The Evolving Field of HIV CTL Epitope Mapping: New Approaches to the Identification of Novel Epitopes

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The past 12 months since the most recent update of the HIV CTL epitope database have brought a large number of new or newly fine mapped HIV protein derived CTL epitopes. In parallel, the important role that CTL play in containing HIV and SIV replication in the infected host has been supported further, especially by viral escape studies in SIV infection. In addition, the dependence of effective CTL activity on HIV specific T-helper responses has become more evident, particularly from data generated by recent treatment interruption studies. Other recent studies have provided further strong evidence that T-helper responses and the magnitude and breadth of CTL responses are tightly linked.

In addition to these studies supporting earlier findings, there have been significantly new directions established in the field of anti-HIV T cell immunity. Once again the value of the SIV animal model has been highlighted in the studies of Allen *et al.*, that identified epitopes within the Tat protein as being a critical part of the apparently crucial acute CTL response [Allen (2000)]. This work drew attention to the disparity between CTL of different specificities, so that CTL escape was observed in 100% of animals targeting the Mamu-A*01-restricted Tat epitope, but in none of the same animals that also generated strong responses towards the Mamu-A*01-restricted Gag epitope. Like the earlier studies from this group, from other work in the lymphocytic choriomeningitis virus (LCMV) animal model, and consistent with data that have shown associations between particular HLA class I alleles and rapid (for example HLA-B35) or slow progression (for example, HLA-B57 or B27) in HIV infection, these studies underlined that CTL of different specificities are not equal. Moreover, the CTL specificities that may characterize chronic infection may not actually be those that are important in considerations of vaccine development as some recent data suggest that the specificities of CTL responses observed in chronic responses can differ form those in the acute phase of infection. This is for instance the case for the HLA-A*0201-restricted response to the SL9 epitope in p17 Gag. This is the best-studied CTL specificity in HIV infection, is detectable in 75% of adults expressing A*0201 in chronic infection, and yet was not detectable in 11 A*0201-positive adults studied during acute infection (most prior to seroconversion) [Goulder (2001b)].

The focus of HIV CTL studies has therefore increasingly turned to characterizing the timing and specificities of the acute CTL response, since this is very likely to significantly contribute to the initial reduction in viremia and in determining the eventual steady-state set-point during chronic infection. This increased appreciation of the importance of the acute CTL response has brought the realization that the CTL response must be more comprehensively screened, and restricting the analyses to the well-studied proteins of Gag, Nef, RT and Env may not be adequate. Novel technologies such as intracellular cytokine stainings and Elispot assays to detect antigen specific T cells (see below) now make it possible to screen for responses using hundreds of overlapping peptides that span all the HIV proteins. Although this is expensive, this approach may be necessary in order to obtain a comprehensive view of the all-important early CTL response.

New methods for the accurate measurement of CTL responses

Many of the above mentioned exiting new results were obtained by applying new technologies that facilitate the detection of CTL and Th responses [Kaul & Rowland-Jones(1999)]. Also, these newer approaches have detected immune responses with a higher sensitivity, allowing the complete breadth of CTL responses to be monitored. Elispot assays combined with intracellular staining (ICS) for Interferon–γ (IFN-γ) allow for the screening of the entire protein sequences of HIV for T cell mediated immune responses and to determine the phenotype of the responding cells. Importantly, this also allows for functional analyses of antigen specific cells, including intracelluar perforin and cytokine contents. However, no real alternative to fresh killing (*ex-vivo*) assays has been developed at this point.

Elispot and ICS have proven useful for epitope fine mapping and definition of HLA restriction without the cumbersome generation of CTL clones and lines. However, analyses using polyclonal PBMC preparation may be inconclusive if different epitopes overlap within the tested peptide and if overlapping epitopes can be presented by different HLA class I molecules. These potential

limitations should be kept in mind if epitope fine mapping and HLA restriction analyses are carried out using PBMC preparation. These considerations also affect the criteria we would like to set forward for epitope inclusion in this section of "optimal epitopes" within the database, especially with regard to the identification of the restricting HLA class I molecules (see below).

Novel CTL epitopes: Immunodominance and Effectiveness

While the new technologies have greatly increased the speed with which novel epitopes can be defined, from the foregoing discussions it is clearer than before that mere descriptions of new epitopes are only a first step, albeit an important one, in understanding the role of specific CTL responses in control of HIV. Epitope identification has greater value when placed in the context of the individual subjects and of the population being studied. Thus, it is important to know the proportion of HIV-infected individuals expressing the appropriate HLA type who make the CTL response, to know the magnitude of the response in relation to other HIV-specific CTL responses, and to know the timing of the response (acute/chronic), and the viral load of the subject. Determining the effectiveness of individual CTL specificities is not straightforward, but the ability to link a reliably dominant response, generated in acute infection, to long-term control of HIV replication (*i.e.,* low viral load) would be of value in consideration of vaccine design.

