

Supplemental Table 1. Peptide binding affinities from the BIRC5 (survivin) protein

Survivin*		Binding scores for various alleles						
Position	Peptide	A*0201	A*0301	A*1101	A*2402	B*0702	B*0801	B*1501
1	MGAPTLPPA	94	1	65	1	2	1	1
2	GAPTLPPAW	4	1	1	74	7	1	0
3	APTLPPAWQ	3	0	0	0	28	2	0
4	PTLPPAWQP	0	0	0	0	0	0	0
5	TLPPAWQPF	69	1	0	110	14	2	90
6	LPPAWQPFL	20	0	0	49	58	2	0
7	PPAWQPFLK	0	28	99	0	2	0	0
8	PAWQPFLKD	0	0	0	0	0	0	0
9	AWQPFLKDH	0	0	0	0	0	0	0
10	WQPFLKDHR	0	0	0	0	0	0	0
11	QPFLKDHRI	8	1	1	11	59	20	0
12	PFLKDHRI	5	1	0	30	0	11	0
13	FLKDHRI	77	0	0	0	4	55	40
14	LKDHRISTF	2	0	1	27	1	6	3
15	KDHRISTFK	1	43	66	0	2	1	1
16	DHRISTFKN	0	0	0	0	0	0	0
17	HRISTFKNW	6	7	9	46	3	2	2
18	RISTFKNWP	21	8	13	5	4	2	4
19	ISTFKNWPF	40	3	6	107	16	9	77
20	STFKNWPFL	86	26	54	117	1	3	3
21	TFKNWPFL	0	0	0	0	0	0	0
22	FKNWPFL	0	0	0	0	0	0	0
23	KNWPFL	37	2	1	0	2	1	1
24	NWPFL	0	0	0	0	0	0	0
25	WPFL	0	1	0	33	23	2	1
26	PFLE	39	0	0	0	0	0	0
27	FLE	0	2	0	3	0	1	1
28	LE	0	0	0	0	0	0	0
29	E	0	0	0	0	0	0	0
30	G	0	0	0	0	0	0	0
31	C	0	0	0	0	0	0	0
32	A	0	0	0	0	0	0	0
33	CT	67	2	1	9	3	3	5
34	T	0	0	0	0	0	0	0
35	P	0	0	0	0	0	0	0
36	E	0	0	0	0	0	0	0
37	R	56	76	100	34	10	3	95
38	M	51	4	1	11	3	3	3
39	A	0	0	0	0	0	0	0
40	E	5	2	1	37	2	4	3
41	A	0	0	1	0	0	0	0
42	G	0	0	0	0	0	0	0
43	F	24	3	0	1	1	2	2
44	I	0	0	0	0	0	0	0
45	H	0	0	0	0	0	0	0

Supplemental Data: Lin *et al.* Evaluation of MHC class I peptide binding prediction servers: applications for vaccine research

46	CPTENEPDL	0	0	0	0	0	0	0
47	PTENEPDLA	0	0	0	0	0	0	0
48	TENEPDLAQ	0	0	0	0	0	0	0
49	ENEPDLAQC	0	0	0	0	0	0	0
50	NEPDLAQCF	1	1	1	25	1	1	0
51	EPDLAQCF	5	0	0	43	3	0	0
52	PDLAQCF	0	41	79	40	0	0	0
53	DLAQCF	0	0	0	65	0	0	0
54	LAQCF	0	0	0	0	1	0	0
55	AQCF	3	1	0	0	1	0	19
56	QCFF	7	0	0	47	3	0	6
57	CFF	0	0	0	70	2	1	0
58	FF	5	1	0	47	1	2	2
59	FCF	37	0	0	43	1	1	45
60	CF	0	0	0	0	0	3	80
61	F	0	0	0	0	0	0	0
62	KE	0	0	0	0	0	0	0
63	E	0	0	0	0	0	0	0
64	LE	0	0	0	0	0	0	0
65	EG	0	0	0	0	0	0	0
66	GW	0	0	0	0	0	0	0
67	WE	0	0	0	0	0	0	0
68	EP	0	0	0	0	0	0	0
69	PD	0	0	0	0	0	0	0
70	DD	0	0	0	0	0	0	0
71	DD	0	0	0	0	0	0	0
72	DD	0	0	0	0	0	0	0
73	DD	0	0	0	0	0	0	0
74	DD	0	0	0	0	0	0	0
75	DD	0	0	0	0	0	0	0
76	DD	0	0	0	0	0	0	0
77	DD	0	0	0	0	0	0	0
78	DD	3	1	2	22	4	0	0
79	DD	26	2	4	86	9	2	2
80	DD	21	3	18	7	5	3	3
81	DD	98	4	8	24	6	3	9
82	DD	7	47	114	18	4	3	2
83	DD	3	62	100	10	4	3	2
84	DD	0	0	0	0	0	0	0
85	DD	8	1	10	121	5	51	6
86	DD	20	2	0	19	4	40	2
87	DD	0	0	0	0	0	0	0
88	DD	24	3	1	29	42	35	20
89	DD	0	0	0	0	0	0	0
90	DD	0	0	0	0	0	0	0
91	DD	61	2	0	5	4	4	24
92	DD	0	0	0	0	0	0	0
93	DD	5	0	0	39	0	1	6
94	DD	0	0	0	0	0	0	0

