-3.71	26214.4
HLA A*3001	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.28	0.57	-3.71	19173.4
HLA A*0212	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.43	0.72	-3.71	26973.0
HLA A*0301	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.33	0.62	-3.71	21400.3
HLA A*3201	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.33	0.62	-3.72	21412.8
HLA A*0219	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.43	0.72	-3.72	27010.7
HLA B*4002	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.52	0.81	-3.72	33268.3
HLA B*1503	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.20	0.48	-3.72	15823.1
HLA B*4403	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.61	0.89	-3.72	40528.9
HLA B*4801	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.43	0.72	-3.72	27094.8
HLA A*0216	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.43	0.71	-3.72	26642.6
HLA B*4801	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.43	0.71	-3.72	26703.1
HLA B*4403	1:28-36	9	HASAAPVIT	1.18	-0.26	-4.64	0.92	-3.72	43326.5
HLA B*4501	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.56	0.84	-3.72	36503.6
HLA A*2902	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.29	0.57	-3.72	19345.6
HLA B*5401	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.53	0.81	-3.72	34149.6
HLA B*1509	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.47	0.75	-3.72	29707.9
HLA A*2902	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.43	0.72	-3.72	27194.7
HLA B*1501	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.13	0.41	-3.72	13475.5
HLA A*3201	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.54	0.82	-3.72	34535.5
HLA A*2403	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.43	0.71	-3.72	27131.9
HLA A*0219	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.43	0.71	-3.72	27151.6
HLA B*4501	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.49	0.77	-3.72	31254.7
HLA A*0101	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.37	0.65	-3.72	23209.1
HLA A*2402	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.53	0.81	-3.72	34047.2
HLA A*0203	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.29	0.57	-3.72	19441.4
HLA A*3002	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.24	0.52	-3.72	17351.2
HLA B*4402	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.44	0.72	-3.72	27347.2
HLA A*8001	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.44	0.71	-3.72	27294.7
HLA A*2402	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.57	0.84	-3.72	36816.4
HLA B*4501	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.53	0.81	-3.72	33732.8
HLA A*0211	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.44	0.72	-3.72	27418.3
HLA A*0301	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.37	0.65	-3.72	23327.0
HLA A*3101	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.43	0.71	-3.72	27010.7
HLA A*0216	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.44	0.72	-3.72	27485.3
HLA A*3101	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.44	0.72	-3.72	27521.3
HLA B*3801	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.53	0.81	-3.72	33877.6
HLA A*2301	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.53	0.81	-3.72	33886.2
HLA B*1509	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.49	0.76	-3.72	30627.0
HLA A*6802	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.43	0.71	-3.72	27112.6
HLA A*2603	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.60	0.87	-3.72	39582.5
HLA A*2301	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.54	0.81	-3.73	34707.0
HLA A*2402	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.53	0.81	-3.73	34019.8
HLA B*5801	1:37-45	9	AVVPPAADP	0.41	0.20	-4.34	0.61	-3.73	21892.5
HLA B*5401	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.21	0.48	-3.73	16225.8
HLA A*2601	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.37	0.65	-3.73	23599.3

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*2902	1:37-45	9	AVVPPAADP	0.41	0.20	-4.34	0.61	-3.73	21948.0
HLA B*5101	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.44	0.71	-3.73	27702.2
HLA B*3801	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.54	0.81	-3.73	34733.3
HLA B*3801	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.54	0.81	-3.73	34996.2
HLA B*1502	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.57	0.84	-3.73	37433.5
HLA B*0702	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.45	0.72	-3.73	27936.1
HLA A*2403	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.44	0.71	-3.73	27471.5
HLA A*0216	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.45	0.72	-3.73	28025.4
HLA B*3501	1:50-58	9	TAAGFSAQG	0.80	-0.61	-3.92	0.19	-3.73	8360.6
HLA B*5101	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.49	0.76	-3.73	31218.7
HLA B*1502	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.54	0.81	-3.73	34513.6
HLA A*8001	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.45	0.72	-3.73	28133.4
HLA A*3301	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.54	0.81	-3.73	34640.6
HLA B*0802	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.45	0.72	-3.73	28167.2
HLA B*5801	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.35	0.62	-3.73	22374.7
HLA A*1101	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.45	0.71	-3.73	28100.2
HLA B*4001	1:59-67	9	VEHAVVTAE	0.87	-0.71	-3.89	0.16	-3.74	7788.0
HLA B*0702	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.45	0.71	-3.74	28233.9
HLA A*3002	1:47-55	9	SLQTAAGFS	1.15	-0.94	-3.95	0.21	-3.74	8856.0
HLA B*0802	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.44	0.70	-3.74	27682.7
HLA B*3501	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.45	0.71	-3.74	28030.8
HLA B*4402	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.38	0.65	-3.74	24227.5
HLA A*2501	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.44	0.70	-3.74	27790.2
HLA A*0206	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.19	0.45	-3.74	15610.7
HLA B*1509	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.44	0.70	-3.74	27837.3
HLA A*2402	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.52	0.77	-3.74	32739.8
HLA A*0203	1:37-45	9	AVVPPAADP	0.41	0.20	-4.35	0.61	-3.74	22614.3
HLA A*3301	1:25-33	9	AAAHASAAP	0.72	0.16	-4.62	0.88	-3.74	41436.6
HLA B*4501	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.63	0.89	-3.74	42923.8
HLA B*2705	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.46	0.71	-3.74	28579.3
HLA B*4002	1:20-28	9	LTARLAAAH	1.06	-0.16	-4.63	0.89	-3.74	43054.7
HLA B*1503	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.46	0.71	-3.74	28680.5
HLA B*0801	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.21	0.46	-3.74	16144.9
HLA A*2602	1:37-45	9	AVVPPAADP	0.41	0.20	-4.36	0.61	-3.74	22803.6
HLA A*2501	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.39	0.65	-3.75	24570.5
HLA B*1517	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.46	0.72	-3.75	28924.6
HLA A*2601	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.31	0.57	-3.75	20574.3
HLA A*0201	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.39	0.65	-3.75	24589.1
HLA B*5101	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.46	0.72	-3.75	28949.8
HLA A*3001	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.23	0.48	-3.75	16953.1
HLA A*2301	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.52	0.77	-3.75	33208.9
HLA A*3101	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.39	0.65	-3.75	24689.1
HLA A*2902	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.46	0.71	-3.75	28597.3
HLA A*2902	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.46	0.72	-3.75	29137.6
HLA A*0203	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.39	0.65	-3.75	24761.6
HLA A*0101	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.36	0.62	-3.75	23141.9
HLA A*8001	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.46	0.72	-3.75	29161.9
HLA B*4002	1:25-33	9	AAAHASAAP	0.72	0.16	-4.63	0.88	-3.75	42214.5
HLA B*5101	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.47	0.72	-3.75	29191.7

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*5301	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.55	0.81	-3.75	35886.8
HLA B*4002	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.62	0.87	-3.75	41989.5
HLA A*2501	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.46	0.71	-3.75	28795.7
HLA A*3201	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.56	0.81	-3.75	36543.1
HLA B*4501	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.57	0.81	-3.75	36836.5
HLA B*4403	1:87-95	9	LAGDAAAAA	1.17	-0.30	-4.62	0.87	-3.75	42116.0
HLA B*7301	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.57	0.81	-3.75	36854.2
HLA B*1509	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.40	0.65	-3.75	24966.6
HLA A*3101	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.37	0.62	-3.75	23392.1
HLA A*6801	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.60	0.84	-3.75	39598.1
HLA A*2603	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.57	0.81	-3.75	37032.7
HLA A*1101	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.47	0.72	-3.75	29510.1
HLA B*2705	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.47	0.72	-3.75	29527.0
HLA A*6802	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.32	0.57	-3.75	21008.6
HLA A*6901	1:50-58	9	TAAGFSAQG	0.80	-0.61	-3.94	0.19	-3.75	8794.8
HLA A*2601	1:37-45	9	AVVPPAADP	0.41	0.20	-4.37	0.61	-3.75	23311.5
HLA B*1501	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.40	0.65	-3.75	25124.3
HLA B*1501	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.21	0.45	-3.76	16206.5
HLA A*2603	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.57	0.81	-3.76	36935.9
HLA B*7301	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.60	0.84	-3.76	39793.1
HLA B*4403	1:25-33	9	AAAHASAAP	0.72	0.16	-4.63	0.88	-3.76	42876.9
HLA B*3501	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.37	0.62	-3.76	23619.0
HLA B*5301	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.56	0.81	-3.76	36651.8
HLA B*4601	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.40	0.65	-3.76	25327.8
HLA B*4001	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.40	0.65	-3.76	25375.0
HLA A*2602	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.57	0.81	-3.76	37523.4
HLA B*1509	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.48	0.72	-3.76	29936.8
HLA B*4002	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.61	0.84	-3.76	40337.6
HLA A*2603	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.57	0.81	-3.76	36915.3
HLA B*3901	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.48	0.71	-3.76	29948.0
HLA A*3001	1:72-80	9	LGRAGVGVG	0.85	-0.77	-3.84	0.08	-3.76	6912.0
HLA A*3301	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.52	0.76	-3.76	33441.9
HLA A*0212	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.38	0.62	-3.76	23934.6
HLA B*0802	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.48	0.71	-3.76	30056.6
HLA A*2602	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.58	0.82	-3.76	38347.3
HLA B*4801	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.41	0.65	-3.77	25731.8
HLA A*0206	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.48	0.71	-3.77	29884.9
HLA B*1801	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.48	0.72	-3.77	30367.0
HLA A*3001	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.23	0.46	-3.77	17021.2
HLA B*3801	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.52	0.75	-3.77	33263.4
HLA B*1503	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.34	0.57	-3.77	21701.2
HLA B*7301	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.54	0.77	-3.77	34972.0
HLA A*0201	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.38	0.62	-3.77	24246.2
HLA A*2402	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.58	0.81	-3.77	38436.8
HLA B*3801	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.53	0.76	-3.77	34038.5
HLA A*3301	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.58	0.81	-3.77	38173.8
HLA B*1501	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.29	0.52	-3.77	19500.0
HLA A*6802	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.23	0.45	-3.77	16822.2
HLA B*4501	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.49	0.71	-3.77	30652.0

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*1503	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.48	0.71	-3.77	30282.2
HLA A*2902	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.39	0.62	-3.77	24471.2
HLA A*3001	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.26	0.49	-3.77	18161.2
HLA B*0802	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.48	0.71	-3.77	30453.0
HLA A*0219	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.42	0.65	-3.77	26322.1
HLA B*4403	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.62	0.84	-3.78	41608.9
HLA A*3201	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.48	0.70	-3.78	30191.2
HLA A*2603	1:25-33	9	AAAHASAAP	0.72	0.16	-4.65	0.88	-3.78	44815.0
HLA A*6801	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.59	0.82	-3.78	39338.2
HLA A*2301	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.54	0.76	-3.78	34503.0
HLA A*2603	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.60	0.82	-3.78	39372.7
HLA A*0212	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.42	0.65	-3.78	26437.2
HLA A*0211	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.49	0.71	-3.78	30991.5
HLA B*5101	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.48	0.70	-3.78	30340.2
HLA A*3301	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.62	0.84	-3.78	41845.7
HLA B*5301	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.59	0.81	-3.78	39130.9
HLA B*1801	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.49	0.72	-3.78	31180.4
HLA B*5801	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.35	0.57	-3.78	22180.2
HLA A*0206	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.39	0.62	-3.78	24766.7
HLA B*4001	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.39	0.62	-3.78	24772.5
HLA A*2501	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.49	0.72	-3.78	31218.8
HLA A*1101	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.49	0.71	-3.78	30739.4
HLA B*5401	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.49	0.71	-3.78	30750.0
HLA B*0702	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.39	0.62	-3.78	24811.2
HLA B*2705	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.49	0.71	-3.78	30780.8
HLA B*4002	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.59	0.81	-3.78	39075.9
HLA A*3201	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.60	0.81	-3.78	39396.0
HLA B*4601	1:37-45	9	AVVPPAADP	0.41	0.20	-4.39	0.61	-3.78	24786.1
HLA A*0201	1:37-45	9	AVVPPAADP	0.41	0.20	-4.39	0.61	-3.78	24801.2
HLA B*4601	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.40	0.62	-3.78	24976.1
HLA B*4002	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.54	0.76	-3.78	34996.8
HLA B*0801	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.40	0.62	-3.78	25001.9
HLA B*0802	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.50	0.72	-3.78	31525.2
HLA B*5701	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.43	0.65	-3.78	26791.1
HLA B*5701	1:37-45	9	AVVPPAADP	0.41	0.20	-4.40	0.61	-3.78	24898.4
HLA B*5701	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.27	0.48	-3.78	18467.3
HLA B*3901	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.50	0.72	-3.78	31608.9
HLA A*0216	1:37-45	9	AVVPPAADP	0.41	0.20	-4.40	0.61	-3.78	24956.1
HLA B*1517	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.35	0.57	-3.78	22508.3
HLA B*4002	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.59	0.81	-3.78	38864.4
HLA A*8001	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.43	0.65	-3.79	26953.4
HLA A*0101	1:37-45	9	AVVPPAADP	0.41	0.20	-4.40	0.61	-3.79	25049.4
HLA B*5101	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.49	0.71	-3.79	31213.3
HLA B*5701	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.40	0.62	-3.79	25186.8
HLA A*3301	1:48-56	9	LQTAAGFSA	1.01	-0.19	-4.60	0.82	-3.79	40248.6
HLA B*0803	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.49	0.71	-3.79	31247.7
HLA A*0301	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.35	0.57	-3.79	22628.6
HLA B*3901	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.50	0.71	-3.79	31307.0
HLA A*3201	1:1-9	9	MTLRVVPEG	0.78	-0.59	-3.97	0.19	-3.79	9413.2

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*2301	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.54	0.75	-3.79	34822.9
HLA A*2902	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.43	0.65	-3.79	27135.6
HLA B*0803	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.50	0.71	-3.79	31827.3
HLA B*1517	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.50	0.71	-3.79	31491.6
HLA A*3101	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.36	0.57	-3.79	22784.7
HLA A*3001	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.00	0.21	-3.79	9990.9
HLA B*0803	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.49	0.70	-3.79	31234.4
HLA A*0206	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.44	0.65	-3.79	27286.9
HLA A*2603	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.51	0.72	-3.79	32137.2
HLA A*2602	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.64	0.84	-3.79	43241.5
HLA A*3002	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.51	0.72	-3.79	32188.5
HLA B*0803	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.51	0.72	-3.79	32192.0
HLA B*1509	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.50	0.71	-3.79	31694.5
HLA B*4001	1:37-45	9	AVVPPAADP	0.41	0.20	-4.41	0.61	-3.79	25448.9
HLA A*2501	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.51	0.71	-3.79	32112.7
HLA A*3101	1:37-45	9	AVVPPAADP	0.41	0.20	-4.41	0.61	-3.79	25463.7
HLA B*5401	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.51	0.72	-3.79	32315.5
HLA B*0801	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.28	0.48	-3.79	18900.5
HLA B*3901	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.28	0.49	-3.79	19025.7
HLA B*1503	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.26	0.46	-3.79	18112.6
HLA A*0216	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.41	0.62	-3.79	25714.1
HLA A*0250	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.36	0.57	-3.79	23072.5
HLA A*2602	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.44	0.65	-3.79	27566.8
HLA B*5401	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.41	0.62	-3.80	25757.4
HLA A*2603	1:42-50	9	AADPVSLQT	1.20	-0.36	-4.64	0.84	-3.80	43719.4
HLA A*6801	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.61	0.81	-3.80	40898.1
HLA B*1501	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.26	0.46	-3.80	18240.9
HLA B*1501	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.37	0.57	-3.80	23220.6
HLA A*0202	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.01	0.21	-3.80	10186.0
HLA B*7301	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.51	0.71	-3.80	32136.0
HLA A*2402	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.55	0.75	-3.80	35764.7
HLA B*5301	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.57	0.77	-3.80	37494.5
HLA A*3301	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.61	0.81	-3.80	41171.4
HLA A*2403	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.45	0.65	-3.80	27892.7
HLA A*0219	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.42	0.62	-3.80	26079.9
HLA B*4402	1:37-45	9	AVVPPAADP	0.41	0.20	-4.42	0.61	-3.80	26020.4
HLA B*4801	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.42	0.62	-3.80	26192.3
HLA A*0211	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.51	0.71	-3.80	32523.0
HLA A*2601	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.32	0.52	-3.80	21023.0
HLA B*1503	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.52	0.72	-3.80	33132.3
HLA A*2402	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.57	0.76	-3.80	36844.3
HLA A*2403	1:37-45	9	AVVPPAADP	0.41	0.20	-4.42	0.61	-3.81	26217.0
HLA B*4801	1:37-45	9	AVVPPAADP	0.41	0.20	-4.42	0.61	-3.81	26259.7
HLA A*2602	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.51	0.70	-3.81	32444.3
HLA B*0702	1:37-45	9	AVVPPAADP	0.41	0.20	-4.42	0.61	-3.81	26304.5
HLA A*2301	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.52	0.72	-3.81	33377.2
HLA A*3002	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.52	0.72	-3.81	33414.6
HLA A*0219	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.27	0.46	-3.81	18697.4
HLA A*0219	1:37-45	9	AVVPPAADP	0.41	0.20	-4.42	0.61	-3.81	26389.1