Epitope prediction

The "reverse immunogenetics" approach to define novel CTL epitopes has been an enormously successful one, rapidly achieving the desired result of the equivalent of finding a needle in a haystack. The elution of peptides from individual class I molecules has generated a huge amount of valuable data regarding the types of peptides that are best-suited for binding to particular class I molecules. Using these peptide-binding motifs to synthesize new peptides that can be tested for binding and for CTL recognition is therefore an attractive method that is continually being refined (SYFPEITHI, Database of MHC ligands and peptide motifs; `http://www.uni- tuebingen.de/uni/kxi`). Combining the reverse immunogenetics and the comprehensive screening methods may today be the most effective approach to quickly reach the optimal epitopes prediction from a 15mer peptide sequence. Having arrived at this putative optimal peptide, confirmation using 4 additional peptides (with one amino acid added or truncated from each terminus of the predicted optimal peptide) will define the optimal epitope sequence with minimal synthesis of truncated peptides.

New viral targets and epitope clustering

Newly identified epitopes that have been reported since the last update of this database confirm previously observed trends. One trend is that an increasing number of CTL epitopes are being identified in proteins outside the traditionally well studied HIV proteins Gag, RT, Env and Nef. This is greatly due to the use of the above described new methodologies that have allowed more sensitive and comprehensive studies of proteins previously not analyzed, especially Tat, Rev and Vpr. Interestingly, a recent report showed that Tat may be targeted frequently in acute infection and may contribute to the containment of the initial viremia, although early escape form these responses was observed [Allen (2000)]. Similarly, more CTL responses to Rev have been reported recently and may prove useful with regard to vaccine design. It will be important to investigate whether early expression of these proteins (especially before Nef mediated downregulation of HLA class I may take place) could lead to rapid elimination of infected cells resulting in diminished viral burst size.

Another trend that has been confirmed by newly identified epitopes is the clustering of epitopes in certain regions of the different HIV proteins. Recently published work now shows that such epitope clustering is maintained even in individuals with HLA backgrounds that have not traditionally been well studied [Goulder (2000c)]. However, one recent study found that the immunodominant HIV Gag response in Caucasians was more often targeting an epitope in Gag p17, whereas in Africans, the immunodominant response mapped more frequently to an epitope in Gag p24 [Goulder (2000c)].

The likely basis for these differences is the identity of the HLA class I molecules prevalent in the different populations. In addition, alternative mechanisms such as race-dependent differences in the unfolding of HIV proteins and proteasomal digestion and differences in T cell repertoire and available HLA class I alleles to bind and present the processed epitopes may contribute to the different clustering. Finally, sequence differences between HIV clade B and clade C may be a constraining factor for the presentation of immunogenic peptides. Further characterization of HIV specific CTL responses and the fine mapping of these responses in non-Caucasian individuals and individuals infected with non-clade B virus will be necessary to identify the major factors leading to the observed differences in epitope clustering. Importantly, a better understanding of these factors will also be required for the design of population tailored vaccine.

HLA restriction analyses and HLA-C alleles

In the past, some epitopes have been excluded form the list of "optimal CTL epitopes" based on inconclusive data on HLA restriction of these epitopes, often caused by high degrees of linkage disequilibrium between certain alleles and the presence of allele subtypes. Some of these epitopes have been reinstated in this list as more HLA restriction analyses data were provided. Since the problem of inconclusive HLA restriction analyses will persist in the future, especially when investigations move into less well characterized ethnicities where the available data of cross–presentation and existence of sub-alleles is limited, it appears important to perform these analyses carefully and with the best available tools. The use of single HLA class I allele transfected cell lines appears as the gold standard for these analyses, provided the correct allele subtype is used (if subtypes are known at all). We would thus like to encourage investigators that have generated such cell lines or face these kind of problems to share their reagents with other investigators for a faster and more accurate characterization of newly discovered CTL epitopes.

