The HIV Immunology Database
- Los Alamos National Laboratory

IEDB User Workshop – 2021

(virtual)

LA-UR-21-30653

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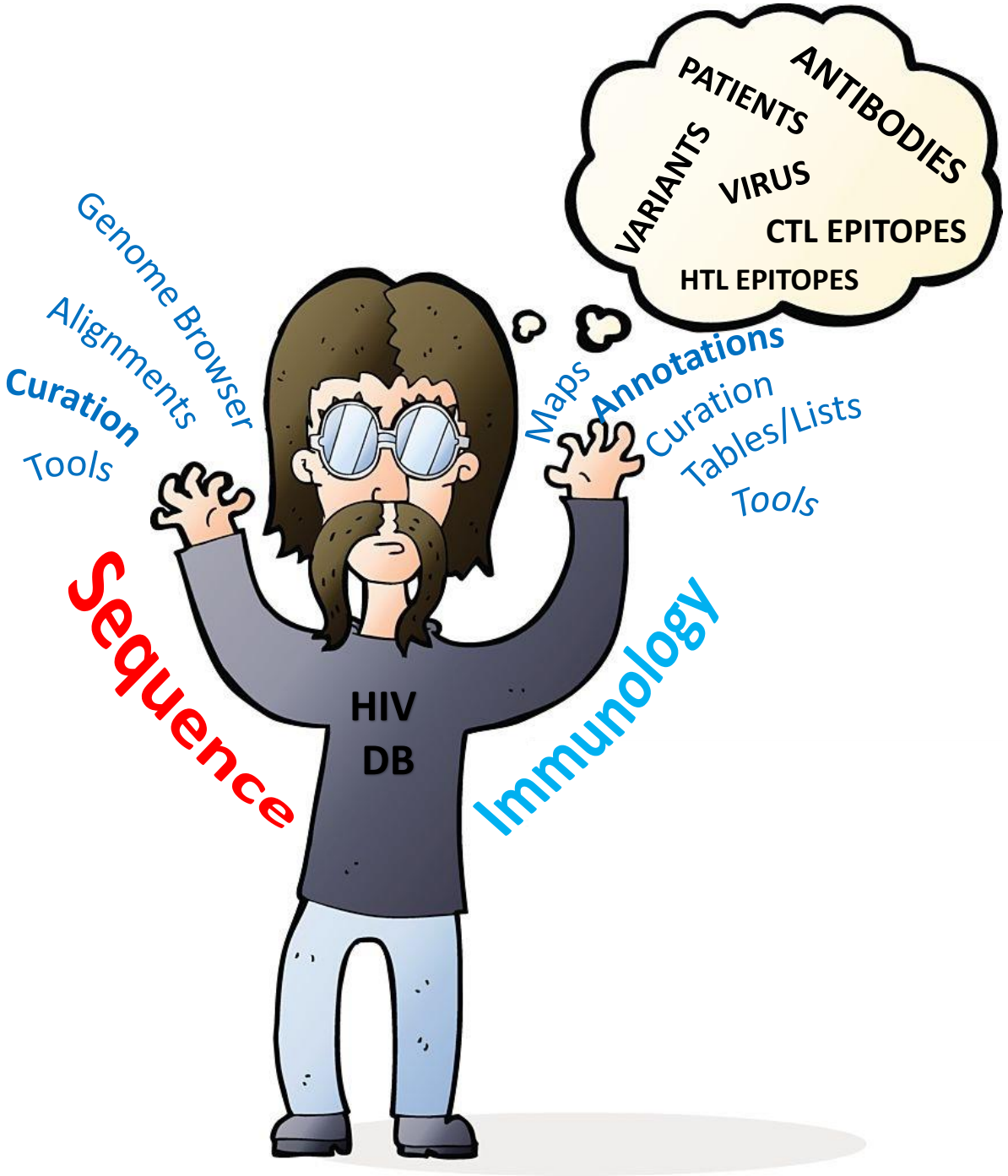

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www.hiv.lanl.gov

Presenters: Brian Foley, Elizabeth-Sharon Fung

Database PI:
Brian Foley

Additional database staff:
Werner Abfalterer, Katie Belobrajdic, Kumkum Ganguly, Jennifer Macke, Elena Romero, James Szinger, Hyejin Yoon