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*3201	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.56	0.75	-3.81	36504.4
HLA B*3501	1:37-45	9	AVVPPAADP	0.41	0.20	-4.42	0.61	-3.81	26394.7
HLA B*1801	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.52	0.71	-3.81	33309.2
HLA B*4601	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.38	0.57	-3.81	23824.3
HLA B*7301	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.56	0.75	-3.81	36604.3
HLA A*0216	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.45	0.65	-3.81	28494.4
HLA B*0803	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.53	0.72	-3.81	33548.2
HLA B*0702	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.33	0.52	-3.81	21299.7
HLA A*0202	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.52	0.71	-3.81	32996.9
HLA B*1801	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.43	0.62	-3.81	26664.8
HLA A*2602	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.38	0.57	-3.81	23928.4
HLA B*5301	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.53	0.71	-3.81	33499.8
HLA A*1101	1:37-45	9	AVVPPAADP	0.41	0.20	-4.42	0.61	-3.81	26562.7
HLA A*2603	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.62	0.81	-3.81	41545.9
HLA B*1801	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.52	0.70	-3.81	32933.6
HLA B*4002	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.63	0.81	-3.81	42509.7
HLA A*2403	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.43	0.62	-3.81	26879.2
HLA A*0250	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.52	0.70	-3.81	33048.5
HLA A*8001	1:37-45	9	AVVPPAADP	0.41	0.20	-4.43	0.61	-3.82	26837.5
HLA B*3901	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.28	0.46	-3.82	19036.5
HLA A*2603	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.58	0.76	-3.82	37860.2
HLA B*0802	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.46	0.65	-3.82	29003.5
HLA B*4402	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.43	0.62	-3.82	27118.7
HLA A*0202	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.43	0.62	-3.82	27120.9
HLA B*2705	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.46	0.65	-3.82	29071.9
HLA B*4403	1:54-62	9	FSAQGVEHA	1.07	-0.26	-4.63	0.81	-3.82	42653.7
HLA A*0211	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.03	0.21	-3.82	10673.0
HLA B*5401	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.52	0.70	-3.82	33360.9
HLA A*6801	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.01	0.19	-3.82	10213.7
HLA B*3501	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.39	0.57	-3.82	24418.4
HLA B*2705	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.44	0.62	-3.82	27238.1
HLA A*6901	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.31	0.49	-3.82	20192.4
HLA A*3201	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.54	0.72	-3.82	34314.4
HLA B*7301	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.58	0.76	-3.82	38219.7
HLA B*5401	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.28	0.46	-3.82	19246.1
HLA A*0101	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.39	0.57	-3.82	24475.4
HLA A*3101	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.30	0.48	-3.82	20120.6
HLA A*0202	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.31	0.49	-3.82	20232.2
HLA B*1509	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.54	0.71	-3.82	34348.4
HLA A*0212	1:37-45	9	AVVPPAADP	0.41	0.20	-4.44	0.61	-3.82	27242.4
HLA A*0250	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.54	0.72	-3.82	34617.6
HLA A*0202	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.39	0.57	-3.82	24631.5
HLA A*2602	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.54	0.72	-3.82	34628.8
HLA A*0250	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.54	0.72	-3.83	34732.4
HLA A*2501	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.44	0.62	-3.83	27617.4
HLA A*0301	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.34	0.52	-3.83	22127.3
HLA A*3301	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.58	0.75	-3.83	38188.1
HLA A*0216	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.04	0.21	-3.83	10906.1
HLA B*1517	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.31	0.49	-3.83	20605.4

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*0201	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.40	0.57	-3.83	24956.8
HLA B*1517	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.02	0.19	-3.83	10449.3
HLA B*0702	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.31	0.48	-3.83	20518.2
HLA B*5801	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.35	0.52	-3.83	22285.2
HLA A*2301	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.55	0.72	-3.83	35083.3
HLA A*3001	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.29	0.46	-3.83	19612.5
HLA B*4402	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.40	0.57	-3.83	25007.0
HLA B*0801	1:37-45	9	AVVPPAADP	0.41	0.20	-4.44	0.61	-3.83	27787.5
HLA A*2301	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.55	0.71	-3.83	35098.6
HLA A*8001	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.45	0.62	-3.83	28026.3
HLA B*4403	1:35-43	9	ITAVVPPAA	1.01	-0.20	-4.64	0.81	-3.83	43383.9
HLA B*5301	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.55	0.72	-3.83	35368.2
HLA A*2402	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.55	0.72	-3.83	35391.3
HLA A*2402	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.54	0.70	-3.83	34526.9
HLA B*4002	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.61	0.77	-3.83	40641.1
HLA A*2301	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.54	0.70	-3.83	34608.6
HLA B*4002	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.59	0.75	-3.83	38794.3
HLA A*0250	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.55	0.71	-3.83	35379.8
HLA B*3801	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.55	0.71	-3.83	35401.3
HLA A*2301	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.54	0.71	-3.83	34968.2
HLA B*5401	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.40	0.57	-3.84	25387.9
HLA B*1517	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.48	0.65	-3.84	30338.1
HLA B*3901	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.45	0.62	-3.84	28334.6
HLA B*5301	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.60	0.76	-3.84	39766.6
HLA B*1509	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.55	0.72	-3.84	35856.1
HLA B*3501	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.36	0.52	-3.84	22843.1
HLA A*0250	1:37-45	9	AVVPPAADP	0.41	0.20	-4.45	0.61	-3.84	28447.4
HLA A*0219	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.41	0.57	-3.84	25643.0
HLA A*1101	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.49	0.65	-3.84	30746.5
HLA A*0203	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.31	0.46	-3.84	20262.8
HLA B*1517	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.46	0.62	-3.84	28777.3
HLA B*7301	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.55	0.70	-3.84	35445.9
HLA B*5701	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.41	0.57	-3.85	25938.6
HLA B*0802	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.46	0.62	-3.85	28931.2
HLA A*0203	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.30	0.45	-3.85	19946.1
HLA A*6801	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.56	0.71	-3.85	36351.9
HLA B*4801	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.42	0.57	-3.85	26048.6
HLA A*3301	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.49	0.65	-3.85	31120.5
HLA B*7301	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.56	0.72	-3.85	36687.3
HLA B*4601	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.33	0.48	-3.85	21450.9
HLA B*3801	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.56	0.72	-3.85	36646.5
HLA A*0301	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.33	0.48	-3.85	21463.6
HLA A*6801	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.57	0.72	-3.85	36739.0
HLA A*6901	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.33	0.48	-3.85	21480.0
HLA B*3801	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.57	0.72	-3.85	36767.0
HLA B*1503	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.31	0.46	-3.85	20529.8
HLA A*3001	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.18	0.33	-3.85	15231.1
HLA B*0801	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.42	0.57	-3.85	26226.3
HLA B*7301	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.57	0.71	-3.85	36741.7

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*5301	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.57	0.72	-3.85	36937.9
HLA B*7301	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.57	0.72	-3.85	36901.5
HLA A*0203	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.34	0.49	-3.85	21734.5
HLA B*4403	1:76-84	9	GVGVGESGA	1.07	-0.25	-4.67	0.81	-3.85	46412.7
HLA B*5301	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.56	0.70	-3.85	36048.9
HLA A*6801	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.57	0.72	-3.85	36985.2
HLA B*4403	1:34-42	9	VITAVVPPA	1.03	-0.23	-4.66	0.81	-3.85	45569.7
HLA A*3201	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.57	0.71	-3.85	36912.5
HLA A*0211	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.42	0.57	-3.85	26417.0
HLA B*5701	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.04	0.19	-3.85	11059.5
HLA B*5101	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.42	0.57	-3.85	26426.4
HLA B*0702	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.34	0.49	-3.85	21863.0
HLA A*6801	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.62	0.76	-3.85	41400.5
HLA B*3801	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.56	0.70	-3.86	36311.0
HLA A*3002	1:37-45	9	AVVPPAADP	0.41	0.20	-4.47	0.61	-3.86	29461.0
HLA B*4403	1:49-57	9	QTAAGFSAQ	0.80	-0.02	-4.63	0.77	-3.86	42822.7
HLA A*0211	1:37-45	9	AVVPPAADP	0.41	0.20	-4.47	0.61	-3.86	29611.6
HLA B*1517	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.05	0.19	-3.86	11097.4
HLA A*1101	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.47	0.62	-3.86	29795.1
HLA B*3801	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.57	0.71	-3.86	37025.1
HLA B*5101	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.48	0.62	-3.86	29929.1
HLA A*0216	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.43	0.57	-3.86	26934.9
HLA A*2501	1:37-45	9	AVVPPAADP	0.41	0.20	-4.48	0.61	-3.86	29930.5
HLA B*5101	1:37-45	9	AVVPPAADP	0.41	0.20	-4.48	0.61	-3.86	29933.1
HLA A*3001	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.27	0.41	-3.86	18762.0
HLA B*4501	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.58	0.72	-3.86	37997.9
HLA A*3002	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.43	0.57	-3.86	27067.1
HLA B*0803	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.51	0.65	-3.86	32338.1
HLA A*1101	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.43	0.57	-3.86	27098.8
HLA B*0702	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.43	0.57	-3.86	27101.0
HLA B*1501	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.35	0.49	-3.86	22401.2
HLA A*0250	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.57	0.71	-3.87	37556.9
HLA B*1502	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.58	0.72	-3.87	38153.0
HLA A*3201	1:37-45	9	AVVPPAADP	0.41	0.20	-4.48	0.61	-3.87	30187.8
HLA A*6802	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.35	0.48	-3.87	22362.1
HLA A*2402	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.58	0.71	-3.87	37636.0
HLA B*0802	1:37-45	9	AVVPPAADP	0.41	0.20	-4.48	0.61	-3.87	30220.6
HLA B*4001	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.44	0.57	-3.87	27241.3
HLA B*3901	1:37-45	9	AVVPPAADP	0.41	0.20	-4.48	0.61	-3.87	30268.2
HLA A*0101	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.39	0.52	-3.87	24353.5
HLA B*2705	1:37-45	9	AVVPPAADP	0.41	0.20	-4.48	0.61	-3.87	30315.1
HLA A*2402	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.58	0.71	-3.87	38307.9
HLA B*0803	1:37-45	9	AVVPPAADP	0.41	0.20	-4.48	0.61	-3.87	30405.6
HLA B*4001	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.39	0.52	-3.87	24457.5
HLA A*0202	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.06	0.19	-3.87	11494.9
HLA B*5801	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.36	0.49	-3.87	22696.4
HLA A*3101	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.39	0.52	-3.87	24519.9
HLA B*0801	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.39	0.52	-3.87	24531.9
HLA A*2603	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.63	0.75	-3.87	42231.4

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*0203	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.36	0.48	-3.87	22651.9
HLA A*0211	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.52	0.65	-3.87	32956.4
HLA A*0211	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.36	0.49	-3.87	22826.9
HLA A*6901	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.39	0.52	-3.87	24657.5
HLA A*2402	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.59	0.72	-3.87	38859.4
HLA A*0212	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.44	0.57	-3.87	27648.6
HLA A*0202	1:37-45	9	AVVPPAADP	0.41	0.20	-4.49	0.61	-3.87	30686.7
HLA A*0301	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.36	0.49	-3.87	22896.9
HLA A*0216	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.36	0.49	-3.87	22903.5
HLA A*0101	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.36	0.49	-3.88	22962.3
HLA B*4001	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.34	0.46	-3.88	21859.5
HLA A*2902	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.40	0.52	-3.88	24855.7
HLA A*3301	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.58	0.70	-3.88	38150.3
HLA A*0201	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.40	0.52	-3.88	24874.9
HLA B*4001	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.36	0.49	-3.88	23049.8
HLA B*3901	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.36	0.48	-3.88	22950.1
HLA A*0202	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.52	0.65	-3.88	33362.5
HLA A*0211	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.49	0.62	-3.88	31163.0
HLA B*4403	1:24-32	9	LAAAHASAA	0.90	-0.14	-4.63	0.75	-3.88	42887.3
HLA B*4601	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.40	0.52	-3.88	24970.3
HLA B*1502	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.59	0.71	-3.88	39169.2
HLA B*1517	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.40	0.52	-3.88	25001.3
HLA B*1502	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.58	0.70	-3.88	38404.0
HLA B*1502	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.60	0.72	-3.88	39443.5
HLA A*3002	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.59	0.71	-3.88	38898.1
HLA A*0201	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.37	0.49	-3.88	23299.3
HLA B*3801	1:37-45	9	AVVPPAADP	0.41	0.20	-4.50	0.61	-3.88	31310.3
HLA A*2403	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.45	0.57	-3.88	28265.4
HLA A*2601	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.37	0.48	-3.89	23350.3
HLA B*4801	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.35	0.46	-3.89	22438.9
HLA B*5801	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.35	0.46	-3.89	22379.6
HLA B*0803	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.50	0.62	-3.89	31826.3
HLA B*3801	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.53	0.65	-3.89	34088.9
HLA A*8001	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.46	0.57	-3.89	28548.0
HLA B*5301	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.60	0.71	-3.89	39588.9
HLA B*5701	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.41	0.52	-3.89	25568.4
HLA A*0203	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.41	0.52	-3.89	25587.8
HLA B*7301	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.53	0.65	-3.89	34248.2
HLA B*4403	1:19-27	9	ALTARLAAA	1.01	-0.25	-4.65	0.76	-3.89	44831.3
HLA A*0101	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.37	0.48	-3.89	23587.6
HLA A*2501	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.46	0.57	-3.89	28763.3
HLA B*5801	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.35	0.45	-3.89	22156.5
HLA A*0101	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.36	0.46	-3.89	22673.0
HLA A*3001	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.16	0.27	-3.89	14561.2
HLA A*8001	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.41	0.52	-3.89	25798.7
HLA A*6901	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.35	0.45	-3.89	22265.4
HLA B*5801	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.36	0.46	-3.89	22796.2
HLA A*2301	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.51	0.62	-3.89	32326.5
HLA B*4001	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.36	0.46	-3.89	22772.8

