HIV CTL Epitopes

PART I: HIV-1 CTL EPITOPES

SUMMARY

Part I includes tables, maps, and alignments of HIV-specific CTL epitopes arranged sequentially according to the location of the proteins in the HIV-1 genome. We attempted to make this section as comprehensive as possible, reflecting the latest data and insights. Bruce Walker in part IV. For a listing of SIV macaque epitopes, please see the summary by Todd Allen and David Watkins.

A. CTL EPITOPE TABLES

Each CTL reference has a six part basic entry:

• Location: The amino acid positions of the epitope coverage in the reference strain. The WEAU (GenBank Accession Number U21135) is used as a reference strain throughout this publication. The WEAU numbering is used in the protein maps in this database.

• Epitope: The amino acid sequence of the epitope of interest as defined in the reference, based on the reference strain used in the study defining the epitope. On rare occasions, when only the WEAU sequence is given, the sequence is taken from the WEAU database.

• Antigen: The antigenic stimulus of the CTL response.

• Species: The species responding and HLA of MHC specificity of the epitope.

• Reference: The primary reference (sometimes two or more directed towards the same or similar sequence)

The information is arranged in the order presented above following the WEAU numbering. When sequences are published in an overlapping format, the contributing references are provided following the reference format. The WEAU numbering is used in the protein maps in this database.

WEAU, 1.60, was chosen as the reference clone because it is one of the best characterized sequences currently available. The sequence was graciously provided prior to publication by George Shaw. The sequence was determined by looking up the reference strain and the numbered location, are followed by a question mark in the table.

• Antigen: The antigenic stimulus of the CTL response.

• Species: The species responding and HLA of MHC specificity of the epitope.

• Reference: The primary reference (sometimes two or more directed towards the same or similar sequence)
The alignments were modified in some cases to optimize the alignment relative sequence. Where alignments were optimized by sequence alignment, the sequence of the sequence used to create the alignment was compared to the published sequence in the HIV-1 genetic sequence database. All epitopes are aligned to the published sequence. The alignments were published in the HIV-1 protein N-terminal region.