The last year has also confirmed the trend that HLA-C alleles can present a number of HIV derived epitopes. This is especially important as HIV Nef does not appear to downregulate C alleles and responses restricted by HLA C may thus not be subject to this immune modulating effect. However, Nef mediated downregulation of HLA class I does not appear to become effective until relatively late in the viral replication cycle and the numbers of HLA-C alleles on the cell surface is low compared to HLA-A and -B alleles. Therefore, the importance of HLA-C alleles restricted CTL responses in HIV infection remains to be established.

As every year, we would like to express our gratitude to the large number of researchers in the field who continuously contribute to this database. We very much welcome any criticism, comments and additions to this list since we are sure that some epitopes will unintentionally escape our attention, despite close monitoring of the literature. Also, pertinent information, such as resources for single HLA allele expressing cell lines, HLA subtype information and new technologies for CTL epitope mapping could be listed or referenced in this list, providing additional help to problems encountered by investigators. Please write or call us with any comments you may have.

Best defined epitope table

In the table that follows, primary anchors are bold faced, secondary anchors are not. The amino acid position numbers shown are those of the analagous epitope in HXB2R, our standard strain as used in other parts of this database.

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Table 1 Best Defined HIV CTL Epitopes

HLA	Protein	AA	Sequence	Reference
A*0201 (A2)			2 6 C	[Falk (1991), Barouch (1995)]
		1° anchor	**L** **L**	
			M **V**	
		2° anchor	V	
	p17	77–85	SLYNTVATL	[Johnson (1991), Parker (1992), Parker (1994)]
	RT	33–41	ALVEICTEM	[Haas (1998), Haas(1999)]
	RT	179–187	VIYQYMDDL	[Harrer (1996a)]
	RT	309–317	ILKEPVHGV	[Walker (1989), Tsomides (1991)]
	gp160	311–320	RGPGRAFVTI	[Alexander-Miller (1996)]
	gp160	813–822	SLLNATDIAV	[Dupuis (1995)]
	Nef	136–145	PLTFGWCYKL	[Haas (1996), Maier & Autran(1999)]
	Nef	180–189	VLEWRFDSRL	[Haas (1996), Maier & Autran(1999)]
	Vpr	58–66	AIIRILQQL	[Altfeld (2001)]
A*0202 (A2)			2 C	[Barouch (1995)]
			L **L**	
			V	
	p17	77–85	SLYNTVATL	[Goulder(2000)]
A*0205 (A2)	p17	77–85	SLYNTVATL	[Goulder(2000)]
A*0301 (A3)			2 C	[DiBrino (1993), Rammensee (1995)]
			L **K**	
			V **Y**	
			M **F**	
	p17	18–26	KIRLRPGGK	[Harrer (1996b)]
	p17	20–28	RLRPGGKKK	[Goulder (1997a), Culmann(1999), Lewinsohn (1999), Wilkes & Ruhl(1999)]
	p17	20–29	RLRPGGKKKY	[Goulder (2000b)]
	RT	33–43	ALVEICTEMEK	[Haas (1998), Haas(1999)]
	RT	93–101	GIPHPAGLK	[Altfeld (2000)]
	RT	158–166	AIFQSSMTK	[Threlkeld (1997)]
	RT	269–277	QIYPGIKVR	[Altfeld (2000)]
	VIF	17–26	RIRTWKSLVK	[Altfeld (2000)]
	gp160	37–46	TVYYGVPVWK	[Johnson (1994)]
	gp160	770–780	RLRDLLLIVTR	[Takahashi (1991)]
	Nef	73–82	QVPLRPMTYK	[Koenig (1990), Culmann (1991)]

Table 1 (cont.) Best Defined HIV CTL Epitopes

HLA	Protein	AA	Sequence	Reference
A*1101 (A11)			2 C **K** V I F Y	[Zhang (1993), Rammensee (1995)]
	p17	84–92	TLYCVHQRI	[Harrer (1998)]
	p24	217–227	ACQGVGGPGHK	[Sipsas (1997)]
	RT	158–166	AIFQSSMTK	[Johnson & Walker(1994), Zhang (1993), Threlkeld (1997)]
	RT	341–350	IYQEPFKNLK	[Culmann(1999)]
	RT	520–528	QIIEQLIKK	[Fukada (1999)]
	Integrase	179–188	AVFIHNFKRK	[Fukada (1999)]
	Nef	73–82	QVPLRPMTYK	[Buseyne(1999)]
	Nef	75–82	PLRPMTYK	[Culmann (1991)]
	Nef	84–92	AVDLSHFLK	[Culmann (1991)]
A*2402 (A24)			2 C **Y** **I** **L** **F**	[Maier (1994)]
	p17	28–36	KYKLKHIVW	[Ikeda-Moore (1998), Lewinsohn(1999)]
	p24	162–172	RDYVDRFFKTL	[Dorrell (1999), Rowland-Jones(1999)]
	gp160	52–61	LFCASDAKAY	[Lieberman (1992), Shankar (1996)]
	gp160	585–593	RYLKDQQLL	[Dai (1992)]
	Nef	134–141	RYPLTFGW	[Goulder (1997b), Ikeda-Moore (1998)]
A*2501 (A25)				
	p24	13–23	QAISPRTLNAW	[Kurane & West(1999)]
	p24	71–80	ETINEEAAEW	[Klenerman (1996), van Baalen (1996)]