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*0219	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.38	0.49	-3.90	24076.8
HLA B*1801	1:37-45	9	AVVPPAADP	0.41	0.20	-4.51	0.61	-3.90	32327.9
HLA A*6801	1:90-98	9	DAAAAATYG	0.74	-0.73	-3.91	0.01	-3.90	8052.8
HLA B*1801	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.36	0.46	-3.90	22982.7
HLA B*1501	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.23	0.33	-3.90	16983.8
HLA B*4403	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.60	0.70	-3.90	40065.7
HLA A*0212	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.38	0.49	-3.90	24194.2
HLA A*6802	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.42	0.52	-3.90	26127.3
HLA A*0211	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.36	0.46	-3.90	23065.8
HLA A*2301	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.54	0.65	-3.90	35022.8
HLA A*0301	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.36	0.46	-3.90	23129.9
HLA A*0301	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.36	0.46	-3.90	23069.9
HLA B*4501	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.36	0.46	-3.90	23143.0
HLA A*3101	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.36	0.45	-3.90	22649.1
HLA A*0250	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.11	0.21	-3.90	12914.9
HLA A*2402	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.52	0.62	-3.90	32875.9
HLA B*1502	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.61	0.71	-3.90	40796.0
HLA A*6801	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.09	0.19	-3.90	12262.0
HLA A*3101	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.39	0.49	-3.90	24431.2
HLA B*4403	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.62	0.72	-3.90	41511.8
HLA A*2601	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.39	0.49	-3.90	24438.9
HLA B*4002	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.62	0.71	-3.90	41394.7
HLA A*3201	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.61	0.71	-3.90	40908.9
HLA B*3501	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.36	0.45	-3.90	22760.3
HLA A*2403	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.42	0.52	-3.90	26427.3
HLA A*0202	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.36	0.45	-3.90	22769.8
HLA A*0202	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.39	0.48	-3.90	24386.7
HLA B*0802	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.47	0.57	-3.90	29719.0
HLA A*0216	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.36	0.45	-3.91	22881.0
HLA B*3901	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.47	0.57	-3.91	29761.0
HLA B*4801	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.42	0.52	-3.91	26562.9
HLA A*0301	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.36	0.45	-3.91	22937.8
HLA A*0201	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.39	0.48	-3.91	24576.4
HLA B*4002	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.61	0.70	-3.91	40973.8
HLA B*4801	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.39	0.48	-3.91	24603.9
HLA A*2602	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.62	0.71	-3.91	41390.9
HLA B*5101	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.39	0.48	-3.91	24616.0
HLA B*0702	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.37	0.46	-3.91	23569.7
HLA B*1509	1:37-45	9	AVVPPAADP	0.41	0.20	-4.52	0.61	-3.91	33247.4
HLA B*4403	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.62	0.71	-3.91	41951.1
HLA A*3301	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.62	0.72	-3.91	42155.2
HLA A*6802	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.40	0.49	-3.91	24845.3
HLA A*2501	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.43	0.52	-3.91	26860.7
HLA A*3301	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.63	0.72	-3.91	42341.0
HLA B*4601	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.40	0.49	-3.91	24894.0
HLA B*0801	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.36	0.45	-3.91	23164.7
HLA A*2602	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.63	0.71	-3.91	42197.6
HLA B*0801	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.40	0.49	-3.91	24943.4
HLA B*4002	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.63	0.72	-3.91	42391.2

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*6801	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.56	0.65	-3.91	36136.8
HLA A*3201	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.63	0.72	-3.91	42543.3
HLA A*0216	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.38	0.46	-3.91	23838.9
HLA A*0212	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.38	0.46	-3.91	23865.2
HLA A*2601	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.38	0.46	-3.91	23896.5
HLA A*2403	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.40	0.49	-3.91	25110.5
HLA A*3301	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.63	0.71	-3.91	42552.2
HLA B*4601	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.38	0.46	-3.91	23924.9
HLA A*3002	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.40	0.48	-3.91	25000.4
HLA A*0201	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.37	0.45	-3.92	23399.8
HLA B*1502	1:37-45	9	AVVPPAADP	0.41	0.20	-4.53	0.61	-3.92	33791.9
HLA A*2603	1:13-21	9	ASAAVEALT	0.86	-0.15	-4.62	0.70	-3.92	41718.4
HLA A*6802	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.33	0.41	-3.92	21234.5
HLA B*4402	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.44	0.52	-3.92	27260.7
HLA A*0212	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.37	0.45	-3.92	23520.3
HLA A*6901	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.38	0.46	-3.92	24009.4
HLA A*0216	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.10	0.19	-3.92	12723.5
HLA A*2403	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.40	0.48	-3.92	25177.4
HLA A*2603	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.63	0.71	-3.92	42388.9
HLA B*4002	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.63	0.72	-3.92	43117.4
HLA A*2603	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.53	0.62	-3.92	34210.0
HLA B*1502	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.38	0.46	-3.92	24137.7
HLA A*2601	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.38	0.46	-3.92	24068.8
HLA B*2705	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.49	0.57	-3.92	30695.2
HLA A*2403	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.11	0.19	-3.92	12752.3
HLA A*0101	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.38	0.46	-3.92	24130.3
HLA A*0201	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.38	0.46	-3.92	24210.1
HLA A*0101	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.37	0.45	-3.92	23702.2
HLA A*0206	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.49	0.57	-3.92	30860.7
HLA B*5401	1:37-45	9	AVVPPAADP	0.41	0.20	-4.54	0.61	-3.92	34280.8
HLA A*2902	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.41	0.48	-3.92	25425.4
HLA B*1503	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.38	0.45	-3.92	23794.7
HLA B*4801	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.39	0.46	-3.92	24281.5
HLA B*4402	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.39	0.46	-3.92	24358.4
HLA B*4402	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.41	0.48	-3.92	25481.0
HLA A*2403	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.39	0.46	-3.92	24392.5
HLA A*2403	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.38	0.45	-3.92	23842.1
HLA B*1502	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.57	0.65	-3.92	37047.9
HLA B*0803	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.49	0.57	-3.92	31020.9
HLA B*4403	1:67-75	9	EGVEELGRA	1.05	-0.34	-4.64	0.72	-3.92	43617.4
HLA B*4801	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.41	0.49	-3.92	25662.8
HLA B*5801	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.33	0.41	-3.92	21608.0
HLA B*4001	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.41	0.48	-3.92	25582.4
HLA A*2301	1:37-45	9	AVVPPAADP	0.41	0.20	-4.54	0.61	-3.93	34550.6
HLA B*1801	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.49	0.57	-3.93	31161.5
HLA A*3002	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.41	0.49	-3.93	25779.3
HLA B*1501	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.39	0.46	-3.93	24474.3
HLA A*2403	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.34	0.41	-3.93	21697.0
HLA B*1509	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.50	0.57	-3.93	31291.2

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*4001	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.38	0.45	-3.93	24080.6
HLA A*3101	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.11	0.19	-3.93	13013.0
HLA B*5701	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.41	0.49	-3.93	25914.8
HLA A*2601	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.38	0.45	-3.93	24112.3
HLA A*0212	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.39	0.46	-3.93	24603.5
HLA B*1509	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.55	0.62	-3.93	35092.9
HLA A*0212	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.41	0.48	-3.93	25866.7
HLA B*5701	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.39	0.46	-3.93	24686.4
HLA B*5301	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.50	0.57	-3.93	31551.8
HLA B*4402	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.42	0.49	-3.93	26077.5
HLA A*3002	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.58	0.65	-3.93	37701.8
HLA A*3301	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.64	0.71	-3.93	43679.2
HLA B*1509	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.39	0.46	-3.93	24794.2
HLA A*3001	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.25	0.32	-3.93	17885.3
HLA A*0212	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.45	0.52	-3.93	28258.6
HLA A*1101	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.45	0.52	-3.93	28270.4
HLA B*0702	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.40	0.46	-3.93	24848.0
HLA B*3801	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.55	0.62	-3.93	35399.9
HLA A*0201	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.40	0.46	-3.93	24900.5
HLA A*8001	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.42	0.48	-3.93	26121.1
HLA A*0250	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.58	0.65	-3.93	38000.2
HLA B*4601	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.39	0.45	-3.94	24517.8
HLA A*2603	1:93-101	9	AAATYGVVG	1.16	-0.45	-4.65	0.72	-3.94	44780.8
HLA A*0202	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.35	0.41	-3.94	22179.6
HLA A*3101	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.40	0.46	-3.94	25106.8
HLA A*6801	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.55	0.62	-3.94	35636.8
HLA A*0202	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.40	0.46	-3.94	25140.1
HLA A*0203	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.40	0.46	-3.94	25099.3
HLA A*0219	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.42	0.48	-3.94	26351.2
HLA A*2902	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.42	0.49	-3.94	26499.7
HLA A*0219	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.46	0.52	-3.94	28661.4
HLA B*4601	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.40	0.46	-3.94	25370.6
HLA B*1517	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.41	0.46	-3.94	25453.5
HLA A*3101	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.41	0.46	-3.94	25412.3
HLA A*1101	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.43	0.48	-3.94	26663.7
HLA A*8001	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.43	0.49	-3.94	26845.3
HLA B*1501	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.13	0.19	-3.94	13598.1
HLA B*3901	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.41	0.46	-3.94	25488.2
HLA A*0206	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.43	0.48	-3.94	26718.3
HLA A*0250	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.56	0.62	-3.94	36255.0
HLA B*5301	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.56	0.62	-3.95	36369.6
HLA A*2603	1:83-91	9	GASYLAGDA	0.98	-0.27	-4.66	0.71	-3.95	45653.1
HLA B*0802	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.46	0.52	-3.95	29173.9
HLA A*2402	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.51	0.57	-3.95	32690.6
HLA A*0216	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.47	0.52	-3.95	29190.0
HLA B*4402	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.40	0.45	-3.95	25211.5
HLA B*1503	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.47	0.52	-3.95	29266.4
HLA B*5701	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.40	0.45	-3.95	25272.1
HLA A*2402	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.59	0.65	-3.95	39314.0

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*4402	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.41	0.46	-3.95	25849.9
HLA A*6802	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.28	0.33	-3.95	18922.9
HLA B*2705	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.40	0.45	-3.95	25392.1
HLA B*4501	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.60	0.65	-3.95	39526.2
HLA A*0219	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.41	0.46	-3.95	25957.0
HLA B*7301	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.57	0.62	-3.95	36963.8
HLA B*0702	1:6-14	9	VPEGLAAAS	1.10	-1.12	-3.93	-0.03	-3.95	8451.0
HLA A*6801	1:37-45	9	AVVPPAADP	0.41	0.20	-4.57	0.61	-3.95	36881.5
HLA A*3301	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.52	0.57	-3.95	33259.3
HLA B*5701	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.42	0.46	-3.95	26229.6
HLA B*3901	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.47	0.52	-3.95	29761.1
HLA A*6901	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.37	0.41	-3.95	23192.1
HLA B*4501	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.23	0.27	-3.96	16899.0
HLA A*2403	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.42	0.46	-3.96	26240.9
HLA A*1101	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.44	0.49	-3.96	27668.7
HLA A*0301	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.37	0.41	-3.96	23298.0
HLA A*2902	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.42	0.46	-3.96	26285.0
HLA B*0801	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.42	0.46	-3.96	26319.4
HLA A*0216	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.42	0.46	-3.96	26333.1
HLA A*0101	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.37	0.41	-3.96	23377.2
HLA A*3201	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.61	0.65	-3.96	40297.0
HLA A*0219	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.41	0.45	-3.96	25998.6
HLA B*4001	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.37	0.41	-3.96	23511.1
HLA A*2603	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.61	0.65	-3.96	40390.6
HLA A*6801	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.48	0.52	-3.96	30208.9
HLA A*8001	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.42	0.46	-3.96	26552.8
HLA A*2402	1:37-45	9	AVVPPAADP	0.41	0.20	-4.58	0.61	-3.96	37602.2
HLA A*3201	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.42	0.45	-3.96	26108.8
HLA B*5101	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.43	0.46	-3.96	26764.3
HLA A*2301	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.53	0.57	-3.96	34095.1
HLA A*6802	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.43	0.46	-3.96	26759.5
HLA A*3001	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.29	0.33	-3.96	19562.6
HLA A*8001	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.43	0.46	-3.96	26852.3
HLA B*7301	1:37-45	9	AVVPPAADP	0.41	0.20	-4.58	0.61	-3.96	37874.3
HLA A*3002	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.58	0.62	-3.97	38205.7
HLA B*2705	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.49	0.52	-3.97	30710.4
HLA B*0802	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.46	0.49	-3.97	28513.2
HLA A*0216	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.45	0.48	-3.97	28365.8
HLA A*2603	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.54	0.57	-3.97	34515.3
HLA A*6801	1:7-15	9	PEGLAAASA	1.26	-0.55	-4.68	0.71	-3.97	47848.0
HLA B*5701	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.38	0.41	-3.97	24107.8
HLA B*1801	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.49	0.52	-3.97	30952.1
HLA B*2705	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.46	0.49	-3.97	28701.9
HLA B*5301	1:37-45	9	AVVPPAADP	0.41	0.20	-4.59	0.61	-3.97	38575.3
HLA B*4002	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.62	0.65	-3.97	41614.7
HLA B*3501	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.38	0.41	-3.97	24261.7
HLA B*4601	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.39	0.41	-3.98	24325.6
HLA B*1801	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.46	0.48	-3.98	28793.0
HLA B*3801	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.54	0.57	-3.98	35057.3

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*0206	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.50	0.52	-3.98	31352.9
HLA B*2705	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.44	0.46	-3.98	27677.5
HLA B*1502	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.55	0.57	-3.98	35229.5
HLA A*3301	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.59	0.62	-3.98	39295.7
HLA B*0803	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.50	0.52	-3.98	31453.5
HLA B*0802	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.46	0.48	-3.98	28990.1
HLA B*4801	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.43	0.45	-3.98	27149.7
HLA B*3501	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.30	0.32	-3.98	19994.4
HLA B*1509	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.46	0.48	-3.98	29068.0
HLA B*5101	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.50	0.52	-3.98	31628.7
HLA B*0802	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.44	0.45	-3.98	27448.5
HLA B*1502	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.60	0.62	-3.99	39899.1
HLA A*2501	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.47	0.48	-3.99	29405.2
HLA B*1801	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.47	0.49	-3.99	29594.8
HLA A*0201	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.40	0.41	-3.99	24898.5
HLA A*2902	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.45	0.46	-3.99	28205.5
HLA A*2601	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.40	0.41	-3.99	25007.6
HLA B*1503	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.17	0.19	-3.99	14944.6
HLA B*4402	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.17	0.18	-3.99	14757.1
HLA A*2902	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.44	0.45	-3.99	27695.6
HLA A*2603	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.45	0.46	-3.99	28355.7
HLA B*0803	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.47	0.48	-3.99	29627.2
HLA A*1101	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.44	0.45	-3.99	27732.0
HLA A*2603	1:37-45	9	AVVPPAADP	0.41	0.20	-4.60	0.61	-3.99	40205.3
HLA A*2501	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.45	0.46	-3.99	28510.0
HLA B*1501	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.18	0.19	-3.99	15066.1
HLA B*3501	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.45	0.46	-3.99	28467.6
HLA A*3101	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.40	0.41	-3.99	25302.1
HLA A*0211	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.45	0.45	-3.99	27998.4
HLA B*4403	1:44-52	9	DPVSLQTAA	1.05	-0.40	-4.64	0.65	-3.99	43571.6
HLA B*5301	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.48	0.48	-3.99	30015.8
HLA B*1503	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.33	0.33	-3.99	21247.6
HLA A*2501	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.48	0.49	-4.00	30266.4
HLA B*2705	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.48	0.48	-4.00	30150.4
HLA A*0203	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.41	0.41	-4.00	25618.3
HLA B*0802	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.46	0.46	-4.00	29025.9
HLA A*0212	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.41	0.41	-4.00	25755.7
HLA A*1101	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.46	0.46	-4.00	29162.7
HLA A*0301	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.32	0.32	-4.00	20975.5
HLA A*1101	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.46	0.46	-4.00	29107.2
HLA A*0206	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.41	0.41	-4.00	25822.8
HLA A*6802	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.21	0.21	-4.00	16351.3
HLA A*3001	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.19	0.19	-4.00	15645.0
HLA A*0211	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.52	0.52	-4.00	33355.5
HLA B*0801	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.41	0.41	-4.00	25991.0
HLA B*4402	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.42	0.41	-4.01	26070.4
HLA B*5401	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.46	0.45	-4.01	28864.6
HLA B*4801	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.42	0.41	-4.01	26257.8
HLA B*5101	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.50	0.49	-4.01	31312.5

