

Table 2: CTL epitopes conserved among HIV-1 proteomes

EPITOPE	C-(1)	Source (2)	Position (3)	HLA I Restriction (4)	Predicted HLA I Restriction (5)	PPC(6)
SPRTLNAWV	K	GAG:p24	148–156:16–24	B0702	B0702 B3501 B5101 B5102 B5103 B5301 B5401 B5502	0.35
AVFIHNFKR	K	POL:Integrase	894–902:179–187	A0301	A0301 A1101 A3101 A3301 A6601 A6801	0.35
TLFCASDAK	A	ENV:gp160	51–59	A0301	A0301 A1101 A3101 A3301 A6801	0.32
FPVRPQVPL	R	NEF	68–76	B3501	A2902 B0702 B3501 B5101 B5102 B5103 B5301 B5401	0.32
RAMASDFNL	P	POL:Integrase	735–743:20–28	A0201	A0201 B2709 C0304	0.31
TLNAWVKVI	E	GAG:p24	151–159:19–27	A0201	A0201 A0202 A0203 A0204 A0206	0.29
VIYQYMDDL	Y	POL: Reverse Transcriptase	334–342:179–187	A0201	A0201 A0205 A0207 A0214	0.28
LVGPTPVNI	I	POL:Protease	132–140:76–84	A0201	A0201 A0202 A0205 A0209 B1501 B1516	0.27
TVLDVGDAY	F	POL: Reverse Transcriptase	262–270:107–115	B3501	B1501 B3501 B5701 C0304	0.26
PLVKLWYQL	E	POL: Reverse Transcriptase	576–584:421–429	A0201	A0201 A0202 A0203	0.26
TLNFPISPI	E	POL: Protease	152–160:96–1004		A0201 A0207	0.23
NTPVFIAIKK	K	POL: Reverse Transcriptase	212–220:57–65	A0301	A0301 A6601 C0102	0.22
EKEGKISKI	G	POL: Reverse Transcriptase	197–205:42–50	B5101	B2701 B3801 B3901 B3909 B4402 B5101 B8	0.19
LLWKGEHAV	V	POL: Reverse Transcriptase	956–964:241–249	A0201	A0201 A0204 A0205 A0209	0.18
LTFGWCFKL	V	NEF	137–145	A0201	A0201	0.18
YQYMDDLIV	G	POL: Reverse Transcriptase	336–344:181–189	A0201	A0201	0.18
GPKVKQWPL	T	POL: Reverse Transcriptase	173–181:18–26	B0801	B0702 B0801 B3501 B8	0.17
RAIEAQQHL	L	ENV:gp41	557–565:46–54	B5101 B1501 C0304	B1501 B1517 B5101 C0304	0.13
GLNKIVRMY	S	GAG:p24	269–277:137–145	B1501	A0203 A1 B1501	0.13
YFPDWQNYT	P	NEF	120–128	A1 B3701 B5701	A1 B3701 B5701	0.07
WYIKIFIMI	V	ENV:gp41	680–688:680–688	A2402	A0203 A0206 A2402	0.05
YVDRFFKTL	R	GAG:p24	296–304:164–172	A2601	A0203 A0204 A0207 A2601 B3801	0.05
FVNTPLLVK	L	POL: Reverse Transcriptase	571–579:416–424	A1101	A1101	0.05
KIQNFRVYY	R	POL:Integrase	934–942:219–227	A3002	A1 A3002	0.03
DRFFKTLRA	E	GAG:p24	298–306:166–174	B1402	B1402 B2701 B2702 B2703 B2704 B2705 B2709	0.03

1) Most proximal C-terminal flanking amino acid residue to the epitope

2) HIV-1 ORF

3) Position in mature protein.

4) HLA-I restriction of the epitope as retrieved from the Los Alamos HIV database

5) Predicted HLA-I binding profiles of epitopes were obtained using PSSMs [16].

6) Protection Population Coverage (PPC) was computed for 5 ethnic groups (Black, Caucasian, Hispanic, North American Natives and Asian) in the USA population. Each PPC value shown in the table is that of the ethnic group with the lowest PPC for that specific HLA I combination.

LVGPTPVNI is predicted to bind to several alleles within the A2 supertype (A0201 A0202 A0205 A0209) but additionally to other non-related alleles of the HLA-B locus (B2701 and B3801).

In order to assess the accuracy of the predicted PPC, five peptide pools were created, each solubilized in DMSO and combining CTL epitopes (200 μ M each) to provide a PPC \geq 95 % (peptides included in the pools are shown in Table 3). Peptide 1 pool contained all 25 selected peptides whereas peptide pools #2 (15 peptides), #3 (13 peptides),

#4 (11 peptides), #5 (7 peptides) comprising 55, 13, 11, 5, 2, respectively, of distinct 5-peptide combinations producing \geq 95% PPC. Peptides pools 1–5 were designed so that peptides in the smaller pools are contained in the larger pools. CD8+ T cell responses to these pools were first checked by IFN γ ELISPOT assay using PBMC samples from a cohort of 47 HIV-1 infected patients. Patients were largely heterogeneous with regard to their HLA I background and included those diagnosed during acute or chronic HIV-1 with or without HAART therapy and some long-term non-progressors (Table 4). Furthermore, these