II-1: HIV Helper T-Cell Epitopes

SUMMARY

Part II includes tables and maps of HIV-specific helper T-cell (Th) epitopes arranged sequentially according to the location of the proteins in the HIV-1 genome. We attempted to make this easy to use, to provide the experiential location of epitopes on a fixed protein, but are limited in our presentation of protein sequences of the WEAU clone 1.60. These maps are included in the presentation of the protein maps of the WEAU (U21135) strain, as are references through the publication. The WEAU strain was used as a reference strain throughout this publication.

A. TABLES:

Each Th epitope has a six-part basic entry:

- **Location:** The amino acid positions of the epitope boundaries and the reference sequence as given in the primary publication. Frequently, these positions as published are inaccurate. Therefore, we have included all human and primate Th epitopes defined to within 21 amino acids of the location and HLA restriction determination.

- **WEAU Location:** The viral strain WEAU (GenBank Accession Number U21135) is used as a reference strain throughout this publication. The position of the defined epitope location on the sequence of the WEAU protein is indicated. Obviously, WEAU may not be identical to a given region in the primary study, and so we simply indicate the location of the aligned positions. The WEAU numbering is used in the protein maps of this database. Nef in the WEAU cloned sequence has a frame shift, but the Nef reference protein sequence was completed past the frame shift, ensuring accurate position location was maintained.

- **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 amino acid sequence was written out in the original publication, and the sequences were numbered inaccurately by the primary authors, we may have misrepresented the epitope's amino acid sequence. Therefore, epitopes that were not explicitly written out in the text in the primary publication, those that we 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 Th response to the defined epitope.

- **Species (HLA):** The species responding and HLA specificity of the epitope.

- **Reference:** The primary reference.

Following each entry for a given Th epitope is a brief comment explaining the context of the study that defined or studied the epitope. If the same epitope was studied in several labs, each study is cited in its own entry.

B. HIV PROTEIN EPITOPE MAPS:

All human and primate Th epitopes defined to within 21 amino acids or less are included on the HIV protein epitope maps. HLA restriction information is included when known.

The location and HLA restriction location are indicated on protein sequences of the WEAU clone 1.60. These maps are used to provide the experiential location of epitopes on a fixed protein, but are limited in their presentation of protein sequences of the WEAU clone 1.60. These maps are included in the presentation of the protein maps of this database. Nef in the WEAU cloned sequence has a frame shift, but the Nef reference protein sequence was completed past the frame shift, ensuring accurate position location was maintained.

Epitopes are numbered, and the numbering on this map is used to reference the corresponding epitope sequence alignments. The WEAU sequence is described on page I-1.

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Epitopes are numbered, and the numbering on this map is used to reference the corresponding epitope sequence alignments. The WEAU sequence is described on page I-1.
Because of space limitations, alignments that correspond to the epitopes are only available from the web site, not in the hard copy of the compendium. All epitope alignments were created are available at the 1998 web site protein alignments (http://hiv-web.lanl.gov/ALIGN-98/ALIGN-INDEX-98.html), and we restricted ourselves to full gene region sequences for these alignments, excluding short fragments of sequences. The subtype designation and the country of isolation are indicated along with the common name of the sequence. Stop codons are indicated with a $, and frameshifts by a #; they are inserted to maintain the alignments.

C. REFERENCES AND NOTES