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*8001	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.46	0.45	-4.01	29167.1
HLA B*0702	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.47	0.45	-4.01	29186.8
HLA B*4501	1:37-45	9	AVVPPAADP	0.41	0.20	-4.63	0.61	-4.01	42172.7
HLA A*3301	1:37-45	9	AVVPPAADP	0.41	0.20	-4.63	0.61	-4.01	42276.0
HLA B*0803	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.50	0.49	-4.01	31509.3
HLA A*0301	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.35	0.33	-4.01	22177.6
HLA A*0211	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.50	0.48	-4.01	31384.1
HLA B*1501	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.07	0.06	-4.01	11775.3
HLA B*1501	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.34	0.32	-4.02	21668.9
HLA B*0802	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.48	0.46	-4.02	30160.7
HLA B*5801	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.35	0.33	-4.02	22292.0
HLA A*3101	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.35	0.33	-4.02	22331.5
HLA A*0202	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.20	0.19	-4.02	16008.2
HLA A*0201	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.20	0.19	-4.02	16031.9
HLA B*1503	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.50	0.49	-4.02	31911.4
HLA B*3501	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.35	0.33	-4.02	22135.8
HLA B*1502	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.50	0.48	-4.02	31754.4
HLA A*2902	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.34	0.32	-4.02	21870.4
HLA B*3901	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.48	0.45	-4.02	29858.4
HLA B*0803	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.49	0.46	-4.02	30569.7
HLA B*5101	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.48	0.45	-4.02	29995.0
HLA A*2301	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.54	0.52	-4.02	34840.4
HLA B*1517	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.49	0.46	-4.02	30638.9
HLA A*1101	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.44	0.41	-4.03	27350.8
HLA B*4002	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.64	0.62	-4.03	43963.7
HLA B*2705	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.44	0.41	-4.03	27449.2
HLA A*0219	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.44	0.41	-4.03	27483.2
HLA B*5801	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.35	0.32	-4.03	22350.6
HLA A*0206	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.24	0.21	-4.03	17389.6
HLA A*6901	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.36	0.33	-4.03	22785.5
HLA B*5401	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.55	0.52	-4.03	35531.5
HLA A*0206	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.49	0.46	-4.03	31231.5
HLA B*1509	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.55	0.52	-4.03	35571.4
HLA B*4002	1:37-45	9	AVVPPAADP	0.41	0.20	-4.65	0.61	-4.03	44268.3
HLA A*6901	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.04	0.01	-4.03	11022.8
HLA B*4501	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.49	0.45	-4.03	30693.5
HLA B*0803	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.50	0.46	-4.03	31311.0
HLA A*2501	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.50	0.46	-4.03	31334.2
HLA B*5801	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.36	0.33	-4.03	22911.8
HLA A*0212	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.24	0.21	-4.03	17546.7
HLA B*0801	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.37	0.33	-4.03	23294.0
HLA B*0702	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.45	0.41	-4.04	27905.3
HLA B*4501	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.65	0.62	-4.04	44776.0
HLA B*4403	1:37-45	9	AVVPPAADP	0.41	0.20	-4.65	0.61	-4.04	44569.8
HLA A*0206	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.36	0.32	-4.04	22724.8
HLA B*3501	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.37	0.33	-4.04	23371.7
HLA A*2902	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.45	0.41	-4.04	27978.7
HLA A*0202	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.56	0.52	-4.04	36033.3
HLA A*0101	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.36	0.33	-4.04	23166.8

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*4601	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.37	0.33	-4.04	23507.4
HLA A*2501	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.49	0.45	-4.04	31114.3
HLA B*1509	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.52	0.49	-4.04	33450.7
HLA B*5301	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.49	0.45	-4.04	31132.5
HLA B*1503	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.45	0.41	-4.04	28184.6
HLA A*0301	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.37	0.33	-4.04	23257.6
HLA A*0211	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.45	0.41	-4.04	28244.6
HLA B*7301	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.61	0.57	-4.04	40779.0
HLA A*0216	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.45	0.41	-4.04	28352.5
HLA B*1509	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.51	0.46	-4.04	32115.3
HLA B*1801	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.51	0.46	-4.04	32059.0
HLA A*0206	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.31	0.27	-4.04	20652.2
HLA A*8001	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.45	0.41	-4.04	28431.3
HLA B*3801	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.56	0.52	-4.04	36550.4
HLA B*1517	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.36	0.32	-4.04	23158.7
HLA A*2403	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.36	0.32	-4.04	23165.7
HLA A*0250	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.56	0.52	-4.05	36692.5
HLA B*5101	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.51	0.46	-4.05	32267.1
HLA A*3201	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.61	0.57	-4.05	41145.8
HLA A*0101	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.37	0.32	-4.05	23267.4
HLA B*5701	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.23	0.19	-4.05	17117.8
HLA B*1502	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.57	0.52	-4.05	36789.9
HLA B*3801	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.51	0.46	-4.05	32345.1
HLA A*0211	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.51	0.46	-4.05	32369.4
HLA B*4001	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.37	0.33	-4.05	23695.8
HLA A*2602	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.53	0.48	-4.05	33993.1
HLA A*3002	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.51	0.46	-4.05	32568.8
HLA B*1501	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.26	0.21	-4.05	18170.8
HLA B*1517	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.46	0.41	-4.05	28850.6
HLA A*0250	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.54	0.49	-4.05	34326.3
HLA B*4501	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.54	0.49	-4.05	34340.0
HLA B*4403	1:33-41	9	PVITAVVPP	0.62	-0.01	-4.67	0.62	-4.05	46346.9
HLA A*3101	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.37	0.32	-4.05	23499.3
HLA A*6901	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.38	0.33	-4.05	24163.2
HLA B*5701	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.38	0.33	-4.05	23847.9
HLA A*2603	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.57	0.52	-4.05	37135.8
HLA A*2301	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.53	0.48	-4.05	34224.3
HLA B*5401	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.51	0.46	-4.05	32684.4
HLA B*1801	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.51	0.45	-4.05	32059.2
HLA B*1502	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.54	0.49	-4.05	34463.8
HLA A*2402	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.57	0.52	-4.05	37329.6
HLA B*3801	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.54	0.49	-4.05	34583.3
HLA A*8001	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.37	0.32	-4.05	23668.6
HLA A*0101	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.39	0.33	-4.05	24326.4
HLA A*2403	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.38	0.33	-4.05	24025.4
HLA A*0202	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.52	0.46	-4.05	32890.9
HLA B*3501	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.24	0.19	-4.05	17426.2
HLA B*5801	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.24	0.19	-4.05	17572.8
HLA A*0201	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.27	0.21	-4.06	18434.1

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*0250	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.54	0.48	-4.06	34668.6
HLA A*2601	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.39	0.33	-4.06	24523.0
HLA A*2402	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.54	0.48	-4.06	34701.8
HLA A*6901	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.38	0.32	-4.06	23870.9
HLA B*4402	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.33	0.27	-4.06	21359.3
HLA A*3101	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.38	0.33	-4.06	24244.4
HLA B*0803	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.51	0.45	-4.06	32580.1
HLA A*3201	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.58	0.52	-4.06	37883.2
HLA B*5401	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.55	0.49	-4.06	35092.6
HLA A*2601	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.38	0.32	-4.06	24055.5
HLA B*4001	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.38	0.32	-4.06	24076.7
HLA A*2301	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.55	0.49	-4.06	35265.6
HLA B*4601	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.38	0.32	-4.06	24149.9
HLA A*6901	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.33	0.27	-4.06	21581.3
HLA A*2602	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.53	0.46	-4.06	33640.6
HLA A*0201	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.40	0.33	-4.06	24941.5
HLA B*0702	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.40	0.33	-4.06	24960.7
HLA B*7301	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.58	0.52	-4.06	38352.9
HLA B*4001	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.34	0.27	-4.07	21729.3
HLA B*1501	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.39	0.33	-4.07	24660.4
HLA A*2403	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.34	0.27	-4.07	21738.4
HLA B*5401	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.25	0.19	-4.07	17886.3
HLA A*2601	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.39	0.33	-4.07	24693.7
HLA B*4001	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.40	0.33	-4.07	25055.9
HLA B*7301	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.53	0.46	-4.07	34023.8
HLA B*0801	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.34	0.27	-4.07	21859.7
HLA A*6802	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.39	0.32	-4.07	24509.1
HLA A*0212	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.34	0.27	-4.07	21919.3
HLA A*0216	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.39	0.32	-4.07	24571.2
HLA A*2403	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.40	0.33	-4.07	25256.4
HLA A*6801	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.53	0.46	-4.07	34247.3
HLA A*6802	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.11	0.04	-4.07	12898.4
HLA B*4402	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.40	0.33	-4.07	25354.0
HLA A*3002	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.53	0.45	-4.07	33566.6
HLA A*0201	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.40	0.33	-4.07	25026.8
HLA B*3801	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.56	0.48	-4.07	35920.6
HLA A*6801	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.40	0.33	-4.07	25068.8
HLA B*1801	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.48	0.41	-4.07	30418.1
HLA B*0802	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.48	0.41	-4.07	30428.1
HLA A*2301	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.54	0.46	-4.07	34452.0
HLA A*0201	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.39	0.32	-4.07	24782.3
HLA B*5701	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.40	0.32	-4.08	24875.9
HLA B*0801	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.26	0.19	-4.08	18288.4
HLA B*5701	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.41	0.33	-4.08	25583.0
HLA B*5301	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.59	0.52	-4.08	39299.5
HLA A*0250	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.54	0.46	-4.08	34766.6
HLA A*2301	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.54	0.46	-4.08	34816.1
HLA A*2501	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.49	0.41	-4.08	30869.0
HLA B*4002	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.65	0.57	-4.08	44464.1

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*0250	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.53	0.45	-4.08	34211.5
HLA B*3901	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.49	0.41	-4.08	30982.3
HLA A*2902	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.41	0.33	-4.08	25920.8
HLA A*0203	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.40	0.32	-4.08	25237.8
HLA B*5101	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.49	0.41	-4.08	31164.5
HLA A*3002	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.55	0.46	-4.08	35206.5
HLA B*1501	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.24	0.16	-4.08	17342.6
HLA B*7301	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.57	0.48	-4.08	36928.7
HLA B*4501	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.65	0.57	-4.08	44991.9
HLA A*0301	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.30	0.21	-4.09	19724.5
HLA B*5801	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.36	0.27	-4.09	22750.2
HLA B*3801	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.55	0.46	-4.09	35435.8
HLA B*4403	1:41-49	9	PAADPVSLQ	0.86	-0.29	-4.66	0.57	-4.09	45188.0
HLA A*0203	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.42	0.33	-4.09	26259.3
HLA B*3501	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.10	0.01	-4.09	12506.9
HLA B*4601	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.41	0.33	-4.09	25969.9
HLA B*1509	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.54	0.45	-4.09	34909.6
HLA A*1101	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.41	0.32	-4.09	25685.2
HLA B*0801	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.42	0.33	-4.09	26173.5
HLA B*4801	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.42	0.33	-4.09	26554.1
HLA B*0801	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.41	0.32	-4.09	25847.9
HLA A*2301	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.55	0.45	-4.09	35209.7
HLA A*6802	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.43	0.33	-4.09	26625.3
HLA A*3201	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.58	0.49	-4.09	37902.6
HLA A*0101	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.37	0.27	-4.09	23179.6
HLA A*0301	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.37	0.27	-4.09	23196.4
HLA A*3002	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.41	0.32	-4.09	26001.0
HLA A*3301	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.61	0.52	-4.10	41177.2
HLA B*7301	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.55	0.45	-4.10	35570.2
HLA B*0803	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.51	0.41	-4.10	32181.5
HLA A*3301	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.58	0.48	-4.10	38085.8
HLA A*2602	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.55	0.45	-4.10	35656.9
HLA A*0203	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.29	0.19	-4.10	19289.7
HLA A*0219	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.37	0.27	-4.10	23474.9
HLA B*7301	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.29	0.19	-4.10	19307.1
HLA A*6801	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.55	0.45	-4.10	35777.7
HLA B*1502	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.56	0.46	-4.10	36612.2
HLA A*0203	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.29	0.19	-4.10	19592.3
HLA B*4001	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.28	0.18	-4.10	19204.1
HLA A*0212	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.42	0.32	-4.10	26501.3
HLA A*8001	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.44	0.33	-4.10	27253.4
HLA B*5301	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.59	0.49	-4.10	38815.0
HLA A*0203	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.38	0.27	-4.10	23726.3
HLA A*6801	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.43	0.32	-4.10	26633.1
HLA B*1501	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.38	0.27	-4.11	23860.7
HLA B*4002	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.57	0.46	-4.11	37176.6
HLA B*3501	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.38	0.27	-4.11	23885.1
HLA B*1509	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.44	0.33	-4.11	27507.0
HLA A*1101	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.32	0.21	-4.11	20765.8

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*0212	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.44	0.33	-4.11	27535.9
HLA B*4801	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.38	0.27	-4.11	23947.7
HLA B*3801	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.56	0.45	-4.11	36452.3
HLA B*5401	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.52	0.41	-4.11	32973.9
HLA A*0212	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.29	0.19	-4.11	19707.7
HLA B*5301	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.57	0.46	-4.11	37335.4
HLA B*1517	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.44	0.33	-4.11	27589.1
HLA B*4501	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.63	0.52	-4.11	42420.1
HLA B*4801	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.44	0.33	-4.11	27322.1
HLA B*1509	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.52	0.41	-4.11	33196.2
HLA B*0702	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.43	0.32	-4.11	27035.7
HLA B*4801	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.43	0.32	-4.11	27047.5
HLA B*0801	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.29	0.18	-4.11	19619.3
HLA A*2902	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.44	0.33	-4.11	27440.1
HLA A*2402	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.60	0.49	-4.11	39639.2
HLA A*3001	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.27	0.16	-4.11	18549.8
HLA B*0702	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.39	0.27	-4.11	24279.4
HLA A*0212	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.44	0.33	-4.11	27589.9
HLA B*4501	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.58	0.46	-4.11	37819.1
HLA A*0201	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.39	0.27	-4.11	24360.2
HLA A*3201	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.60	0.48	-4.12	39734.8
HLA B*4402	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.44	0.32	-4.12	27345.9
HLA A*3101	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.39	0.27	-4.12	24487.5
HLA A*0250	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.58	0.46	-4.12	38091.9
HLA A*3002	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.39	0.27	-4.12	24537.2
HLA A*0101	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.33	0.21	-4.12	21292.5
HLA A*6901	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.33	0.21	-4.12	21292.8
HLA A*0219	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.44	0.32	-4.12	27505.4
HLA B*4402	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.45	0.33	-4.12	27948.2
HLA B*4601	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.39	0.27	-4.12	24633.6
HLA A*1101	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.45	0.33	-4.12	28445.9
HLA B*0802	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.45	0.33	-4.12	28473.8
HLA B*1503	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.44	0.32	-4.12	27724.8
HLA A*2402	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.59	0.46	-4.12	38597.1
HLA A*2402	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.59	0.46	-4.12	38615.6
HLA B*4002	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.64	0.52	-4.12	43964.9
HLA A*2301	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.53	0.41	-4.12	34253.9
HLA B*1502	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.33	0.21	-4.12	21597.3
HLA A*2602	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.61	0.49	-4.12	40737.6
HLA A*3101	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.33	0.21	-4.12	21611.4
HLA A*0219	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.31	0.19	-4.13	20534.6
HLA B*3501	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.16	0.04	-4.13	14615.8
HLA A*1101	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.45	0.33	-4.13	28349.4
HLA A*6901	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.18	0.06	-4.13	15236.6
HLA A*2601	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.34	0.21	-4.13	21703.8
HLA B*4002	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.61	0.49	-4.13	40955.4
HLA A*3201	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.59	0.46	-4.13	38900.2
HLA A*0216	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.40	0.27	-4.13	25072.9
HLA A*2601	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.40	0.27	-4.13	25084.3

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*0203	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.45	0.33	-4.13	28474.2
HLA B*0801	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.34	0.21	-4.13	21770.1
HLA B*5701	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.40	0.27	-4.13	25126.5
HLA A*0219	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.34	0.21	-4.13	21829.1
HLA A*0301	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.32	0.19	-4.13	20703.1
HLA A*3001	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.31	0.18	-4.13	20441.0
HLA B*3901	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.46	0.33	-4.13	28990.6
HLA B*1502	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.58	0.45	-4.13	38385.5
HLA B*7301	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.62	0.49	-4.13	41265.9
HLA A*2403	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.34	0.21	-4.13	21925.4
HLA A*0219	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.46	0.33	-4.13	28701.6
HLA A*2603	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.62	0.49	-4.13	41401.2
HLA A*2402	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.59	0.45	-4.13	38535.9
HLA A*0206	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.32	0.19	-4.13	20982.6
HLA A*2902	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.34	0.21	-4.13	21998.8
HLA A*0219	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.47	0.33	-4.13	29262.1
HLA B*1517	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.07	-0.06	-4.13	11764.3
HLA A*3001	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.27	0.13	-4.13	18448.7
HLA B*4403	1:62-70	9	AVVTAEGVE	1.05	-0.53	-4.66	0.52	-4.14	45265.5
HLA B*1801	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.41	0.27	-4.14	25628.1
HLA A*3201	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.60	0.46	-4.14	39946.4
HLA A*8001	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.46	0.33	-4.14	29160.9
HLA A*8001	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.41	0.27	-4.14	25710.8
HLA B*4501	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.62	0.48	-4.14	41928.9
HLA B*1801	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.32	0.18	-4.14	20936.9
HLA A*6802	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.41	0.27	-4.14	25831.5
HLA A*2501	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.47	0.33	-4.14	29716.7
HLA A*2603	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.62	0.48	-4.14	42056.8
HLA B*5301	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.60	0.46	-4.14	40139.5
HLA B*0802	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.47	0.33	-4.14	29339.1
HLA A*8001	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.35	0.21	-4.14	22452.6
HLA B*4403	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.61	0.46	-4.14	40421.0
HLA B*2705	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.46	0.32	-4.14	29049.5
HLA B*0702	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.47	0.33	-4.14	29487.9
HLA B*1801	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.48	0.33	-4.14	29907.4
HLA B*1517	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.47	0.33	-4.14	29521.1
HLA A*2902	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.42	0.27	-4.14	26047.2
HLA B*3901	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.17	0.02	-4.14	14680.8
HLA A*0216	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.48	0.33	-4.14	30010.6
HLA A*2602	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.61	0.46	-4.14	40522.8
HLA B*5801	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.35	0.21	-4.15	22644.8
HLA B*2705	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.47	0.33	-4.15	29719.3
HLA A*3002	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.56	0.41	-4.15	36116.2
HLA A*6801	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.61	0.46	-4.15	40765.1
HLA A*0211	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.42	0.27	-4.15	26275.5
HLA A*3301	1:8-16	9	EGLAAASAA	0.96	-0.49	-4.61	0.46	-4.15	41058.4
HLA B*1801	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.47	0.32	-4.15	29558.0
HLA A*3201	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.56	0.41	-4.15	36415.8
HLA A*0202	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.47	0.32	-4.15	29654.3