Contract Officer Representative: Anjali Singh, NIAID, NIH

Theoretical Biology and Biophysics, T-6
Los Alamos National Laboratory

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IN MEMORY:

Karina Yusim : former PI and architect of the Immunology DB

New compendium and updated A-list (CTL epitopes) dedicated to her memory

Los Alamos HIV Databases – www.hiv.lanl.gov/

The 2021 update includes all sequences through Dec 2020

- HIV Immunology Database: Searchable annotated T cell epitopes and Antibody entries

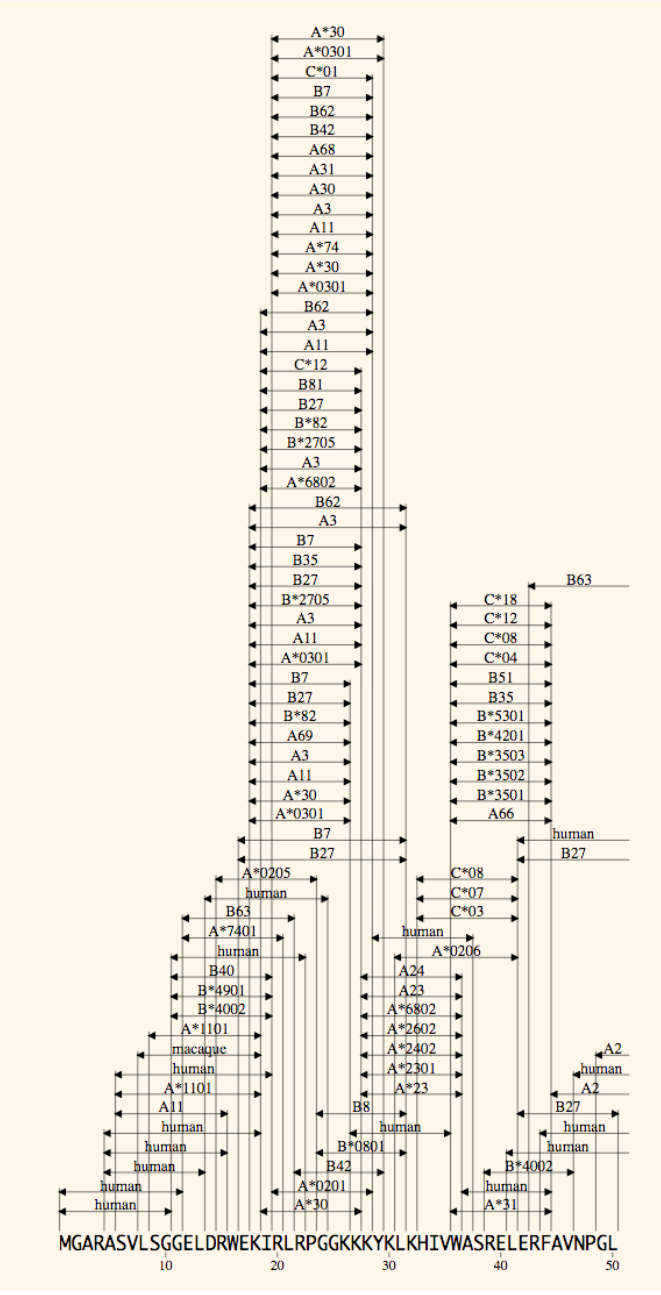
Database	# Entries	# Papers
CD8+ Epitope	11,138	1,407
CD4+ Epitope	1,656	393
Antibody	3,586	2,220

- Neutralization data accessible through CATNAP for
  - 470 Abs,
  - 40 antibody mixtures
  - 20 polyclonal sera,
  - 1,191 pseudoviruses tested, including 1,170 with sequences

- 69 bioinformatics tools with simple web interfaces

- Links to external tools, including IEDB's
  - Tools split ~ 1/3rd between HIV-specific and 2/3rds general-use

- HIV Sequence Database: Over 955,845 searchable annotated HIV/SIV sequences total.
  - Stored metadata enables us to provide custom made alignments or pre-made 1-sequence-per-person alignments.