Supplemental Data: Lin *et al.* Evaluation of MHC class I peptide binding prediction servers: applications for vaccine research

95	ELTLGEFLK	5	4	49	11	0	1	0
96	LTLGEFLKL	92	8	44	97	8	3	3
97	TLGEFLKLD	41	1	0	66	0	4	1
98	LGEFLKLDLDR	0	0	0	0	0	0	0
99	GEFLKLDRE	0	0	0	0	0	0	0
100	EFLKLDLDRER	0	0	0	0	0	0	0
101	FLKLDLDRERA	65	8	3	0	1	37	8
102	LKLDLDRERAK	0	0	0	0	0	0	0
103	KLDLDRERAKN	38	21	0	11	1	3	0
104	LDRERAKNKN	0	0	0	0	0	0	0
105	DRERAKNKNKI	0	0	0	0	0	0	0
106	RERAKNKNKIA	0	0	0	0	0	0	0
107	ERAKNKNKIAK	0	0	0	0	0	0	0
108	RAKNKNKIAKE	0	0	0	0	0	0	0
109	AKNKNKIAKET	0	0	0	0	0	0	0
110	KNKNKIAKETN	0	0	0	0	0	0	0
111	NKNKIAKETNN	0	0	0	0	0	0	0
112	KIAKETNNKN	8	54	86	1	1	3	3
113	IAKETNNKKN	4	52	90	1	3	2	3
114	AKETNNKKNK	0	0	0	0	0	0	0
115	KETNNKKNKKE	0	0	0	0	0	0	0
116	ETNNKKNKKEF	0	0	0	0	0	0	0
117	TNNKKNKKEFE	0	0	0	0	0	0	0
118	NNKKNKKEFEE	0	0	0	0	0	0	0
119	NKKKKEFEET	0	0	0	0	0	0	0
120	KKKKEFEETA	0	0	0	0	0	0	0
121	KKKEFEETAK	0	0	0	0	0	0	0
122	KEFEETAKK	0	0	0	0	0	0	0
123	EFEETAKKV	0	0	0	0	0	0	0
124	FEETAKKVR	0	0	0	0	0	0	0
125	EETAKKVRR	0	0	0	0	0	0	0
126	ETAKKVRRRA	0	0	0	0	0	0	0
127	TAKKVRRRAI	3	2	0	6	42	64	3
128	AKKVRRRAIE	0	0	0	0	0	0	0
129	KKVRRRAIEQ	0	0	0	0	0	0	0
130	KVRRRAIEQL	48	19	1	36	74	26	48
131	VRRRAIEQLA	0	0	0	0	0	0	0
132	RRAIEQLAA	0	0	0	0	0	0	0
133	RAIEQLAAM	71	3	25	46	67	5	73
134	AIEQLAAMD	0	0	0	0	0	0	0

* Bachinsky MM, Guillen DE, Patel SR, Singleton J, Chen C, Soltis DA, Tussey LG: **Mapping and binding analysis of peptides derived from the tumor-associated antigen survivin for eight HLA alleles.** *Cancer Immun* 2005, 5:6.