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*4403	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.64	0.49	-4.15	43361.9
HLA B*3901	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.48	0.33	-4.15	30101.8
HLA B*2705	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.49	0.33	-4.15	30561.6
HLA A*0202	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.48	0.33	-4.15	30182.7
HLA A*2603	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.62	0.46	-4.15	41302.5
HLA B*4002	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.64	0.48	-4.15	43386.3
HLA B*1502	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.56	0.41	-4.15	36724.9
HLA B*4403	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.62	0.46	-4.15	41447.8
HLA B*1503	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.31	0.16	-4.16	20437.0
HLA A*0211	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.48	0.32	-4.16	29921.0
HLA A*1101	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.34	0.19	-4.16	22001.4
HLA A*0206	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.49	0.33	-4.16	30822.0
HLA B*7301	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.49	0.33	-4.16	30837.8
HLA A*0301	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.35	0.19	-4.16	22220.5
HLA B*7301	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.57	0.41	-4.16	36925.5
HLA A*3301	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.64	0.49	-4.16	43893.6
HLA A*0216	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.48	0.33	-4.16	30465.2
HLA A*3301	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.61	0.45	-4.16	40893.4
HLA A*2601	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.35	0.19	-4.16	22283.2
HLA A*0202	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.29	0.13	-4.16	19587.2
HLA A*2501	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.49	0.33	-4.16	30718.8
HLA B*0802	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.48	0.32	-4.16	30303.8
HLA B*0801	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.35	0.19	-4.16	22460.5
HLA A*2501	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.48	0.32	-4.16	30336.8
HLA B*1517	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.43	0.27	-4.16	27130.9
HLA B*2705	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.37	0.21	-4.16	23573.1
HLA B*5101	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.50	0.33	-4.16	31279.2
HLA A*6901	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.29	0.13	-4.16	19710.2
HLA B*5101	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.48	0.32	-4.16	30482.5
HLA B*3801	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.57	0.41	-4.16	37504.1
HLA A*0250	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.57	0.41	-4.16	37512.2
HLA B*3901	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.35	0.19	-4.16	22592.5
HLA B*3901	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.49	0.32	-4.16	30559.1
HLA A*6802	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.22	0.06	-4.17	16669.4
HLA B*5101	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.49	0.33	-4.17	31043.5
HLA B*4002	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.63	0.46	-4.17	42526.9
HLA B*1501	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.35	0.18	-4.17	22248.3
HLA A*2902	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.35	0.19	-4.17	22572.8
HLA B*4403	1:10-18	9	LAAASAAVE	1.14	-0.66	-4.65	0.48	-4.17	44808.2
HLA A*0250	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.49	0.32	-4.17	30896.3
HLA B*4601	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.36	0.19	-4.17	22707.6
HLA A*2601	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.36	0.19	-4.17	22793.1
HLA A*3301	1:73-81	9	GRAGVGVGE	1.10	-0.64	-4.63	0.46	-4.17	43118.4
HLA A*3001	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.11	-0.06	-4.17	12841.1
HLA B*4403	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.63	0.45	-4.17	42303.2
HLA B*0803	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.49	0.32	-4.17	31143.3
HLA B*4001	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.38	0.21	-4.17	24166.9
HLA B*4002	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.63	0.45	-4.17	42497.0
HLA B*5801	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.36	0.18	-4.17	22703.4

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*5301	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.59	0.41	-4.18	38516.5
HLA B*0702	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.39	0.21	-4.18	24278.1
HLA B*3501	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.11	-0.06	-4.18	12896.6
HLA A*3101	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.37	0.19	-4.18	23208.8
HLA B*3901	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.15	-0.03	-4.18	14100.9
HLA A*6901	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.36	0.18	-4.18	22803.3
HLA A*2402	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.59	0.41	-4.18	38677.1
HLA A*6801	1:88-96	9	AGDAAAAAT	0.90	-0.42	-4.66	0.49	-4.18	45981.3
HLA B*1517	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.22	0.04	-4.18	16511.8
HLA A*2902	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.37	0.19	-4.18	23394.8
HLA B*0803	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.51	0.33	-4.18	32470.8
HLA A*3001	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.24	0.06	-4.18	17233.3
HLA A*2602	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.50	0.32	-4.18	31660.0
HLA B*0802	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.45	0.27	-4.18	28319.7
HLA B*0803	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.51	0.33	-4.18	32173.0
HLA B*4002	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.45	0.27	-4.18	28356.8
HLA A*0101	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.37	0.19	-4.18	23547.9
HLA A*0201	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.37	0.19	-4.18	23565.5
HLA B*5401	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.37	0.19	-4.18	23570.2
HLA B*1509	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.45	0.27	-4.18	28489.2
HLA B*4601	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.38	0.19	-4.19	23729.4
HLA A*0101	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.37	0.19	-4.19	23558.4
HLA A*1101	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.46	0.27	-4.19	28668.7
HLA A*2602	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.37	0.19	-4.19	23575.9
HLA A*0211	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.51	0.33	-4.19	32566.0
HLA B*4601	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.40	0.21	-4.19	24940.3
HLA A*0301	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.37	0.18	-4.19	23365.6
HLA B*1517	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.25	0.06	-4.19	17615.1
HLA B*4801	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.38	0.19	-4.19	23954.3
HLA B*1502	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.52	0.33	-4.19	33268.5
HLA B*5301	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.52	0.33	-4.19	32921.1
HLA A*0219	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.38	0.19	-4.19	24063.5
HLA A*2603	1:94-102	9	AATYGVVGG	0.92	-0.47	-4.65	0.45	-4.19	44220.9
HLA B*5401	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.52	0.33	-4.19	33001.7
HLA B*4501	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.60	0.41	-4.19	40027.1
HLA A*0211	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.52	0.33	-4.19	33493.3
HLA B*4801	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.35	0.16	-4.19	22314.5
HLA A*2301	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.51	0.32	-4.19	32672.4
HLA B*1509	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.52	0.33	-4.19	33167.3
HLA A*2602	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.60	0.41	-4.19	40243.4
HLA A*2301	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.53	0.33	-4.19	33645.8
HLA A*2403	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.38	0.18	-4.20	23774.5
HLA B*1801	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.52	0.33	-4.20	33252.6
HLA A*0206	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.52	0.33	-4.20	33311.3
HLA A*2601	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.38	0.18	-4.20	24129.8
HLA A*2403	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.39	0.19	-4.20	24670.6
HLA A*0211	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.39	0.19	-4.20	24676.3
HLA A*3001	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.15	-0.05	-4.20	14184.1
HLA B*4601	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.36	0.16	-4.20	22859.8

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*0301	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.36	0.16	-4.20	22882.7
HLA B*4001	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.40	0.19	-4.20	24833.9
HLA B*0801	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.36	0.16	-4.21	22918.7
HLA A*2501	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.48	0.27	-4.21	30002.0
HLA B*5401	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.53	0.32	-4.21	33608.0
HLA A*6802	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.23	0.02	-4.21	16909.6
HLA A*3201	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.53	0.32	-4.21	33679.9
HLA B*5801	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.36	0.16	-4.21	23007.1
HLA A*3002	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.39	0.19	-4.21	24806.0
HLA A*0101	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.39	0.18	-4.21	24488.7
HLA B*4403	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.62	0.41	-4.21	41528.6
HLA A*6802	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.34	0.13	-4.21	21857.8
HLA B*3501	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.42	0.21	-4.21	26191.0
HLA A*2301	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.54	0.33	-4.21	34384.1
HLA B*5701	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.42	0.21	-4.21	26291.7
HLA B*5101	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.48	0.27	-4.21	30354.0
HLA B*0801	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.27	0.06	-4.21	18502.6
HLA A*0212	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.40	0.19	-4.21	25158.5
HLA B*4402	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.40	0.19	-4.21	24973.5
HLA B*0702	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.39	0.18	-4.21	24651.3
HLA B*5101	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.40	0.19	-4.21	24977.3
HLA B*7301	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.39	0.18	-4.21	24662.4
HLA B*1502	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.53	0.32	-4.21	34014.2
HLA B*4001	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.40	0.19	-4.21	24997.0
HLA B*1501	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.34	0.13	-4.21	22029.7
HLA A*1101	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.40	0.19	-4.21	25247.8
HLA A*0202	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.54	0.33	-4.21	35064.8
HLA B*1509	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.54	0.32	-4.21	34317.6
HLA A*0201	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.40	0.18	-4.22	24910.1
HLA B*1503	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.41	0.19	-4.22	25470.8
HLA A*3101	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.37	0.16	-4.22	23529.6
HLA B*5401	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.55	0.33	-4.22	35440.7
HLA A*2603	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.63	0.41	-4.22	42568.8
HLA B*4002	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.63	0.41	-4.22	42719.7
HLA B*3901	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.38	0.16	-4.22	23751.7
HLA B*4601	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.40	0.18	-4.22	25221.0
HLA A*3001	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.26	0.04	-4.22	18200.4
HLA B*5301	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.54	0.32	-4.22	34839.6
HLA B*3501	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.28	0.06	-4.22	18996.9
HLA B*3901	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.40	0.18	-4.22	25311.4
HLA B*1503	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.55	0.33	-4.22	35386.1
HLA B*0803	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.49	0.27	-4.22	31201.5
HLA A*0202	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.49	0.27	-4.22	31213.9
HLA A*0203	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.38	0.16	-4.22	23864.5
HLA B*0803	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.43	0.21	-4.22	27105.8
HLA B*4801	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.43	0.21	-4.22	27136.0
HLA A*3101	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.41	0.18	-4.22	25412.6
HLA A*8001	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.41	0.19	-4.22	25755.0
HLA B*5801	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.36	0.13	-4.22	22720.7

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*1517	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.30	0.08	-4.23	20068.4
HLA B*1503	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.44	0.21	-4.23	27307.6
HLA A*0101	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.38	0.16	-4.23	24073.8
HLA A*0203	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.36	0.13	-4.23	22844.2
HLA B*4402	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.44	0.21	-4.23	27391.8
HLA A*6901	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.27	0.04	-4.23	18480.3
HLA B*4801	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.41	0.19	-4.23	25982.9
HLA B*3801	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.55	0.32	-4.23	35363.6
HLA B*3801	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.56	0.33	-4.23	36384.5
HLA B*4801	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.41	0.18	-4.23	25690.2
HLA A*6901	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.38	0.16	-4.23	24202.8
HLA A*0301	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.36	0.13	-4.23	22933.5
HLA B*1801	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.42	0.19	-4.23	26072.6
HLA A*3301	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.64	0.41	-4.23	43707.1
HLA B*2705	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.42	0.19	-4.23	26167.9
HLA B*4403	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.50	0.27	-4.23	31930.3
HLA A*2601	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.39	0.16	-4.23	24420.0
HLA B*1517	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.44	0.21	-4.23	27825.2
HLA B*0801	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.37	0.13	-4.23	23239.0
HLA A*0101	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.37	0.13	-4.23	23245.4
HLA B*1502	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.51	0.27	-4.24	32130.6
HLA B*0702	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.43	0.19	-4.24	26644.9
HLA B*4402	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.43	0.19	-4.24	26710.0
HLA A*0216	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.43	0.19	-4.24	26736.2
HLA B*3901	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.45	0.21	-4.24	27994.5
HLA A*0201	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.39	0.16	-4.24	24700.6
HLA A*6801	1:75-83	9	AGVGVGESG	0.98	-0.57	-4.65	0.41	-4.24	44638.1
HLA A*0212	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.42	0.18	-4.24	26331.5
HLA A*2501	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.42	0.18	-4.24	26344.5
HLA B*5701	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.42	0.18	-4.24	26498.7
HLA A*0250	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.43	0.19	-4.24	26857.1
HLA B*0802	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.45	0.21	-4.24	28334.6
HLA A*6801	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.58	0.33	-4.24	37586.5
HLA A*2402	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.56	0.32	-4.24	36585.6
HLA A*0101	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.30	0.06	-4.24	19948.1
HLA A*3001	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.26	0.01	-4.24	18022.3
HLA A*0250	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.57	0.33	-4.24	37239.4
HLA B*4002	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.43	0.18	-4.24	26642.9
HLA A*0201	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.38	0.13	-4.24	23779.4
HLA A*6802	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.43	0.18	-4.24	26662.9
HLA B*0801	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.32	0.08	-4.24	21005.6
HLA A*0212	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.40	0.16	-4.25	25142.3
HLA B*3801	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.57	0.33	-4.25	37338.5
HLA B*2705	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.44	0.19	-4.25	27314.8
HLA A*2402	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.57	0.33	-4.25	37409.6
HLA A*2501	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.43	0.19	-4.25	27163.1
HLA A*3101	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.38	0.13	-4.25	23928.0
HLA A*2501	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.44	0.19	-4.25	27389.1
HLA A*6802	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.40	0.16	-4.25	25306.3

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*5401	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.52	0.27	-4.25	33110.8
HLA A*8001	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.40	0.16	-4.25	25391.6
HLA A*0203	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.43	0.18	-4.25	27117.5
HLA B*5701	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.41	0.16	-4.25	25539.7
HLA B*0802	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.44	0.19	-4.25	27516.1
HLA B*0702	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.41	0.16	-4.25	25587.1
HLA A*2601	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.38	0.13	-4.25	24257.9
HLA B*0702	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.44	0.19	-4.25	27619.5
HLA A*2402	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.59	0.33	-4.25	38654.5
HLA B*3501	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.41	0.16	-4.25	25699.1
HLA A*0250	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.59	0.33	-4.26	38697.2
HLA B*3801	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.53	0.27	-4.26	33750.1
HLA B*1509	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.45	0.19	-4.26	27981.0
HLA A*3301	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.58	0.32	-4.26	37806.6
HLA A*8001	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.45	0.19	-4.26	28014.0
HLA A*3201	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.53	0.27	-4.26	33810.2
HLA A*2501	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.47	0.21	-4.26	29374.5
HLA A*3201	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.59	0.33	-4.26	39001.1
HLA A*3002	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.39	0.13	-4.26	24573.7
HLA A*3002	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.59	0.33	-4.26	38533.6
HLA B*3501	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.44	0.18	-4.26	27581.4
HLA A*0219	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.44	0.18	-4.26	27622.3
HLA A*3301	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.59	0.33	-4.26	38742.2
HLA A*0206	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.39	0.13	-4.26	24739.1
HLA A*2602	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.60	0.33	-4.26	39398.9
HLA A*2403	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.42	0.16	-4.26	26208.7
HLA A*2301	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.54	0.27	-4.26	34316.1
HLA B*0802	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.46	0.19	-4.27	28548.1
HLA B*1801	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.48	0.21	-4.27	29941.7
HLA B*5401	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.31	0.04	-4.27	20247.9
HLA A*3201	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.60	0.33	-4.27	39441.4
HLA A*3001	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.28	0.01	-4.27	19015.7
HLA B*4601	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.40	0.13	-4.27	25197.3
HLA B*3901	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.46	0.19	-4.27	28614.1
HLA A*0101	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.35	0.08	-4.27	22245.9
HLA B*7301	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.59	0.32	-4.27	38957.5
HLA B*1501	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.28	0.01	-4.27	19222.5
HLA B*7301	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.60	0.33	-4.27	39676.1
HLA B*4601	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.35	0.08	-4.27	22358.3
HLA B*5301	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.61	0.33	-4.27	40273.2
HLA B*1517	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.41	0.13	-4.28	25524.4
HLA B*4501	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.33	0.06	-4.28	21484.7
HLA A*2603	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.60	0.32	-4.28	39575.2
HLA A*3001	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.30	0.02	-4.28	19915.7
HLA A*8001	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.46	0.18	-4.28	28730.0
HLA A*0250	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.55	0.27	-4.28	35402.6
HLA B*4501	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.61	0.33	-4.28	40854.8
HLA B*4002	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.61	0.33	-4.28	40882.4
HLA B*2705	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.46	0.18	-4.28	28882.7