Databases' Statistics (continued) –

The 2021 update includes all sequences through Dec 2020

- HIV Immunology Database: Searchable annotated T cell epitopes and Antibody entries
  - 11, 138 CD8+ epitope entries from 1, 407 papers
  - 1,656 CD4+ epitope entries from 393 papers
  - 3,586 Antibody entries from 2,220 papers
  - Neutralization data accessible through CATNAP
    - For 470 Abs, 40 antibody mixtures, and 20 polyclonal sera, 1,191 pseudoviruses tested, including 1,170 with sequences

- 69 bioinformatics tools with simple web interfaces

- Links to external tools, including IEDB's
  - Tools split ~ 1/3rd between HIV-specific and 2/3rds general-use

- HIV Sequence Database: Over 955,845 searchable annotated HIV/SIV sequences total.

  - Stored metadata enables us to provide custom made alignments or pre-made 1-sequence-per-person alignments.

In addition to Annotations, tools and maps, and Compendia,
UPGRADES to
Immunology Database include:

Patient Data expanded and searchable

JSON and CSV Download

HLA Nomenclature updated

A^+-list (CTL epitopes) Upgrade, soon to be published at hiv.lanl.gov

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Integration of HIV Sequence and Immunology databases

- Los Alamos HIV Database: the first pathogen-specific database
  - HIV Sequence Database – founded in 1986 by G. Myers
  - HIV Immunology Database – founded in 1994 by B. Korber

- Integration of HIV sequence and immunological data via multiple tools, for example:

  - HIV Genome Browser provides an interactive detailed view of the HIV genome or proteome with HIV sequence variability, functional domains and antibody and T cell epitopes marked by genome position
  - AnalyzeAlign, Quick Align, Motif Search show the diversity and HIV variability of epitopes

  - CATNAP superimposes Ab neutralization data on virus data, and has links to structures, germline V/D/J genes, Ab sequences, Ab contact residues, Env alignments, positions associated with neutralization sensitivity …
  - Multiple tools tap into the Donors (or Patient) Data, containing available donor HIV sequences, Ab sequences, monoclonal and polyclonal Ab data, HLAs, and T-cell epitopes

Beyond HIV

- **Twenty two of our computational tools (32%) are strictly HIV-specific.**
  The remaining 68% are partially or fully *applicable to other organisms*

- A striking example of successful extension beyond HIV is Mosaic/Epigraph vaccine design:
  - Rabies in bats (Stading *et al*, Plos Negl Trop Dis, 2017)
  - Filoviruses (Theiler *et al*, Sci Rep. 2016, Fenimore, PLoS One, 2012)
  - Chlamydia trachomatis (Badamchi-Zadeh *et al*, Front Immunol, 2016)
  - Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) in pigs (Cui *et al*, Vaccine reports, 2016)
  - Hepatitis C (Yusim *et al*, Clin Vaccine Immunol, 2013)
  - Foot-and-Mouth Disease in livestock (Devendra *et al*, in preparation)
  - Hepatitis B (Yusim *et al*, in preparation)
  - **... and the HIV-1 mosaic designs moved into Phase III human trials**

Beyond HIV (continued) …

- The database structure and tools are transferrable to other pathogens.

We have created several pathogen databases prototyped on the HIV database, with multiple tools being tailored to those databases: (***https://www.hiv.lanl.gov/content/otherviruses.html***):

- **COVID-19 Genome Analysis Pipeline** *
- HCV Sequence (Kuiken et al, Nucleic Acid Res, 2008) and Immunology (Yusim et al, Appl Bioinformatics, 2005) Databases
- Hemorrhagic Fever Viruses (HFV) Sequence Database (80 viral species, found in 10 different genera comprising five different families: arena-, bunya-, flavi-, filo- and togaviridae) (Kuiken et al, Nucleic Acid Res, 2012)
- Filovirus Sequence and Immunology Database (Yusim et al, Database, 2016) (hfv.lanl.gov)

Because of a lack of individual funding, only the sequence portions of these latter databases are automatically updated

immuno@lanl.gov

seq-info@lanl.gov

www.hiv.lanl.gov/

HIV DATABASES

The **HIV databases** contain comprehensive data on HIV genetic sequences and immunological epitopes. The website also gives access to a large number of tools that can be used to analyze and visualize these data. This project has been funded in whole or in part with Federal funds from the National Institute of Allergy and Infectious Diseases, National Institutes of Health, Department of Health and Human Services, under Interagency Agreement No. AAI12007-001-00000. Our content is reviewed by an Editorial Board.

