Table 8: **Protease**

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
Protease(3–11)	Protease(71–79 LAI)	ITLWQRPLV		human(A*6802, A*7401, A19)	[Dong (1998)]
	• Predicted on binding motif, no truncations analyzed • Clade A/B/D consensus, S. Rowland-Jones, pers. comm.				
Protease(30–38)	Pol( )	DTVLEEMNL	HIV-1 exposure	human(A*6802)	[Rowland-Jones (1998b)]
	• HIV specific-CTL were found in exposed seronegative prostitutes from Nairobi – these CTL may confer protection • Seroprevalence in this cohort is 90-95% and their HIV-1 exposure is among the highest in the world • Most isolated HIV strains are clade A in Nairobi, although clades C and D are also found – B clade epitopes are often cross-reactive, however stronger responses are frequently observed using A or D clade versions of epitopes • This epitope is conserved among B and D clade viruses • The Clade A version of the epitope: DTVLEDINL • This epitope was recognized by two different exposed and uninfected prostitutes • This epitope was identified by screening HIV-1 49 peptides with the predicted A*6802 anchor residue motif x(VT)xxxxxx(VL)			
Protease(75–84)	Protease(75–84 MN)	VLVGPTPVNI	*in vitro* stimulation	human(A*0201)	[Konya (1997)]
	• Peptide predicted to be reactive based on HLA-A*0201 binding motif • Peptide could stimulate CTL in PBMC from 5/6 seronegative donors • Peptide located in a highly conserved region of protease • Both 9-mer and 10-mer could stimulate CTL: VLVGPTPVNI and LVGPTPVNI • Binding affinity to A*0201 was measured, $C_{1/2\max}\mu M = 6$ for 10-mer, 3 for 9-mer • MAL variant of Pr(75-84 MN), with substitutions V77, G78, and P79 gave reduced binding and CTL recognition			