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*6801	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.49	0.21	-4.28	30983.1
HLA A*0206	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.44	0.16	-4.28	27312.3
HLA A*2403	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.41	0.13	-4.28	25886.2
HLA B*5801	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.34	0.06	-4.28	21789.6
HLA B*3501	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.41	0.13	-4.28	25905.4
HLA A*0212	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.41	0.13	-4.28	25941.1
HLA A*0216	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.41	0.13	-4.28	25955.5
HLA B*5101	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.47	0.19	-4.28	29815.3
HLA A*2602	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.56	0.27	-4.29	36089.1
HLA A*3301	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.47	0.19	-4.29	29689.3
HLA A*2501	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.34	0.06	-4.29	22024.4
HLA B*1801	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.48	0.19	-4.29	29958.4
HLA A*0301	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.36	0.08	-4.29	23109.4
HLA B*1517	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.47	0.18	-4.29	29415.7
HLA A*0203	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.36	0.08	-4.29	23164.9
HLA B*1502	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.62	0.33	-4.29	41256.5
HLA B*5801	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.37	0.08	-4.29	23288.9
HLA A*2902	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.47	0.18	-4.29	29591.5
HLA B*5701	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.42	0.13	-4.29	26446.5
HLA A*0216	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.45	0.16	-4.29	27945.6
HLA B*4001	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.42	0.13	-4.29	26482.0
HLA A*2602	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.62	0.33	-4.29	41621.7
HLA A*0219	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.45	0.16	-4.29	28057.5
HLA A*2902	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.45	0.16	-4.29	28134.6
HLA B*4402	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.43	0.13	-4.29	26695.0
HLA A*6901	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.37	0.08	-4.29	23567.3
HLA A*3301	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.63	0.33	-4.30	42444.9
HLA A*8001	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.43	0.13	-4.30	26810.8
HLA B*5101	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.51	0.21	-4.30	32121.9
HLA A*0216	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.48	0.18	-4.30	30103.0
HLA B*4403	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.63	0.33	-4.30	42665.9
HLA B*1503	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.36	0.06	-4.30	22696.3
HLA A*1101	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.48	0.18	-4.30	30227.7
HLA B*4801	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.34	0.04	-4.30	21810.0
HLA A*1101	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.46	0.16	-4.30	28518.5
HLA B*0702	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.43	0.13	-4.30	27022.6
HLA A*6901	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.32	0.02	-4.30	21007.2
HLA A*3002	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.24	-0.06	-4.30	17258.3
HLA A*0301	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.36	0.06	-4.30	22779.1
HLA A*1101	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.43	0.13	-4.30	27073.7
HLA A*2402	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.49	0.19	-4.30	30752.8
HLA A*3101	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.38	0.08	-4.30	23904.9
HLA B*0802	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.48	0.18	-4.30	30369.6
HLA A*2301	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.49	0.19	-4.30	30813.6
HLA B*1517	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.46	0.16	-4.30	28700.5
HLA A*2601	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.31	0.01	-4.30	20525.5
HLA B*1509	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.46	0.16	-4.30	28750.5
HLA A*2403	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.38	0.08	-4.30	24051.8
HLA B*0803	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.46	0.16	-4.30	28771.5

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*0206	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.49	0.18	-4.30	30623.5
HLA A*2602	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.52	0.21	-4.31	32740.3
HLA B*4801	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.44	0.13	-4.31	27346.6
HLA B*4501	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.63	0.33	-4.31	42901.5
HLA B*0803	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.49	0.18	-4.31	30694.3
HLA A*3201	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.50	0.19	-4.31	31337.0
HLA A*2902	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.44	0.13	-4.31	27430.6
HLA A*2501	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.46	0.16	-4.31	28979.0
HLA B*0802	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.46	0.16	-4.31	28987.1
HLA A*2601	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.36	0.06	-4.31	23135.2
HLA B*5801	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.35	0.04	-4.31	22218.5
HLA A*0219	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.44	0.13	-4.31	27540.4
HLA A*2601	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.39	0.08	-4.31	24387.1
HLA A*2402	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.58	0.27	-4.31	38213.7
HLA B*5801	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.32	0.01	-4.31	20935.2
HLA A*0211	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.47	0.16	-4.31	29284.4
HLA B*5101	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.49	0.18	-4.31	31196.7
HLA A*3101	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.35	0.04	-4.31	22496.3
HLA A*2603	1:52-60	9	AGFSAQGVE	0.95	-0.62	-4.65	0.33	-4.31	44275.9
HLA B*7301	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.47	0.16	-4.31	29444.7
HLA A*3001	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.29	-0.03	-4.31	19396.5
HLA A*0301	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.35	0.04	-4.31	22588.5
HLA B*0803	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.50	0.19	-4.31	31748.9
HLA B*2705	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.47	0.16	-4.32	29596.7
HLA A*3101	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.37	0.06	-4.32	23623.7
HLA B*4601	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.36	0.04	-4.32	22685.8
HLA A*0201	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.39	0.08	-4.32	24806.5
HLA B*0803	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.51	0.19	-4.32	32334.2
HLA A*0250	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.51	0.19	-4.32	32359.8
HLA B*4002	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.64	0.32	-4.32	43710.5
HLA A*2603	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.59	0.27	-4.32	39182.3
HLA B*4002	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.65	0.33	-4.32	44548.4
HLA B*1502	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.51	0.19	-4.32	32547.5
HLA B*1509	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.50	0.18	-4.32	31885.4
HLA B*4001	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.38	0.06	-4.32	23991.4
HLA B*1501	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.26	-0.06	-4.33	18281.0
HLA B*4501	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.65	0.32	-4.33	44374.7
HLA B*1501	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.34	0.01	-4.33	21694.2
HLA B*5101	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.48	0.16	-4.33	30345.3
HLA B*1501	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.37	0.04	-4.33	23253.4
HLA B*3501	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.41	0.08	-4.33	25450.5
HLA B*5301	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.52	0.19	-4.33	33026.0
HLA B*5301	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.60	0.27	-4.33	39889.9
HLA A*6901	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.34	0.01	-4.33	21965.9
HLA B*0702	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.41	0.08	-4.33	25530.2
HLA B*5701	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.41	0.08	-4.33	25541.4
HLA A*2603	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.66	0.33	-4.33	45494.3
HLA A*2603	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.39	0.06	-4.33	24438.4
HLA A*0201	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.39	0.06	-4.33	24585.2

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*2301	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.54	0.21	-4.33	35002.3
HLA B*4403	1:65-73	9	TAEGVEELG	0.96	-0.63	-4.66	0.33	-4.34	45953.7
HLA B*3801	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.55	0.21	-4.34	35273.0
HLA B*5801	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.36	0.02	-4.34	22910.1
HLA B*3501	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.36	0.02	-4.34	22923.1
HLA A*2402	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.55	0.21	-4.34	35360.3
HLA B*5801	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.35	0.01	-4.34	22449.2
HLA A*2501	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.47	0.13	-4.34	29566.2
HLA B*4402	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.40	0.06	-4.34	24914.9
HLA B*3501	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.29	-0.05	-4.34	19507.4
HLA B*3901	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.38	0.04	-4.34	23997.9
HLA B*5301	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.32	-0.03	-4.34	20686.2
HLA B*1509	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.55	0.21	-4.34	35651.9
HLA B*2705	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.47	0.13	-4.34	29779.2
HLA A*0211	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.47	0.13	-4.34	29799.2
HLA B*1503	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.52	0.18	-4.34	33420.3
HLA B*4601	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.40	0.06	-4.34	25128.7
HLA A*3002	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.53	0.19	-4.34	34177.1
HLA B*4403	1:63-71	9	VVTAEGVEE	0.86	-0.54	-4.67	0.32	-4.34	46249.5
HLA B*3901	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.48	0.13	-4.34	29938.9
HLA A*3201	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.56	0.21	-4.35	35909.9
HLA A*3001	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.28	-0.06	-4.35	19073.3
HLA A*0301	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.37	0.02	-4.35	23314.5
HLA B*4001	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.42	0.08	-4.35	26540.9
HLA A*0101	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.39	0.04	-4.35	24320.1
HLA A*0212	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.42	0.08	-4.35	26575.5
HLA A*0212	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.36	0.01	-4.35	22867.8
HLA A*2402	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.54	0.19	-4.35	34500.7
HLA B*4001	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.36	0.01	-4.35	22909.8
HLA A*2301	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.54	0.19	-4.35	34521.8
HLA A*3301	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.54	0.19	-4.35	34560.3
HLA B*1801	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.32	-0.03	-4.35	21006.1
HLA A*2403	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.29	-0.06	-4.35	19314.4
HLA B*7301	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.37	0.02	-4.35	23542.0
HLA B*4402	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.39	0.04	-4.35	24483.9
HLA A*0211	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.53	0.18	-4.35	34025.3
HLA A*0202	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.51	0.16	-4.35	32049.7
HLA B*5401	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.56	0.21	-4.35	36410.7
HLA A*6802	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.43	0.08	-4.35	26832.8
HLA A*2601	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.39	0.04	-4.35	24577.2
HLA B*1501	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.30	-0.05	-4.35	20038.4
HLA B*4801	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.43	0.08	-4.35	26934.2
HLA A*0301	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.37	0.01	-4.35	23175.8
HLA A*0301	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.36	0.01	-4.35	23050.3
HLA B*1801	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.49	0.13	-4.35	30552.2
HLA A*6901	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.33	-0.03	-4.35	21246.6
HLA A*0212	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.41	0.06	-4.35	25762.3
HLA B*5401	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.43	0.08	-4.35	27020.2
HLA B*5701	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.39	0.04	-4.35	24767.1

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*0802	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.49	0.13	-4.36	30665.3
HLA A*3201	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.51	0.16	-4.36	32376.9
HLA B*0801	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.37	0.01	-4.36	23190.4
HLA B*1501	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.38	0.02	-4.36	23890.8
HLA A*2601	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.37	0.01	-4.36	23348.4
HLA A*2403	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.38	0.02	-4.36	23930.6
HLA A*0101	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.38	0.02	-4.36	23943.0
HLA A*2601	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.38	0.02	-4.36	23943.8
HLA B*4402	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.38	0.02	-4.36	23973.4
HLA A*2403	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.41	0.06	-4.36	25972.5
HLA A*3101	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.29	-0.06	-4.36	19722.2
HLA A*0201	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.40	0.04	-4.36	24990.4
HLA B*4801	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.42	0.06	-4.36	26082.9
HLA A*0101	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.37	0.01	-4.36	23573.8
HLA A*3301	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.63	0.27	-4.36	42929.4
HLA B*5701	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.42	0.06	-4.36	26191.2
HLA A*0203	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.42	0.06	-4.36	26201.2
HLA B*5401	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.54	0.18	-4.36	35046.5
HLA A*0219	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.42	0.06	-4.36	26366.9
HLA B*7301	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.55	0.19	-4.36	35862.2
HLA B*5301	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.55	0.19	-4.37	35650.7
HLA A*0101	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.38	0.01	-4.37	23721.3
HLA B*5101	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.25	-0.11	-4.37	17940.1
HLA A*2301	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.55	0.18	-4.37	35328.8
HLA B*3801	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.55	0.19	-4.37	35793.0
HLA B*1502	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.52	0.16	-4.37	33296.7
HLA B*1509	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.55	0.19	-4.37	35822.6
HLA B*5701	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.38	0.01	-4.37	23821.6
HLA A*1101	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.42	0.06	-4.37	26604.7
HLA A*2902	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.43	0.06	-4.37	26686.5
HLA A*0201	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.39	0.02	-4.37	24663.9
HLA B*0801	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.35	-0.03	-4.37	22152.7
HLA B*1503	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.50	0.13	-4.37	31876.1
HLA B*4601	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.38	0.01	-4.37	24220.5
HLA B*1501	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.31	-0.06	-4.37	20306.4
HLA A*0203	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.31	-0.06	-4.37	20376.5
HLA B*4601	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.39	0.02	-4.37	24824.7
HLA B*1503	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.45	0.08	-4.37	28226.8
HLA A*6801	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.40	0.02	-4.37	24871.6
HLA A*2603	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.56	0.18	-4.37	35892.6
HLA B*4402	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.45	0.08	-4.37	28269.8
HLA A*8001	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.43	0.06	-4.37	26985.4
HLA A*8001	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.45	0.08	-4.37	28311.4
HLA B*0702	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.43	0.06	-4.37	27020.6
HLA B*4501	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.56	0.19	-4.38	36487.0
HLA A*2602	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.57	0.19	-4.38	36797.6
HLA B*5801	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.31	-0.06	-4.38	20581.3
HLA B*5101	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.51	0.13	-4.38	32324.4
HLA A*0201	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.39	0.01	-4.38	24554.7

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*1517	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.39	0.01	-4.38	24428.0
HLA B*3501	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.39	0.01	-4.38	24589.4
HLA B*5401	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.53	0.16	-4.38	34222.8
HLA B*0801	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.39	0.01	-4.38	24633.9
HLA A*0219	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.46	0.08	-4.38	28640.3
HLA B*5101	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.46	0.08	-4.38	28643.6
HLA A*6801	1:22-30	9	ARLAAAHAS	1.08	-0.81	-4.65	0.27	-4.38	44849.0
HLA A*0219	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.40	0.02	-4.38	25247.9
HLA B*4001	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.42	0.04	-4.38	26301.1
HLA B*1502	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.46	0.08	-4.38	28733.9
HLA B*0702	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.42	0.04	-4.38	26322.6
HLA B*4001	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.40	0.02	-4.38	25326.0
HLA A*3002	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.54	0.16	-4.38	34396.7
HLA B*0801	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.42	0.04	-4.38	26352.2
HLA B*0801	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.40	0.02	-4.38	25353.8
HLA A*3101	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.40	0.02	-4.38	25354.9
HLA B*0801	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.33	-0.05	-4.38	21480.4
HLA A*0201	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.39	0.01	-4.38	24667.0
HLA A*1101	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.46	0.08	-4.38	28851.2
HLA A*2902	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.46	0.08	-4.38	28861.2
HLA B*3801	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.57	0.19	-4.38	37468.6
HLA B*1502	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.56	0.18	-4.38	36720.1
HLA B*1801	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.46	0.08	-4.39	28997.5
HLA B*5701	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.41	0.02	-4.39	25546.7
HLA A*2301	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.54	0.16	-4.39	34727.9
HLA B*4403	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.57	0.19	-4.39	37363.9
HLA A*3301	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.60	0.21	-4.39	39439.0
HLA A*0212	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.41	0.02	-4.39	25645.9
HLA A*0203	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.41	0.02	-4.39	25765.6
HLA B*4601	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.40	0.01	-4.39	25052.7
HLA A*2602	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.57	0.18	-4.39	37251.1
HLA B*4501	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.60	0.21	-4.39	39812.9
HLA A*0216	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.47	0.08	-4.39	29344.8
HLA B*2705	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.47	0.08	-4.39	29370.1
HLA A*3101	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.40	0.01	-4.39	25162.5
HLA A*0301	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.37	-0.03	-4.39	23175.2
HLA A*2902	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.43	0.04	-4.39	27013.7
HLA B*0803	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.53	0.13	-4.39	33531.2
HLA A*0203	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.40	0.01	-4.39	25351.2
HLA A*0203	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.41	0.01	-4.39	25509.0
HLA B*4001	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.40	0.01	-4.39	25371.4
HLA B*5801	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.37	-0.03	-4.40	23391.1
HLA B*4501	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.59	0.19	-4.40	38534.9
HLA B*7301	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.61	0.21	-4.40	40356.8
HLA B*3801	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.58	0.18	-4.40	37826.4
HLA A*6901	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.35	-0.05	-4.40	22307.1
HLA A*0203	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.44	0.04	-4.40	27431.2
HLA B*5301	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.61	0.21	-4.40	40682.7
HLA A*8001	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.44	0.04	-4.40	27466.3