SEQUENCE DATABASE ▸ IMMUNOLOGY DATABASE ▸

OTHER VIRUSES ▸

News: Archived News ▸

Variant Visualizer
Variant Visualizer is a new tool that provides new options and output styles for visualizing variants in an alignment of nucleotide or protein sequences. The tool is similar to Highlighter, but the Variant Visualizer has more options for refining the graphical output. The output can be refined interactively without rerunning the tool. *21 July 2021*

Questions or comments? Contact us at seq-info@lanl.gov

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Databases Search Tools Products Publications search site Search Site

HIV Molecular Immunology Database

The HIV Molecular Immunology Database is an annotated, searchable collection of HIV-1 cytotoxic and helper T-cell epitopes and antibody binding sites.

Search Interfaces

- CTL/CD8+ search
- T Helper/CD4+ search
- Antibody search
- CTL variant search
- T Helper variant search
- Patient search

- Search help
- Variant search help

- JSON API for search

Database Products

- All Database products and publications
- Epitope maps
- Epitope tables
- Epitope alignments
- Epitope density plots
- T cell epitope variants and escape mutations
- Neutralizing antibody resources & CATNAP
- The HIV Molecular Immunology Compendium
- About the HIV Molecular Immunology Database
- How to cite this database
- Frequently-asked Questions (FAQ)

Tools and Data Sets

- Tools & Links for immunologists
- SIV Epitopes (PDF) review article summarizing known SIV epitopes
- Identifying HLA-Associated Polymorphisms in HIV-1 (PDF) review article summarizing HIV polymorphism associated with escape mutations. Also a table of polymorphisms.
- HLATEM HLA Typing and Epitope Mapping Data Sets
- Standardized Assessments of Neutralizing Antibodies for HIV/AIDS Vaccine Development Assay protocols from Duke Central Reference Laboratory

