New Computational Tools at Los Alamos HIV Immunology Database (www.hiv.lanl.gov)

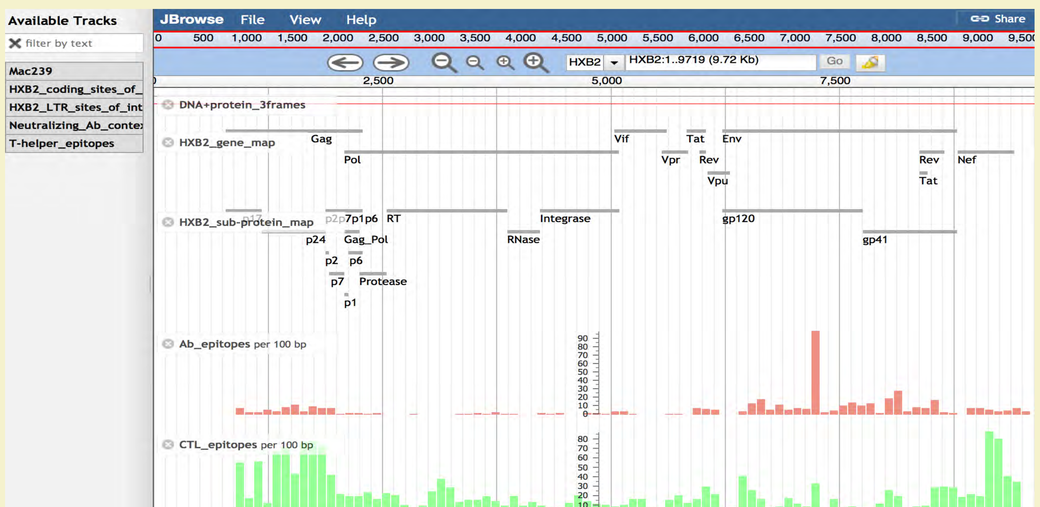
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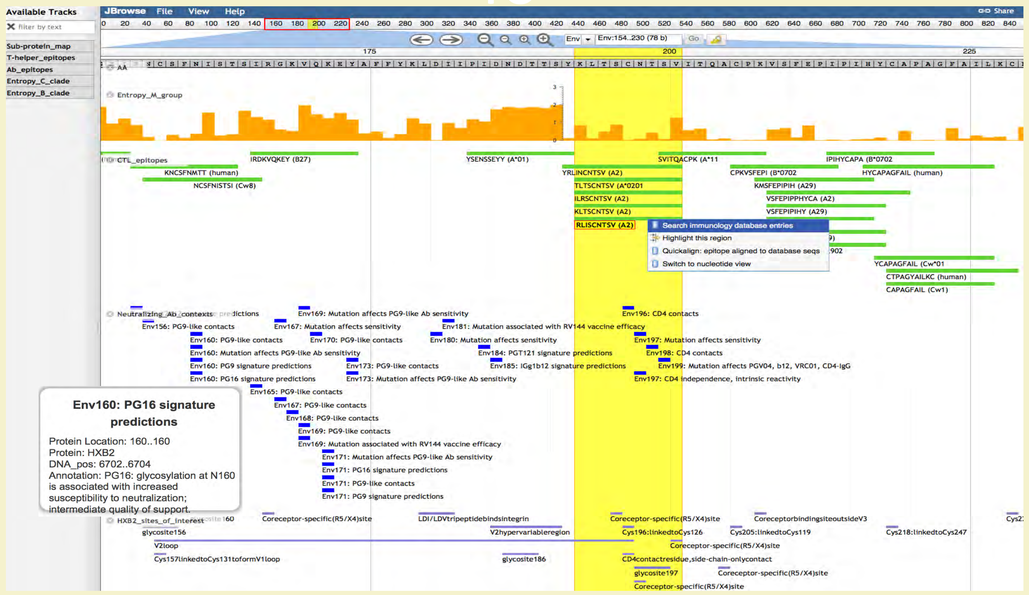
BACKGROUND: Los Alamos HIV immunology database is an annotated, searchable inventory of more than 17,000 of entries of HIV-1 cytotoxic and helper T-cell epitopes and antibody binding sites, integrated with the sequence variability data from the HIV Sequence Database. The database is extensively used and is being cited in majority of publications on HIV. We strive to provide latest information, summaries and tools for the HIV field, and considering the explosion of HIV antibody research in the recent years, 2 global and useful computational tools have been recently added to the database to assist the researchers.

HIV Genome Browser: HIV Genome Browser retrieves and summarizes the vast and diverse information and tools available at HIV Immunology database. The browser allows to look at the whole HIV genome and to zoom in to every HIV region of interest and see main information we have in the database about this position (epitopes, antibody binding sites, antibody contact residues, functional domains, sequence variability, alignments etc). This tool also provides links to the database annotation, database tools, pubmed etc. This tool is a one-stop source of information about HIV genome and immunological data and will be useful for scientific community and for vaccine design efforts.

HIV Genome Browser: Nucleotide view



HIV Genome Browser: Protein view



HIV genome browser combines:

- HXB2 gene map, HXB2 sub-protein map, Mac239 map, overlapping epitopes, antibody binding sites
  - HXB2 coding sites of interest (e.g. functional domains, drug resistance sites, motifs, glycosylation sites, etc.)
  - HXB2 LTR sites of interest (RNA structural elements, primer binding sites, etc.)
  - Neutralizing Ab contact residues, signatures and other NAb-associated features
  - HIV sequence variability (Entropy: M group, B clade, C clade)
  - Links to the database annotation, alignments, tools, Pubmed etc.

CATNAP (Compile, Analyze and Tally NAb Panels): CATNAP was Inspired by Anthony West (*West et al, PNAS 2013*) and includes the initial data he collected from published sources, augmented my extensive additional data collected by the HIV Database staff.

CATNAP is a relational database of HIV sequences, antibodies and neutralization data from multiple recent neutralization studies, coupled with analysis tools. This tool allows for a meta-analysis of multiple neutralization studies to potentially search for antibody neutralization signatures and sites of vulnerability. In addition, most large neutralization studies studies do not supply sufficient HIV sequence information (large Env panels are published without accession numbers, with a huge discrepancy in sequence names), making subsequent signature analysis of even one study difficult, let alone multiple studies. CATNAP provides an easy one-to-one correspondence between the various short names, database names and accession numbers, simplifying analysis for meta-studies.



CATNAP: Theoretical approximation …
By Peter Hraber

CATNAP: IC_{50}/HIV-1 alignment



CATNAP combines:

- Env sequence data superimposed with IC50 or IC80 values
- Antibody potency and breadth summarized over multiple studies
- Alignments and virus details
- Antibody details

CATNAP analysis options for the chosen HXB2 alignment position:

- AA composition, N-glycosylation sites, basic statistics
- What is known about this position in terms of entropy, functional domain, neutralizing antibody contexts, Ab contacts and signatures