Supplemental Table 2. Peptide binding affinities from the CMV construct protein

CMV construct*		Binding scores for various alleles						
Position	Peptide	A*0201	A*0301	A*1101	A*2402	B*0702	B*0801	B*1501
1	MGVIGDQYV	60	0	0	5	5	5	5
2	GVIGDQYVK	35	90	130	10	5	5	5
3	VIGDQYVKV	95	0	35	50	5	5	5
4	IGDQYVKVD	15	0	0	20	5	5	5
5	GDQYVKVDP	10	0	0	15	5	5	5
6	DQYVKVDPV	13	0	0	0	5	35	5
7	QYVKVDPVA	1	0	0	5	5	5	5
8	YVKVDPVAA	60	0	0	0	5	40	50
9	VKVDPVAAL	10	0	0	35	5	5	5
10	KVDPVAALF	70	0	0	110	5	5	70
11	VDPVAALFF	3	0	0	75	5	5	5
12	DPVAALFFF	0	0	0	0	5	0	0
13	PVAALFFFD	3	0	0	5	5	5	5
14	VAALFFFDI	68	0	0	120	5	5	5
15	AALFFFDID	12	0	0	5	5	5	5
16	ALFFFDIDL	60	10	0	10	5	5	30
17	LFFFDIDLQ	5	0	0	10	5	5	5
18	FFFDIDLQA	90	0	0	35	5	5	5
19	FFDIDLQAG	15	0	0	5	5	5	5
20	FDIDLQAGI	50	0	0	5	5	5	5
21	DIDLQAGIL	10	0	0	5	5	5	5
22	IDLQAGILA	25	0	0	60	5	10	5
23	DLQAGILAR	2	0	0	0	5	5	5
24	LQAGILARN	28	0	0	0	5	5	5
25	QAGILARNL	15	0	0	35	5	5	5
26	AGILARNLV	85	0	0	60	5	80	5
27	GILARNLVP	30	0	0	15	10	5	5
28	ILARNLVPM	105	80	35	90	130	200	120
29	LARNLVPMV	80	0	0	10	110	10	10
30	ARNLVPMVA	3	0	0	0	5	5	5
31	RNLVPMVAT	10	0	5	5	5	5	5
32	NLVPMVATV	103	0	0	40	5	5	5
33	LVPMVATVQ	20	0	0	5	0	5	5
34	VPMVATVQG	2	0	0	5	80	5	5
35	PMVATVQGQ	2	0	0	0	5	5	5
36	MVATVQGQN	2	0	0	0	5	5	5
37	VATVQGQNL	25	0	0	80	5	5	5
38	ATVQGQNLK	2	85	120	0	5	5	5
39	TVQGQNLKY	3	70	125	10	5	5	90
40	VQGQNLKYQ	5	0	0	0	5	5	5
41	QGQNLKYQE	2	0	0	5	5	5	5
42	GQNLKYQEF	2	0	5	110	5	5	125

* Movassagh M, Monseaux S, Arnaud L, Necker A, Montero-Julian FA: **Identification of T cell epitopes by iTopia™ epitope discovery system.** *Cytometry A* 2004, **59A**(1):32.

Supplemental Table 3. Well-characterized T-cell epitopes from a selection of tumor-related proteins.