News

News Archive

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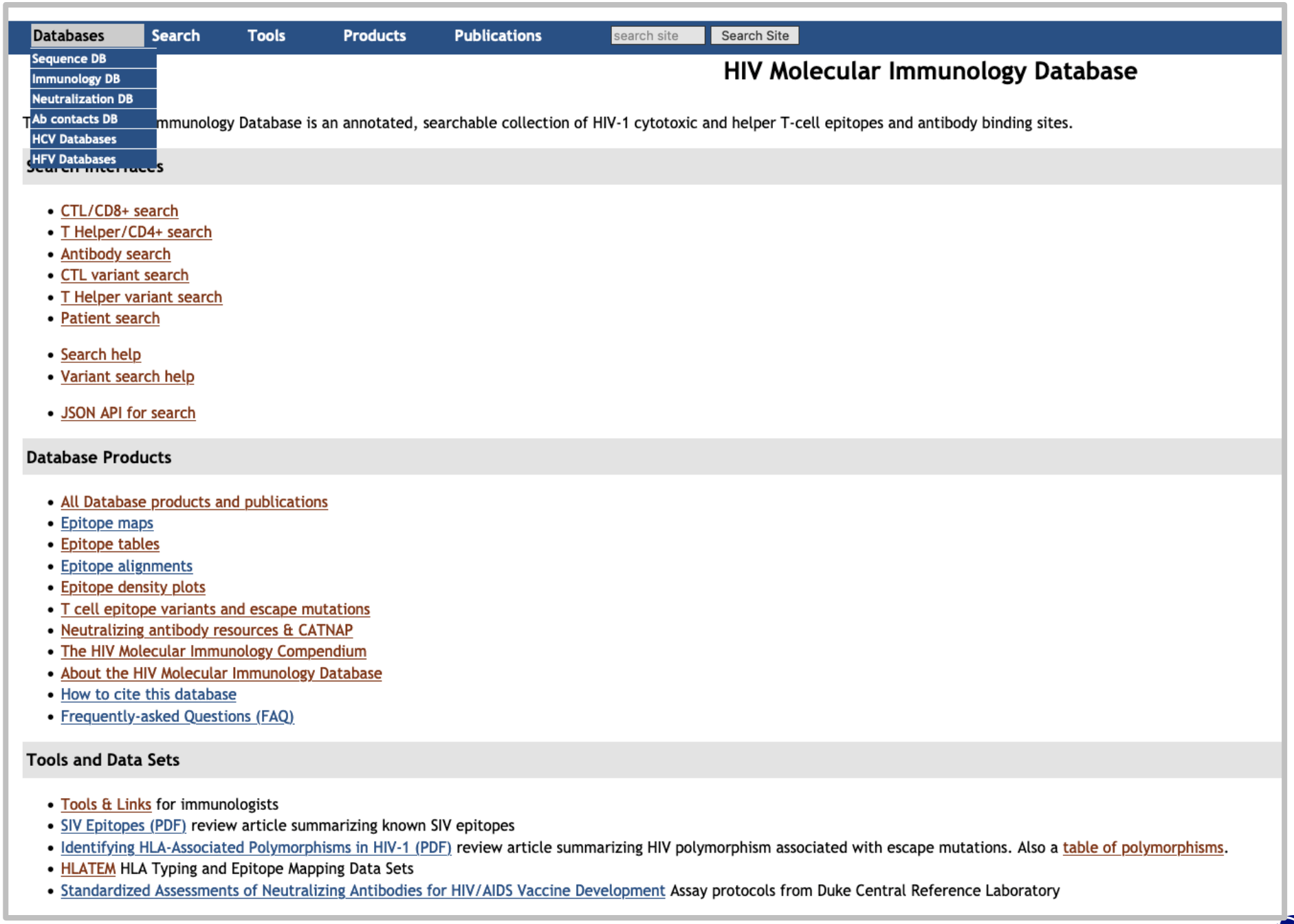

https://www.hiv.lanl.gov/content/immunology/index.html

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Databases Search Tools Products Publications search site Search Site

Search CTL/CD8+ T-Cell Epitope Database

HIV protein	- ALL - Gag p17 p24 p2p7p1p6	
HXB2 protein location	–	Results contained within query location
HXB2 DNA location	–	Results overlap with query location
Epitope	SLYNTVATL	Results contain query sequence
Epitope name		
Record number		
Subtype	- ALL -	
Immunogen	- ALL - computer prediction engineered HIV-1 and HCV co-infection HIV-1 exposed seronegative HIV-1 infected monocyte-derived HIV-1 infection	
Vaccine details if Immunogen is Vaccine	Vaccine type: - ALL - Vaccine strain: - ALL - Vaccine component: - ALL - Adjuvant: - ALL -	
Species	- ALL -	
MHC/HLA	- ALL - A*01 A*01:01 A*01:23 A*02 A*02:01 A*02:02	
Author		First Last
Country	- ALL -	
Keywords	early-expressed proteins early treatment elite controllers enhancing activity epitope processing escape genital and mucosal immunity	
Note		

Search Reset Click for Search Help

Search CTL/CD8+ variants

https://www.hiv.lanl.gov/content/immunology/ctl_search.html

HIV molecular immunology database

Databases Search Tools Products Publications search site Search Site

Search CTL/CD8+ T-Cell Epitope Database

Found 301 matching records:

Displaying record number 57

Download this epitope record as JSON.

HXB2 Location	Gag(69-93) p17(69-93) DNA(994..1068)	Gag Epitope Map
Author Location	p17(69-93 BH10)	
Epitope	QTGSEELRSLYNTVATLYCVHQRIE	Epitope Alignment
Species (MHC/HLA)	human(A2)	
Immunogen	HIV-1 infection	
Experimental methods		
Keywords		

Notes

- Gag CTL response studied in three individuals.

References

Johnson1991 R. P. Johnson, A. