Table 1. Binding of human cdr2-derived nonamers to HLA-A2.1

Rank	Position	Sequence	ED50	$t_{1/2}$	iScore
1	290-298	LLEEMFL**TV**	6.00E-07	5.9	0.815
2	203-211	TMLQAQLSL	8.00E-07	9.8	0.811
3	289-297	SLLEEMFL**T**	6.00E-06	13.9	0.803
4	341-349	RGISLLHEV	1.00E-06	7	0.752
5	65-73	YLTKQVELL	2.00E-06	8.1	0.645
6	260-268	MLQ**S**EHPFV	2.00E-06	5.4	0.584
7	424-432	ALFKEIFSC	3.00E-05	18.7	0.546
8	217-225	VTM**EEEYG**L	2.00E-06	6.5	0.528
9	114-122	SLTETIECL	4.00E-06	9.3	0.518
10	111-119	KILSLTETI	7.00E-06	10.5	0.512
11	273-281	KLVPDSLYV	3.00E-06	6.1	0.499
12	384-392	**AAAK**DLTG**V**	3.00E-06	6.5	0.469
13	246-254	RALELEAV	1.00E-06	2.7	0.352
14	128-136	HLQSQVEEL	1.00E-05	7.7	0.323
15	168-176	RQHFVYDHV	6.00E-06	3.7	0.304
16	391-399	G**VNAQSE**PV	1.00E-05	6.4	0.292
17	372-380	DSLSHKAVQ	9.00E-06	6.3	0.262
18	171-179	FVYDHVFAE	1.00E-05	5.5	0.282
19	405-413	**LASVN**P**E**PV	4.00E-06	1.9	0.244
20	313-221	T**I**LSSLAGS	2.00E-06	1.1	0.238
21	204-212	MLQAQLSLE	5.00E-06	5.1	0.235
22	345-353	LLHEVDTQY	7.00E-06	3.5	0.204
23	197-205	HLKK**T**VTML	1.00E-05	2.5	0.199
24	164-172	LYDLRQHFV	5.00E-07	0.4	0.199
25	400-408	ASGWE**LAS**V	1.00E-06	0.5	0.187
26	120-128	ECLQTNIDH	3.00E-05	5.4	0.178
27	121-129	CLQTNIDHL	2.00E-05	2.4	0.176
28	107-113	ASQQKILSL	8.00E-06	3.4	0.174
29	125-133	NIDHLQSQV	6.00E-06	1.3	0.166
30	29-37	QLAAELGKT	2.00E-05	1.4	0.15
31	274-282	LVPDSLYVP	1.00E-05	2.4	0.154
32	82-90	KVYEQLDVT	8.00E-06	1.3	0.139
33	201-209	**T**VTMLQAQL	3.00E-06	0.6	0.132
34	237-245	LGAT**G**AYRA	1.00E-05	1.2	0.13
35	373-381	SLSHKAVQT	4.00E-06	0.8	0.129
36	225-233	**L**VLKENSEL	7.00E-06	0.8	0.119
37	355-363	ALKVKYEEL	7.00E-06	0.8	0.107
38	176-184	VFAEKITSL	5.00E-06	0.4	0.106

The top peptides bound to HLA-A2.1, ranked by iTopia iScore, are shown. This ranking is a composite of three variables: relative HLA-A2.1 binding (which was >30% of the control for all peptides shown), the concentration of peptide required to fold 50% of the plate-bound monomer (ED50), and the amount of time in hours required for 50% of the formed complexes to decay ($t_{1/2}$). Residues in bold are nonhomologous to the murine sequence.