	Tumor protein	Epitope	Length	Allele	Reference
1	BING-4	CQWGRLWQL	9	A2	62
2	p53	LLGRNSFEV	9	A2	31
3	p53	RMPEAAPPV	9	A2	10
4	TRP-2	SVYDFVWL	9	A2	9
5	TRP-2	TLDSQVMSL	9	A2	32
6	TRP-2-6b	ATTNILEHV	9	A2	64
7	IL13R α 2	WLPFGFILI	9	A2	47
8	MAGE-A1	KVLEYVIKV	9	A2	18
9	MAGE-A1	KMVELVHFL	9	A2	34
10	MAGE-A3	FLWGPRALV	9	A2	11
11	MAGE-A3	KVAELVHFL	9	A2	56
12	MAGE-A9	ALSVMGVYV	9	A2	25
13	MAGE-A10	GLYDGMEHL	9	A2	26
14	MAGE-B2	FLWGPRAYA	9	A2	61
15	MAGE C2	ALKDVEERV	9	A2	2
16	NY-ESO-1	SLLMWITQC	9	A2	63
17	NY-ESO-1	QLSLLMWIT	9	A2	1
18	BCR-ABL	FMVELVEGA	9	A2	3
19	BCR-ABL	KLSEQESLL	9	A2	4
20	BCR-ABL	MLTNSCVKL	9	A2	5
21	bcr-abl p210	SSKALQRPV	9	A2	6
22	ETV6-AML1	RIAECILGM	9	A2	7
23	SSX2	KASEKIFYV	9	A2	7
24	Malic Enzyme	FLDEFMEGV	9	A2	7
25	Adipophilin	SVASTITGV	9	A2	8
26	AFP	GVALQTMKQ	9	A2	12
27	CLCA2	LLGNCLPTV	9	A2	13
28	CLCA2	SLQALKVTV	9	A2	14
29	CPSF	KVHPVIWSL	9	A2	14
30	G250	HLSTAFARV	9	A2	19
31	Gnt-V	VLPDVFIRC	9	A2	20
32	Her2/neu	KIFGSLAFL	9	A2	20
33	Her2/neu	IISAVVGIL	9	A2	21
34	Her2/neu	ALCRWGLLL	9	A2	21
35	Her2/neu	ILHNGAYSL	9	A2	22
36	Her2/neu	RLLQETELV	9	A2	23
37	Her2/neu	VVLGVVFGI	9	A2	23
38	Her2/neu	HLYQGCQVV	9	A2	23
39	Her2/neu	PLQPEQLQV	9	A2	24
40	Her2/neu	TLEEITGYL	9	A2	4
41	Her2/neu	ALIHNTL	9	A2	27
42	Her2/neu	PLTSIISAV	9	A2	27
43	hTERT	ILAKFLHWL	9	A2	28
44	hTERT	RLVDDFLLV	9	A2	28
45	ML-IAP	SLGSPVLGL	9	A2	28

Supplemental Data: Lin *et al.* Evaluation of MHC class I peptide binding prediction servers: applications for vaccine research

46	MUC1	STAPPVHNV	9	A2	29
47	MUC1	LLLLTVLTV	9	A2	29
48	MUC2	LLNQLQVNL	9	A2	30
49	MUC2	MLWGWREHV	9	A2	30
50	PRAME	VLDGLDVLL	9	A2	33
51	PRAME	SLLQHLIGL	9	A2	33
52	RAGE1	LKLSGVVRL	9	A2	35
53	SART3	LLQAEAPRL	9	A2	36
54	SART3	RLAEYQAYI	9	A2	37
55	SOX10	AWISKPPGV	9	A2	38
56	WT1	RMFPNAPYL	9	A2	39
57	CEACAM5	YLSGANLNL	9	A2	40
58	CEACAM5	IMIGVLVGV	9	A2	41
59	ep-CAM	GLKAGVIAV	9	A2	42
60	gp100	KTWGQYWQV	9	A2	42
61	gp100	MLGTHTEV	9	A2	43
62	gp100	ITDQVPFSV	9	A2	44
63	gp100	YLEPGPVTA	9	A2	45
64	gp100	RLMKQDFS	9	A2	46
65	gp100	RLPRIFCSC	9	A2	48
66	MC1R	TILGIFFL	9	A2	49
67	MC1R	FLALIICNA	9	A2	50
68	Melan-A	AAGIGILTV	9	A2	51
69	Melan-A	ILTVILGVL	9	A2	51
70	Polypeptide 15	IMLCLIAAV	9	A2	52
71	Tyrosinase	MLLAVLYCL	9	A2	53
72	Tyrosinase	YMDGTMSQV	9	A2	54
73	CASP-5	FLIHWQNTM	9	A2	54
74	HERV-K-MEL	MLAVISCAV	9	A2	55
75	NY-BR-1	SLSKILDTV	9	A2	55
76	NY-MEL-1	VLHWDPETV	9	A2	55
77	MMP2	GLPPDVQRV	9	A2	55
78	RNF43	ALWPWLLMA	9	A2	55
79	Secernin 1	KMDAEHPEL	9	A2	57
80	STEAP1	MIAVFLPIV	9	A2	58
81	707-AP	RVAALARDA	9	A2	59
82	TGFbRII	RLSSCVPVA	9	A2	60
83	FATE	ILLRDAGLV	9	A*0201	15
84	ephA2	IMNDMPIYM	9	A*0201	16
85	ephA2	VLAGVGFFI	9	A*0201	17

*See supplemental references

Supplemental Table 4. Well-characterized HLA-A*0201 restricted T-cell epitopes from a selection of medically important viruses.

	Virus protein	Epitope	Length	Allele	Reference
1	Adenovirus 3 E3	LIVIGILIL	9	A*0201	65
2	EBV BMLF-1	GLCTLVAML	9	A*0201	66
3	EBV EBNA-3	SVRDLRLARL	9	A*0201	67
4	EBV-encoded BARFO ORF protein	LLWAARPRL	9	A*0201	68
5	EBV gp350	VLQWASLAV	9	A*0201	69
6	EBV gp85	LMIIPLINV	9	A*0201	69
7	EBV gp85	TLFIGSHVV	9	A*0201	69
8	EBV gp85	SLVIVTTFV	9	A*0201	69
9	EBV LMP-1	YLLEMLWRL	9	A*0201	70
10	EBV LMP-2	CLGGLTMV	9	A*0201	71
11	EBV LMP-2	LLWTLVVLL	9	A*0201	72
12	HBV DNA pol	GLSRYVARL	9	A*0201	73
13	HBV surface antigen	WLSLLVPFV	9	A*0201	74
14	HBV surface antigen	FLLTRILTI	9	A*0201	73
15	HCMV IE 1	VLEETSVML	9	A*0201	75
16	HCMV pp65	NLVPMVATV	9	A*0201	76
17	HCMV pp65	MLNIPSINV	9	A*0201	76
18	HCMV pp65	RIFAELEGV	9	A*0201	77
19	HCMV pp65	VLGPISGHV	9	A*0201	78
20	HCV-1 env E	SMVGNWAKV	9	A*0201	79
21	HCV-1 MP	DLMGYIPLV	9	A*0201	80
22	HCV-1 NS3	CINGVCWTV	9	A*0201	81
23	HCV-1 NS3	YLVTRHADV	9	A*0201	82
24	HCV-1 NS5	GLQDCTMLV	9	A*0201	83
25	HIV-1 (BRU) gag p17	SLYNTVATL	9	A*0201	84
26	HIV-1 (BRU) gag p24	TLNAWVKVV	9	A*0201	85
27	HIV-1 (BRU) nef	AFHHVAREL	9	A*0201	86
28	HIV-1 (BRU) RT	ILKEPVHGV	9	A*0201	87
29	HIV-1 (BRU) RT	VIYQYMDDL	9	A*0201	88
30	HIV-1 (MAL) gp120	KLTPLCVTL	9	A*0201	89
31	HPV11 E7	RLVTLKDIV	9	A*0201	90
32	HPV16E7	LLMGTLGIV	9	A*0201	91
33	HPV 6b E7	GLHCYEQLV	9	A*0201	90
34	HPV 6b E7	PLKQHFQIV	9	A*0201	90
35	HSV-1 gp C	GIGIGVLAA	9	A*0201	65
36	HSV-2 gp C	GAGIGVAVL	9	A*0201	65
37	HSV-2 UL47	FLVDAIVRV	9	A*0201	92
38	HSV-2 UL47	GLADTVVAC	9	A*0201	92
39	HTLV-1 tax	LLFGYPVYV	9	A*0201	93
40	Influenza A MP	GILGFVFTL	9	A*0201	94
41	Influenza A (PR8) NS1	AIMDKNIIL	9	A*0201	95
42	Vaccinia virus 49.8 kD protein	ILDDNLYKV	9	A*0201	96
43	Vaccinia virus protein H3L	SLSAYIIRV	9	A*0201	97
44	VP1	SITEVECFL	9	A*0201	98

*See supplemental references

Supplemental references

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