

Resource Summary Report

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HIV Molecular Immunology Database

RRID:SCR_002893

Type: Tool

Proper Citation

HIV Molecular Immunology Database (RRID:SCR_002893)

Resource Information

URL: <http://www.hiv.lanl.gov/content/immunology/index>

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Description: An annotated, searchable collection of HIV-1 cytotoxic and helper T-cell epitopes and antibody binding sites, plus related tools and information. The goal of this database is to provide a comprehensive listing of defined HIV epitopes. These data are also printed in the HIV Molecular Immunology compendium, which is updated yearly and provided free of charge to scientific researchers, both by online download and as a printed copy. The data included in this database are extracted from the HIV immunology literature. HIV-specific B-cell and T-cell responses are summarized and annotated. Immunological responses are divided into three sections, CTL (CD8+), T helper (CD4+), and antibody. Within these sections, defined epitopes are organized by protein and binding sites within each protein, moving from left to right through the coding regions spanning the HIV genome. We include human responses to natural HIV infections, as well as vaccine studies in a range of animal models and human trials. Responses that are not specifically defined, such as responses to whole proteins or monoclonal antibody responses to discontinuous epitopes, are summarized at the end of each protein sub-section. Studies describing general HIV responses to the virus, but not to any specific protein, are included at the end of each section. The annotation includes information such as cross-reactivity, escape mutations, antibody sequence, TCR usage, functional domains that overlap with an epitope, immune response associations with rates of progression and therapy, and how specific epitopes were experimentally defined. Basic information such as HLA specificities for T-cell epitopes, isotypes of monoclonal antibodies, and epitope sequences are included whenever possible. All studies that we can find that incorporate the use of a specific monoclonal antibody are included in the entry for that antibody. A single T-cell epitope can have multiple entries, generally one entry per study. Finally, tables and maps of all defined linear epitopes relative to the HXB2 reference proteins are provided. Alignments of CTL, helper T-cell, and antibody epitopes are available through the search interfaces. Only responses to HIV-1 and HIV-2 are included in the database.

Abbreviations: HIV Molecular Immunology Database

Synonyms: Human Immunodeficiency Virus Molecular Immunology Database

Resource Type: data or information resource, database

Keywords: cytotoxic t cell, cytotoxic t lymphocyte, helper t-cell, antibody, binding site, epitope, t cell epitope, human immunodeficiency virus, immunology, molecule, genome, protein, alignment, b-cell, t-cell, annotation, ctl, t helper, coding region, cross-reactivity, escape mutation, antibody sequence, tcr usage, functional domain, immune response, progression, therapy

Related Condition: Human immunodeficiency virus

Funding: NIAID

Resource Name: HIV Molecular Immunology Database

Resource ID: SCR_002893

Alternate IDs: nif-0000-02965

Old URLs: <http://hiv-web.lanl.gov/immunology/>

Record Creation Time: 20220129T080216+0000

Record Last Update: 20260729T044041+0000

Ratings and Alerts

No rating or validation information has been found for HIV Molecular Immunology Database.

No alerts have been found for HIV Molecular Immunology Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at [nidm-terms](#) .

Sun P, et al. (2013) Bioinformatics resources and tools for conformational B-cell epitope prediction. Computational and mathematical methods in medicine, 2013, 943636.

Charoentong P, et al. (2012) Bioinformatics for cancer immunology and immunotherapy. Cancer immunology, immunotherapy : CII, 61(11), 1885.