Table 1 (cont.) Best Defined HIV CTL Epitopes

HLA	Protein	AA	Sequence	Reference
A*2601 (A26)			12 6 C **V** **Y** **T** **F** **I** **L** **F** D I E L V	[Dumrese (1998)]
	p24	35–43	EVIPMFSAL	[Goulder (1996a)]
A*2902 (A29)				
	gp160	209–217	SFEPIPIHY	[Altfeld (2000)]
A*3002 (A30)			12 C **Y** **Y** **F** **L** **V** R	[Rammensee (1999)]
	p17	76–86	RSLYNTVATLY	[Goulder (2001a)]
	RT	173–181	KQNPDIVIY	[Goulder (2001a)]
	RT	263–271	KLNWASQIY	[Goulder (2001a)]
	gp160	704–712	IVNRNRQGY	[Goulder (2001a)]
	gp41	794–802	KYCWNLLQY	[Goulder (2001a)]
A*3101 (A31)			2 C **R** L V Y F	[Falk (1994), Rammensee (1999)]
	gp160	770–780	RLRDLLLIVTR	[Safrit (1994a), Safrit (1994b)]
A*3201 (A32)				
	RT	392–401	PIQKETWETW	[Harrer (1996b)]
	gp160	419–427	RIKQIINMW	[Harrer (1996b)]

Table 1 (cont.) Best Defined HIV CTL Epitopes

HLA	Protein	AA	Sequence	Reference
A*6802 (A68)				
	Protease	3–11	ITLWQRPLV	[Rowland-Jones(1999)]
	Protease	30–38	DTVLEEWNL	[Rowland-Jones(1999)]
	gp160	777–785	IVTRIVELL	[Wilkes(1999)]*
A*7401 (A19)				
	Protease	3–11	ITLWQRPLV	[Rowland-Jones(1999)]
B*0702 (B7)			123 C **P L** A R R K	[Englehard (1993), Rammensee (1999)]
	p24	16–24	SPRTLNAWV	[Lewinsohn(1999)]
	p24	48–56	TPQDLNTML	[Wilson (1999a), Wilkes & Ruhl & Goulder (1999),* Jin00, Wilson (1997)]
	p24	223–231	GPGHKARVL	[Goulder(2000)]
	gp160	298–307	RPNNNTRKSI	[Safrit (1994b)]
	gp160	843–851	IPRRIRQGL	[Wilkes & Ruhl(1999)]*
	Nef	68–77	FPVTPQVPLR	[Haas (1996), Maier & Autran(1999)]
	Nef	71–79	TPQVPLRPM	[Goulder(1999)]*
	Nef	77–85	RPMTYKAAL	[Bauer (1997)]
	Nef	106–115	RQDILDLWIY	[Goulder(2000)]
	Nef	128–137	TPGPGVRYPL	[Culmann-Penciolelli (1994), Haas (1996)]
B*0801 (B8)			23 5 C **K K L** **R** PR L	[Hill (1992), Sutton (1993), DiBrino (1994a)]
	p17	24–32	GGKKKYKLK	[Rowland-Jones (1993), Goulder (1997d)]
	p17	74–82	ELRSLYNTV	[Goulder (1997d)]
	p24	128–135	EIYKRWII	[Sutton (1993), Goulder (1997d)]
	p24	197–205	DCKTILKAL	[Sutton (1993)]
	RT	18–26	GPKVKQWPL	[Walker (1989), Sutton (1993)]
	gp160	2–10	RVKEKYQHL	[Sipsas (1997)]
	gp160	586–593	YLKDQQLL	[Johnson (1992), Shankar (1996)]
	Nef	13–20	WPTVRERM	[Goulder (1997d)]
	Nef	90–97	FLKEKGGL	[Culmann-Penciolelli (1994), Price (1997)]

Table 1 (cont.) Best Defined HIV CTL Epitopes

HLA	Protein	AA	Sequence	Reference
?B*1401 or B*1402 (B14)				
	Rev	67–75	SAEPVPLQL	[van Baalen & Gruters(2000)]
B*1402 (B14)			23 5 C **R R L** **K H** L Y F	[DiBrino (1994b)]
	p24	166–174	DRFYKTLRA	[Harrer (1996b)]
	gp160	584–592	ERYLKDQQL	[Johnson (1992)]
B*1501 (B62)			2 C **Q Y** **L F** **M**	[Barber (1997)] [Barber (1997)] [Barber (1997)]
	p24	137–145	GLNKIVRMY	[Johnson (1991), Goulder(1999)]*
	RT	260–271	LVGKLNWASQIY	[Johnson(1999)]
	RT	309–318	ILKEPVHGVY	[Johnson (1991), Johnson(1999)]
	Nef	117–127	TQGYFPDWQNY	[Culmann(1999)]
B*1516 (B63)			2 9 **T Y** **S I** **V** **F**	[Barber (1997), Seeger (1998)]
	gp160	375–383	SFNCGGEFF	[Wilson (1997), Wilson(1999b)]
B*1801 (B18)				
	p24	161–170	FRDYVDRFYK	[Ogg (1998)]
	Nef	135–143	YPLTFGWCY	[Culmann (1991), Culmann-Penciolelli (1994)]
B*2703 (B27)				
	p24	131–140	RRWIQLGLQK	[Rowland-Jones (1998), Rowland-Jones(1999)]

Table 1 (cont.) Best Defined HIV CTL Epitopes

HLA	Protein	AA	Sequence	Reference
B*2705 (B27)			12 C **R** **L** **F** K K R R G I A	[Jardetzky91, Rammensee (1995)]
	p17	19–27	IRLRPGGKK	[McKinney (1999), Lewinsohn(1999)]
	p24	131–140	KRWIILGLNK	[Nixon (1988), Buseyne (1993), Goulder (1997c)]
	gp160	786–795	GRRGWEALKY	[Lieberman (1992), Lieberman(1999)]
	Nef	105–114	RRQDILDLWI	[Goulder (1997a)]
B*3501 (B35)			2 C **P** **Y** A F V M S L I	[Hill (1992), Rammensee (1999)]
	p17	36–44	WASRELERF	[Goulder (1997b)]
	p17	124–132	NSSKVSQNY	[Rowland-Jones (1995)]
	p24	122–130	PPIPVGDIY	[Rowland-Jones (1995)]
	p24	122–130	NPVPVGNIY	[Rowland-Jones (1995)]
	RT	107–115	TVLDVGDAY	[Wilson (1999a), Wilkes & Ruhl(1999),*]
	RT	118–127	VPLDEDFRKY	[Sipsas (1997), Shiga (1996)]
	RT	175–183	NPDIVIYQY	[Sipsas (1997), Shiga (1996)]
	RT	175–183	HPDIVIYQY	[Rowland-Jones (1995)]
	gp160	42–52	VPVWKEATTTL	[Wilkes & Ruhl(1999)]*
	gp160	78–86	DPNPQEVVL	[Shiga (1996)]
	gp160	606–614	TAVPWNASW	[Johnson (1994)]
	Nef	74–81	VPLRPMTY	[Culmann (1991), Culmann-Penciolelli (1994)]

Table 1 (cont.) Best Defined HIV CTL Epitopes

HLA	Protein	AA	Sequence	Reference
B*3701 (B37)			2 C **D F** **E M** **L** **I**	[Falk (1993)]
B*3701 (B37)	Nef	120–128	YFPDWQNYT	[Culmann (1991), Culmann(1999)]
B*3901 (B39)			2 C **R L** **H**	[Falk95]
B*3901 (B39)	p24	61–69	GHQAAMQML	[Kurane & West(1999)]
B*4001 (B60)			2 C **E L**	[Falk (1995a)]
	p17	92–101	IEIKDTKEAL	[Altfeld (2000)]*
	p24	44–52	SEGATPQDL	[Altfeld (2000)]*
	p2p7p1p6	118–126	KELYPLTSL	[Yu & Altfeld(2001)]
	RT	202–210	IEELRQHLL	[Altfeld (2000)]*
	gp160	805–814	QELKNSAVSL	[Altfeld (2000)]*
	Nef	92–100	KEKGGLEGL	[Altfeld (2000)]*
B*4201 (B42)				
	p24	48–56	TPQDLNTML	[Goulder (2000c)]
	RT	271–279	YPGIKVRQL	[Wilkes & Ruhl(1999)]*
	Nef	128–137	TPGPGVRYPL	[Goulder(1999)]*
B*4402 (B44)			2 C **E F** **Y**	[Rammensee (1999)]
	p24	162–172	RDYVDRFYKTL	[Ogg (1998)]
	p24	174–184	AEQASQDVKNW	[Lewinsohn(1999)]*
	gp160	31–40	AENLWVTVYY	[Borrow (1997)]

Table 1 (cont.) Best Defined HIV CTL Epitopes

HLA	Protein	AA	Sequence	Reference
B*5101 (B51)				
			2 C	[Falk95]
			A F	
			P I	
			G	
	RT	42–50	EKEGKISKI	[Haas (1998), Haas(1999)]
	RT	128–135	TAFTIPSI	[Sipsas (1997)]
	gp160	416–424	LPCRIKQII	[Tomiyama (1999)]
	gp160	557–565	RAIEAQQHL	[Sipsas (1997)]
B*5201 (B52)				
			2 C	[Rammensee (1999)]
			I	
			V	
			Q	
	p24	143–150	RMYSPTSI	[Wilkes & Ruhl(1999),* Wilson97]
B*5301 (B53)			2 C	
			P L	[Hill (1992)]
	p24	48–56	TPYDINQML	[Gotch (1993)]
	p24	176–184	QASQEVKNW	[Buseyne (1996), Buseyne (1997), Buseyne(1999)]
	Tat	2–11	EPVDPRLEPW	[Addo (2001)]
B*5501 (B55)				
			2 C	[Barber (1995)]
			P	
			A	
	gp160	42–51	VPVWKEATTT	[Shankar (1996), Lieberman(1999)]

Table 1 (cont.) Best Defined HIV CTL Epitopes

HLA	Protein	AA	Sequence	Reference
B*5701 (B57)			12 C **A F** **T W** **S** K Y	[Barber (1997)]
	p24	15–23	ISPRTLNAW	[Johnson (1991), Goulder (1996b)]
	p24	30–40	KAFSPEVIPMF	[Goulder (1996b)]
	p24	108–118	TSTLQEQIGWF	[Goulder (1996b)]
	p24	176–184	QASQEVKNW	[Goulder (1996b)]
	RT	244–252	IVLPEKDSW†	[van der Burg (1997), Hay(1999)]
	Integrase	173–181	KTAVQMAVF†	[Goulder (1996b), Hay(1999)]
	Rev	14–23	KAVRLIKFLY	[Addo(2001)]
	Nef	116–125	HTQGYFPDWQ†	[Culmann (1991)]
	Nef	120–128	YFPDWQNYT†	[Culmann (1991)]
B*5703 (B57)				
	p24	30–37	KAFSPEVI	[Goulder (2000b)]
	p24	30–40	KAFSPEVIPMF	[Goulder (2000b)]
B*5801 (B58)			12 C **A F** **T W** **S** K V I	[Barber (1997), Falk (1995a)]
	p24	108–117	TSTVEEQQIW	[Bertoletti (1998)]
	p24	108–117	TSTLQEQIGW	[Goulder (1996b)]
	Rev	14–23	KAVRLIKFLY	[Addo (2001)]
B*8101 (B81)				
	p24	48–56	TPQDLNTML	[Goulder (2000c)]

Table 1 (cont.) Best Defined HIV CTL Epitopes

HLA	Protein	AA	Sequence	Reference
C*0102 (Cw1)			23 C **A** **L** **L** P	[Barber (1997)]
	p24	36–43	VIPMFSAL	[Goulder (1997b)]
C*0401 (Cw4)			2 6 C **Y** **L** **P** **F** **F** **M** V I L	[Falk (1994)]
	gp160	375–383	SFNCGGEFF	[Wilson (1997), Johnson (1993)]
	p24	176–184	QASQEVKNW	[Buseyne (1997), Buseyne(1999)]
Cw*0501 (Cw5)				
	Rev	67–75	SAEPVPLQL	[Addo (2001)]
C*0802 (Cw8)				
	p24	48–56	TPQDLNTML	[Goulder (2000c)]
	Nef	82–91	KAAVDLSHFL	[Nixon (1999)]

* indicates personal communications in which truncation/titration data was provided

† subtype of B57 not determined

Primary anchors are bold faced, secondary anchors are not.

The amino acid position numbers are those of the analagous epitope in HXB2R our standard strain as used in other parts of this database.

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