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*0212	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.44	0.04	-4.40	27472.2
HLA B*0702	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.41	0.01	-4.40	25865.2
HLA B*1509	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.53	0.13	-4.40	34084.1
HLA B*3901	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.46	0.06	-4.40	28688.2
HLA A*2603	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.56	0.16	-4.40	36000.6
HLA B*3801	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.56	0.16	-4.40	36011.9
HLA A*0301	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.35	-0.05	-4.40	22444.4
HLA A*3101	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.41	0.01	-4.40	25962.9
HLA B*4001	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.38	-0.03	-4.40	23783.6
HLA A*2403	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.44	0.04	-4.40	27656.1
HLA A*2402	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.59	0.18	-4.40	38465.9
HLA B*4601	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.34	-0.06	-4.40	21923.0
HLA B*5401	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.54	0.13	-4.41	34412.4
HLA A*0101	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.35	-0.05	-4.41	22625.4
HLA A*2301	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.54	0.13	-4.41	34431.4
HLA B*3901	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.48	0.08	-4.41	30405.4
HLA B*0802	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.48	0.08	-4.41	30433.3
HLA A*3001	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.29	-0.11	-4.41	19665.8
HLA B*4801	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.42	0.01	-4.41	26189.2
HLA B*1503	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.45	0.04	-4.41	27865.6
HLA A*2403	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.42	0.01	-4.41	26037.0
HLA B*1801	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.42	0.01	-4.41	26053.2
HLA A*0101	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.38	-0.03	-4.41	24000.9
HLA B*4402	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.42	0.01	-4.41	26083.1
HLA B*5701	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.42	0.01	-4.41	26252.2
HLA A*0219	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.42	0.01	-4.41	26093.0
HLA B*2705	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.46	0.06	-4.41	29163.5
HLA B*5801	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.36	-0.05	-4.41	22827.4
HLA A*3002	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.34	-0.06	-4.41	22101.2
HLA B*0803	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.49	0.08	-4.41	30688.4
HLA A*2403	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.42	0.01	-4.41	26424.3
HLA B*2705	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.42	0.01	-4.41	26441.4
HLA B*1502	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.60	0.19	-4.41	39585.2
HLA B*0802	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.47	0.06	-4.41	29351.8
HLA B*4002	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.60	0.19	-4.41	39603.5
HLA A*0219	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.45	0.04	-4.41	28199.5
HLA B*5101	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.45	0.04	-4.41	28245.0
HLA B*1503	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.43	0.02	-4.41	27181.9
HLA B*4601	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.35	-0.06	-4.41	22280.9
HLA A*0202	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.59	0.18	-4.41	39295.9
HLA B*0702	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.44	0.02	-4.41	27290.5
HLA B*4801	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.44	0.02	-4.41	27290.9
HLA A*6802	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.36	-0.05	-4.41	23082.9
HLA A*0216	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.47	0.06	-4.41	29572.4
HLA B*5301	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.60	0.18	-4.41	39404.9
HLA A*6802	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.39	-0.03	-4.41	24452.9
HLA A*0250	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.60	0.18	-4.42	39458.5
HLA A*0301	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.35	-0.06	-4.42	22468.8
HLA B*4402	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.43	0.01	-4.42	26753.3

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*4601	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.39	-0.03	-4.42	24501.9
HLA A*0216	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.43	0.01	-4.42	26634.7
HLA A*2602	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.57	0.16	-4.42	37312.4
HLA B*5801	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.35	-0.06	-4.42	22483.5
HLA A*3201	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.60	0.18	-4.42	39646.5
HLA A*2501	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.50	0.08	-4.42	31262.6
HLA A*2501	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.44	0.02	-4.42	27564.7
HLA A*2902	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.43	0.01	-4.42	26949.5
HLA A*2603	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.63	0.21	-4.42	42502.5
HLA A*2902	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.43	0.01	-4.42	26823.2
HLA A*3101	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.39	-0.03	-4.42	24720.9
HLA A*2601	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.39	-0.03	-4.42	24743.9
HLA A*6901	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.36	-0.06	-4.42	22734.5
HLA A*0201	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.39	-0.03	-4.42	24828.1
HLA A*0250	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.58	0.16	-4.42	37759.4
HLA B*5101	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.40	-0.03	-4.42	24878.6
HLA B*4801	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.43	0.01	-4.42	27030.8
HLA A*2501	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.46	0.04	-4.42	28958.8
HLA A*1101	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.46	0.04	-4.42	28976.0
HLA A*3002	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.60	0.18	-4.42	40239.5
HLA A*2602	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.56	0.13	-4.42	35925.7
HLA A*2902	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.45	0.02	-4.42	27952.7
HLA B*1509	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.46	0.04	-4.42	29097.7
HLA A*0212	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.43	0.01	-4.43	27199.2
HLA A*0212	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.40	-0.03	-4.43	25053.3
HLA A*0203	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.40	-0.03	-4.43	25079.1
HLA A*2402	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.58	0.16	-4.43	38133.0
HLA A*0211	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.44	0.01	-4.43	27498.5
HLA A*3002	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.50	0.08	-4.43	31964.1
HLA A*0301	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.36	-0.06	-4.43	23041.2
HLA A*6802	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.44	0.01	-4.43	27531.0
HLA A*8001	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.45	0.02	-4.43	28179.2
HLA B*4002	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.64	0.21	-4.43	43490.1
HLA A*6802	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.36	-0.06	-4.43	23130.4
HLA A*0216	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.47	0.04	-4.43	29400.9
HLA A*2603	1:1-9	9	MTLRVVPEG	0.78	-0.59	-4.62	0.19	-4.43	41340.3
HLA A*6801	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.47	0.04	-4.43	29420.0
HLA A*2902	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.40	-0.03	-4.43	25317.5
HLA B*0801	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.37	-0.06	-4.43	23247.3
HLA B*1801	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.49	0.06	-4.43	30676.9
HLA B*4001	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.37	-0.06	-4.43	23348.7
HLA A*0219	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.41	-0.03	-4.43	25486.0
HLA B*0802	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.47	0.04	-4.43	29647.2
HLA A*0101	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.37	-0.06	-4.43	23464.5
HLA A*6901	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.37	-0.06	-4.43	23397.2
HLA A*0211	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.51	0.08	-4.43	32533.0
HLA A*0203	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.37	-0.06	-4.44	23446.3
HLA A*2601	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.38	-0.05	-4.44	24243.3
HLA A*0203	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.38	-0.05	-4.44	24255.5

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*4403	1:47-55	9	SLQTAAGFS	1.15	-0.94	-4.65	0.21	-4.44	44235.0
HLA A*0250	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.57	0.13	-4.44	37037.9
HLA A*3301	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.62	0.18	-4.44	41526.4
HLA A*0201	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.37	-0.06	-4.44	23648.1
HLA B*1501	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.41	-0.03	-4.44	25770.9
HLA A*2602	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.49	0.06	-4.44	31215.5
HLA A*0212	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.39	-0.05	-4.44	24383.3
HLA B*5701	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.41	-0.03	-4.44	25782.5
HLA B*5101	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.49	0.06	-4.44	31235.2
HLA B*0802	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.46	0.02	-4.44	28849.2
HLA B*5301	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.59	0.16	-4.44	39201.9
HLA A*0101	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.37	-0.06	-4.44	23681.0
HLA B*3801	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.57	0.13	-4.44	37237.4
HLA B*4801	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.41	-0.03	-4.44	25913.7
HLA B*1801	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.48	0.04	-4.44	30187.6
HLA A*0216	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.45	0.01	-4.44	28412.1
HLA A*2602	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.48	0.04	-4.44	30225.5
HLA B*5101	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.45	0.01	-4.44	28319.2
HLA A*0219	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.46	0.01	-4.44	28518.2
HLA A*0202	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.45	0.01	-4.45	28479.0
HLA B*1517	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.47	0.02	-4.45	29331.3
HLA A*0206	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.52	0.08	-4.45	33306.5
HLA B*4001	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.40	-0.05	-4.45	24855.4
HLA B*1517	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.42	-0.03	-4.45	26302.8
HLA A*0202	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.52	0.08	-4.45	33415.6
HLA A*2603	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.64	0.19	-4.45	43334.0
HLA A*0202	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.47	0.02	-4.45	29439.8
HLA A*3301	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.60	0.16	-4.45	39980.0
HLA B*3501	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.38	-0.06	-4.45	24195.0
HLA A*3101	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.40	-0.05	-4.45	24935.2
HLA A*8001	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.46	0.01	-4.45	28812.0
HLA A*2902	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.40	-0.05	-4.45	24944.5
HLA B*0803	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.50	0.06	-4.45	31968.1
HLA A*2402	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.58	0.13	-4.45	38008.8
HLA A*6801	1:59-67	9	VEHAVVTAE	0.87	-0.71	-4.60	0.16	-4.45	40201.8
HLA B*4001	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.38	-0.06	-4.45	24229.3
HLA A*0201	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.40	-0.05	-4.45	25099.3
HLA B*1801	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.46	0.01	-4.45	29007.5
HLA A*0201	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.39	-0.06	-4.45	24356.9
HLA B*0702	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.40	-0.05	-4.45	25176.6
HLA B*0702	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.34	-0.11	-4.45	21844.8
HLA A*6801	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.58	0.13	-4.45	38380.5
HLA B*1509	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.51	0.06	-4.45	32337.6
HLA B*4002	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.64	0.19	-4.45	43983.0
HLA A*0212	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.39	-0.06	-4.45	24550.6
HLA B*5101	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.48	0.02	-4.45	29906.4
HLA A*2403	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.43	-0.03	-4.45	26817.9
HLA A*0211	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.51	0.06	-4.46	32496.1
HLA A*0216	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.48	0.02	-4.46	30050.3

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*8001	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.47	0.01	-4.46	29199.3
HLA A*6802	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.39	-0.06	-4.46	24687.4
HLA A*2501	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.47	0.01	-4.46	29202.6
HLA B*1502	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.59	0.13	-4.46	38692.6
HLA B*4403	1:50-58	9	TAAGFSAQG	0.80	-0.61	-4.65	0.19	-4.46	44279.8
HLA A*1101	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.48	0.02	-4.46	30186.3
HLA B*0702	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.47	0.01	-4.46	29341.0
HLA B*5701	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.39	-0.06	-4.46	24824.5
HLA A*2601	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.39	-0.06	-4.46	24751.0
HLA A*2601	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.40	-0.06	-4.46	24957.6
HLA B*3901	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.47	0.01	-4.46	29704.7
HLA A*0206	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.40	-0.06	-4.46	24885.4
HLA B*5401	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.48	0.02	-4.46	30443.5
HLA B*4601	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.41	-0.05	-4.46	25774.4
HLA A*8001	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.44	-0.03	-4.46	27255.5
HLA B*2705	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.50	0.04	-4.46	31692.8
HLA A*2301	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.54	0.08	-4.46	34654.5
HLA B*0802	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.47	0.01	-4.46	29687.7
HLA B*1801	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.49	0.02	-4.46	30577.2
HLA B*7301	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.54	0.08	-4.46	34760.8
HLA B*1509	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.54	0.08	-4.46	34789.2
HLA B*4402	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.44	-0.03	-4.46	27422.5
HLA B*4801	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.40	-0.06	-4.46	25104.4
HLA B*2705	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.47	0.01	-4.47	29843.5
HLA A*6801	1:70-78	9	EELGRAGVG	0.91	-0.72	-4.65	0.18	-4.47	44401.6
HLA B*5701	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.42	-0.05	-4.47	26073.0
HLA B*3901	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.48	0.01	-4.47	30001.5
HLA A*0206	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.52	0.06	-4.47	33463.9
HLA B*2705	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.49	0.02	-4.47	30942.8
HLA A*1101	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.48	0.01	-4.47	30060.0
HLA B*0803	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.49	0.02	-4.47	31002.1
HLA A*1101	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.48	0.01	-4.47	30387.0
HLA B*0802	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.48	0.01	-4.47	30460.1
HLA A*2501	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.48	0.01	-4.47	30471.8
HLA B*5401	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.53	0.06	-4.47	33784.6
HLA A*8001	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.41	-0.06	-4.47	25571.4
HLA A*0206	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.51	0.04	-4.47	32545.4
HLA B*5801	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.36	-0.11	-4.47	22977.5
HLA A*2403	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.42	-0.05	-4.47	26486.0
HLA B*1517	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.49	0.01	-4.47	30657.2
HLA B*5301	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.61	0.13	-4.48	40440.5
HLA B*7301	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.53	0.06	-4.48	34065.8
HLA A*0211	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.51	0.04	-4.48	32721.9
HLA B*0803	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.49	0.01	-4.48	30780.5
HLA A*8001	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.41	-0.06	-4.48	25900.2
HLA B*0702	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.41	-0.06	-4.48	25909.3
HLA B*7301	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.61	0.13	-4.48	40652.1
HLA B*0702	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.41	-0.06	-4.48	25867.9
HLA A*2301	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.53	0.06	-4.48	34234.1

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*1517	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.41	-0.06	-4.48	25905.9
HLA B*5401	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.49	0.01	-4.48	30795.3
HLA A*0202	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.43	-0.05	-4.48	26834.1
HLA B*2705	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.45	-0.03	-4.48	28383.8
HLA B*4801	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.43	-0.05	-4.48	26873.8
HLA A*0301	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.37	-0.11	-4.48	23334.6
HLA B*5701	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.42	-0.06	-4.48	26073.8
HLA A*3201	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.61	0.13	-4.48	41099.0
HLA B*2705	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.42	-0.06	-4.48	26244.6
HLA A*2403	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.42	-0.06	-4.48	26156.8
HLA A*2501	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.43	-0.05	-4.48	27048.1
HLA B*0801	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.42	-0.06	-4.48	26179.6
HLA A*6801	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.54	0.06	-4.48	34708.9
HLA A*2902	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.42	-0.06	-4.48	26250.6
HLA B*0802	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.46	-0.03	-4.48	28734.0
HLA A*0206	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.50	0.01	-4.49	31451.4
HLA B*1503	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.50	0.01	-4.49	31265.2
HLA A*0219	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.42	-0.06	-4.49	26436.0
HLA A*0219	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.44	-0.05	-4.49	27249.0
HLA A*3301	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.50	0.01	-4.49	31298.2
HLA A*0216	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.46	-0.03	-4.49	28822.8
HLA A*0101	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.37	-0.11	-4.49	23685.1
HLA B*4402	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.44	-0.05	-4.49	27354.6
HLA A*0212	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.42	-0.06	-4.49	26468.4
HLA B*4801	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.42	-0.06	-4.49	26596.0
HLA A*3301	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.53	0.04	-4.49	33766.2
HLA A*2403	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.38	-0.11	-4.49	23875.4
HLA A*6901	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.38	-0.11	-4.49	23895.9
HLA A*0206	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.50	0.01	-4.49	31643.8
HLA A*0216	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.43	-0.06	-4.49	26765.3
HLA B*5101	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.50	0.01	-4.49	31897.5
HLA B*4402	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.43	-0.06	-4.49	26864.8
HLA B*0803	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.53	0.04	-4.49	34016.1
HLA A*0202	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.55	0.06	-4.49	35441.7
HLA B*4501	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.62	0.13	-4.49	42145.6
HLA A*1101	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.47	-0.03	-4.49	29295.5
HLA A*0206	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.47	-0.03	-4.49	29316.9
HLA B*1502	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.53	0.04	-4.49	34121.5
HLA A*2301	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.53	0.04	-4.49	34191.4
HLA A*3201	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.55	0.06	-4.50	35705.0
HLA A*8001	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.45	-0.05	-4.50	27930.2
HLA A*2902	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.43	-0.06	-4.50	27156.9
HLA A*0206	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.43	-0.06	-4.50	27196.4
HLA B*5401	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.51	0.01	-4.50	32397.1
HLA B*0801	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.39	-0.11	-4.50	24336.6
HLA B*3801	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.52	0.02	-4.50	33207.7
HLA B*0803	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.51	0.01	-4.50	32298.0
HLA A*2402	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.56	0.06	-4.50	36156.3
HLA A*2602	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.52	0.02	-4.50	33435.7

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*3101	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.44	-0.06	-4.50	27379.0
HLA A*3301	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.63	0.13	-4.50	43099.9
HLA A*0219	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.44	-0.06	-4.50	27429.2
HLA A*0250	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.58	0.08	-4.50	38105.1
HLA A*2603	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.64	0.13	-4.50	43233.0
HLA B*3801	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.58	0.08	-4.50	38161.3
HLA A*2301	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.53	0.02	-4.50	33614.5
HLA A*0211	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.53	0.02	-4.50	33658.0
HLA B*1503	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.44	-0.06	-4.51	27680.6
HLA A*0216	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.46	-0.05	-4.51	28535.9
HLA A*0211	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.44	-0.06	-4.51	27701.5
HLA B*0802	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.44	-0.06	-4.51	27781.7
HLA A*0202	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.52	0.01	-4.51	33075.4
HLA A*3101	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.40	-0.11	-4.51	24869.6
HLA A*2601	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.40	-0.11	-4.51	24891.4
HLA A*2501	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.48	-0.03	-4.51	30334.1
HLA A*0211	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.52	0.01	-4.51	32991.7
HLA A*0201	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.40	-0.11	-4.51	24945.7
HLA B*1501	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.40	-0.11	-4.51	24972.0
HLA A*2402	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.59	0.08	-4.51	38729.2
HLA B*4403	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.64	0.13	-4.51	43931.6
HLA A*3002	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.57	0.06	-4.51	36981.2
HLA B*4402	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.45	-0.06	-4.51	27996.6
HLA A*0206	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.53	0.02	-4.51	34223.2
HLA A*2402	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.53	0.02	-4.51	34223.7
HLA B*1509	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.52	0.01	-4.51	33251.2
HLA A*3201	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.53	0.01	-4.51	33501.8
HLA A*3002	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.55	0.04	-4.51	35655.2
HLA B*4002	1:82-90	9	SGASYLAGD	1.08	-0.95	-4.65	0.13	-4.51	44258.4
HLA B*1503	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.53	0.01	-4.51	33655.7
HLA B*4601	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.40	-0.11	-4.52	25327.9
HLA B*0803	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.49	-0.03	-4.52	30899.9
HLA A*1101	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.45	-0.06	-4.52	28327.7
HLA A*0216	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.45	-0.06	-4.52	28343.3
HLA A*1101	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.46	-0.06	-4.52	28541.2
HLA B*5301	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.60	0.08	-4.52	39512.1
HLA B*4501	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.54	0.02	-4.52	34826.3
HLA B*1502	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.53	0.01	-4.52	34031.7
HLA A*3301	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.58	0.06	-4.52	37836.0
HLA A*3002	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.54	0.02	-4.52	35018.6
HLA B*5301	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.56	0.04	-4.52	36426.7
HLA B*3801	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.58	0.06	-4.52	37964.2
HLA B*0802	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.47	-0.05	-4.52	29789.8
HLA B*1502	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.58	0.06	-4.53	38170.1
HLA B*3901	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.46	-0.06	-4.53	28982.7
HLA A*0212	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.41	-0.11	-4.53	25905.2
HLA B*3801	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.54	0.01	-4.53	34530.6
HLA B*5701	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.41	-0.11	-4.53	25990.9
HLA B*1517	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.48	-0.05	-4.53	29969.4

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*2602	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.60	0.08	-4.53	40241.2
HLA A*0202	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.57	0.04	-4.53	36892.5
HLA B*5301	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.59	0.06	-4.53	38461.6
HLA B*7301	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.57	0.04	-4.53	37071.4
HLA A*0211	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.50	-0.03	-4.53	31898.1
HLA B*3801	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.57	0.04	-4.53	37109.1
HLA B*3801	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.50	-0.03	-4.53	31967.4
HLA B*1801	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.48	-0.05	-4.53	30261.2
HLA A*3201	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.48	-0.05	-4.53	30266.6
HLA A*2501	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.47	-0.06	-4.53	29423.4
HLA A*0250	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.59	0.06	-4.53	38962.9
HLA A*6802	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.42	-0.11	-4.53	26417.4
HLA B*2705	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.47	-0.06	-4.54	29532.6
HLA A*2301	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.55	0.01	-4.54	35280.6
HLA B*2705	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.49	-0.05	-4.54	30585.3
HLA A*2501	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.42	-0.11	-4.54	26568.2
HLA A*1101	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.49	-0.05	-4.54	30670.8
HLA A*2301	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.55	0.01	-4.54	35296.5
HLA A*8001	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.43	-0.11	-4.54	26703.9
HLA A*0203	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.43	-0.11	-4.54	26720.0
HLA A*2402	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.58	0.04	-4.54	37959.3
HLA B*3901	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.49	-0.05	-4.54	30926.0
HLA B*1509	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.55	0.01	-4.54	35728.9
HLA B*0803	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.49	-0.05	-4.54	30977.8
HLA B*4801	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.43	-0.11	-4.54	26918.9
HLA A*2603	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.58	0.04	-4.54	38157.3
HLA A*0219	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.43	-0.11	-4.54	27040.5
HLA B*3901	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.48	-0.06	-4.54	30174.4
HLA B*4001	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.43	-0.11	-4.54	27063.0
HLA A*0211	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.48	-0.06	-4.54	30191.5
HLA B*1509	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.49	-0.05	-4.55	31228.0
HLA A*3201	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.62	0.08	-4.55	42052.0
HLA A*0250	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.59	0.04	-4.55	38553.0
HLA A*2603	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.62	0.08	-4.55	42137.8
HLA B*4403	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.60	0.06	-4.55	40258.4
HLA B*1509	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.52	-0.03	-4.55	33246.1
HLA B*5401	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.50	-0.05	-4.55	31456.4
HLA A*2501	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.48	-0.06	-4.55	30546.2
HLA B*1801	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.44	-0.11	-4.55	27316.5
HLA A*3002	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.52	-0.03	-4.55	33417.1
HLA A*0250	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.56	0.01	-4.55	36533.4
HLA A*3201	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.59	0.04	-4.55	38879.3
HLA B*7301	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.56	0.01	-4.55	36351.1
HLA B*5101	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.50	-0.05	-4.55	31673.4
HLA B*1801	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.49	-0.06	-4.55	30644.1
HLA B*1503	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.52	-0.03	-4.55	33489.3
HLA B*1503	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.49	-0.06	-4.55	30662.1
HLA B*3901	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.44	-0.11	-4.55	27533.8
HLA B*5301	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.58	0.02	-4.55	37596.1

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*0216	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.44	-0.11	-4.55	27620.2
HLA B*5101	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.49	-0.06	-4.55	30895.1
HLA B*5301	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.44	-0.11	-4.56	27759.5
HLA B*0802	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.49	-0.06	-4.56	31013.0
HLA A*3301	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.58	0.02	-4.56	37909.0
HLA A*3301	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.63	0.08	-4.56	43109.3
HLA A*3002	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.57	0.01	-4.56	36973.8
HLA B*4402	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.45	-0.11	-4.56	27953.9
HLA B*4002	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.64	0.08	-4.56	43330.7
HLA B*4002	1:81-89	9	ESGASYLAG	0.82	-0.76	-4.62	0.06	-4.56	41354.0
HLA A*0206	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.51	-0.05	-4.56	32433.9
HLA B*5301	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.57	0.01	-4.56	37326.4
HLA B*5101	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.50	-0.06	-4.56	31564.9
HLA B*5401	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.50	-0.06	-4.56	31569.6
HLA B*1502	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.50	-0.06	-4.56	31609.7
HLA A*3002	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.58	0.01	-4.57	37891.4
HLA B*1502	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.58	0.01	-4.57	37864.5
HLA A*2602	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.58	0.01	-4.57	37870.4
HLA B*1801	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.51	-0.06	-4.57	32075.0
HLA B*1503	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.52	-0.05	-4.57	33044.2
HLA B*1517	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.46	-0.11	-4.57	28682.8
HLA B*4501	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.65	0.08	-4.57	44405.7
HLA A*2301	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.54	-0.03	-4.57	34999.5
HLA A*2902	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.46	-0.11	-4.57	28729.1
HLA A*0250	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.59	0.02	-4.57	39202.9
HLA A*0250	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.58	0.01	-4.57	38109.1
HLA A*0211	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.52	-0.05	-4.57	33450.4
HLA A*2603	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.60	0.02	-4.58	39568.3
HLA A*2602	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.52	-0.05	-4.58	33478.8
HLA B*1502	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.60	0.02	-4.58	39594.5
HLA B*3801	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.58	0.01	-4.58	38449.5
HLA A*2402	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.59	0.01	-4.58	38505.5
HLA A*0206	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.47	-0.11	-4.58	29337.2
HLA B*1502	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.55	-0.03	-4.58	35786.6
HLA A*0202	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.52	-0.06	-4.58	32923.6
HLA A*3201	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.60	0.02	-4.58	40212.3
HLA A*0202	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.52	-0.06	-4.58	32906.7
HLA A*2402	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.60	0.01	-4.59	39647.6
HLA B*5301	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.60	0.01	-4.59	39962.0
HLA A*2603	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.60	0.01	-4.59	40010.7
HLA A*2602	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.60	0.01	-4.59	40042.5
HLA B*2705	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.48	-0.11	-4.59	30112.3
HLA A*1101	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.48	-0.11	-4.59	30114.1
HLA B*0802	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.48	-0.11	-4.59	30168.5
HLA A*0202	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.57	-0.03	-4.59	36869.8
HLA B*4403	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.62	0.02	-4.59	41259.9
HLA A*6801	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.67	0.08	-4.59	46885.1
HLA A*3002	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.54	-0.05	-4.60	35036.0
HLA B*0803	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.53	-0.06	-4.60	34009.8

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA B*7301	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.61	0.01	-4.60	40588.4
HLA A*2301	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.55	-0.05	-4.60	35135.7
HLA B*4501	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.64	0.04	-4.60	43270.7
HLA B*4403	1:72-80	9	LGRAGVGVG	0.85	-0.77	-4.67	0.08	-4.60	47287.6
HLA B*5401	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.54	-0.06	-4.60	34278.4
HLA B*1503	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.49	-0.11	-4.60	30738.5
HLA B*0803	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.54	-0.06	-4.60	34287.5
HLA A*2301	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.54	-0.06	-4.60	34300.5
HLA A*0250	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.57	-0.03	-4.60	37508.5
HLA A*3201	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.61	0.01	-4.60	40882.8
HLA A*2301	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.54	-0.06	-4.61	34829.1
HLA B*4002	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.65	0.04	-4.61	44191.5
HLA A*3002	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.49	-0.11	-4.61	31249.3
HLA B*3801	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.55	-0.06	-4.61	35127.7
HLA A*2602	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.58	-0.03	-4.61	38329.9
HLA A*3301	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.62	0.01	-4.61	42045.6
HLA B*1509	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.55	-0.06	-4.61	35358.6
HLA B*4002	1:60-68	9	EHAVVTAEG	0.69	-0.66	-4.64	0.02	-4.61	43251.3
HLA A*3201	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.59	-0.03	-4.62	38824.7
HLA B*1509	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.55	-0.06	-4.62	35662.9
HLA B*4403	1:36-44	9	TAVVPPAAD	0.78	-0.74	-4.66	0.04	-4.62	45210.2
HLA A*2402	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.59	-0.03	-4.62	39062.8
HLA A*2402	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.57	-0.05	-4.62	37381.3
HLA A*0250	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.56	-0.06	-4.62	36316.7
HLA B*3801	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.57	-0.05	-4.62	37469.4
HLA A*2402	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.56	-0.06	-4.63	36469.1
HLA B*4002	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.64	0.01	-4.63	43425.7
HLA B*4501	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.64	0.01	-4.63	43502.1
HLA A*0250	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.58	-0.05	-4.63	37686.1
HLA B*7301	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.58	-0.05	-4.63	37884.0
HLA A*3201	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.57	-0.06	-4.63	36995.3
HLA A*2603	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.64	0.01	-4.63	43889.1
HLA B*4403	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.64	0.01	-4.63	43941.9
HLA B*4501	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.61	-0.03	-4.63	40482.7
HLA B*5301	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.57	-0.06	-4.63	37171.8
HLA B*5301	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.58	-0.05	-4.63	38316.0
HLA A*3301	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.58	-0.05	-4.63	38326.4
HLA B*3801	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.57	-0.06	-4.63	37138.4
HLA B*4501	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.64	0.01	-4.63	44082.3
HLA A*0211	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.52	-0.11	-4.64	33348.8
HLA B*7301	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.61	-0.03	-4.64	40788.5
HLA B*1502	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.57	-0.06	-4.64	37538.8
HLA B*4002	1:90-98	9	DAAAAATYG	0.74	-0.73	-4.65	0.01	-4.64	44546.0
HLA B*3801	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.53	-0.11	-4.64	33771.1
HLA A*0250	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.58	-0.06	-4.64	37798.6
HLA B*4501	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.58	-0.06	-4.64	37934.4
HLA B*0803	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.53	-0.11	-4.64	33911.0
HLA A*3301	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.62	-0.03	-4.64	41421.4
HLA B*4403	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.66	0.01	-4.65	45541.9

Allele	Position	PepLength	Sequence	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA A*2301	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.54	-0.11	-4.65	34377.0
HLA B*5301	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.59	-0.06	-4.65	38478.6
HLA A*6801	1:68-76	9	GVEELGRAG	0.77	-0.76	-4.66	0.01	-4.65	46131.5
HLA B*1502	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.54	-0.11	-4.65	34692.2
HLA A*2402	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.59	-0.06	-4.65	38828.9
HLA B*1502	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.60	-0.05	-4.65	40141.4
HLA A*2602	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.59	-0.06	-4.66	39115.8
HLA B*7301	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.59	-0.06	-4.66	39157.3
HLA B*7301	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.59	-0.06	-4.66	39035.7
HLA A*2603	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.61	-0.05	-4.66	40477.0
HLA A*2602	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.60	-0.06	-4.66	39398.3
HLA B*4002	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.64	-0.03	-4.67	43788.1
HLA A*2603	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.64	-0.03	-4.67	43969.0
HLA A*6801	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.64	-0.03	-4.67	44006.8
HLA A*3201	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.61	-0.06	-4.67	40372.0
HLA B*1509	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.56	-0.11	-4.67	36286.0
HLA B*4403	1:6-14	9	VPEGLAAAS	1.10	-1.12	-4.65	-0.03	-4.68	44744.3
HLA A*6801	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.63	-0.05	-4.68	42524.6
HLA B*4002	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.62	-0.06	-4.68	41395.4
HLA A*2402	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.57	-0.11	-4.68	37155.3
HLA A*2602	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.57	-0.11	-4.68	37259.2
HLA A*6801	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.62	-0.06	-4.68	41774.9
HLA B*7301	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.57	-0.11	-4.69	37450.3
HLA A*3301	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.63	-0.06	-4.69	42283.3
HLA A*2603	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.63	-0.06	-4.69	42365.7
HLA A*0250	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.58	-0.11	-4.70	38423.7
HLA A*3301	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.64	-0.06	-4.70	43153.1
HLA B*4002	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.65	-0.05	-4.70	44684.5
HLA B*4501	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.64	-0.06	-4.70	43519.3
HLA A*2603	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.64	-0.06	-4.71	43836.9
HLA B*4002	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.64	-0.06	-4.71	43736.9
HLA A*0202	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.59	-0.11	-4.71	39244.1
HLA B*4501	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.66	-0.05	-4.71	45301.8
HLA A*6801	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.64	-0.06	-4.71	43993.5
HLA B*4403	1:77-85	9	VGVGESGAS	0.98	-1.04	-4.66	-0.06	-4.72	45313.6
HLA B*4403	1:74-82	9	RAGVGVGES	0.87	-0.93	-4.66	-0.06	-4.72	45710.0
HLA B*4403	1:45-53	9	PVSLQTAAG	0.77	-0.82	-4.68	-0.05	-4.73	47581.1
HLA B*4002	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.62	-0.11	-4.73	41646.1
HLA A*3201	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.62	-0.11	-4.73	41870.2
HLA A*3301	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.64	-0.11	-4.75	43542.9
HLA B*4501	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.65	-0.11	-4.77	45063.7
HLA A*2603	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.66	-0.11	-4.77	45450.1
HLA A*6801	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.66	-0.11	-4.77	45568.5
HLA B*4403	1:39-47	9	VPPAADPVS	0.96	-1.07	-4.67	-0.11	-4.78	46514.0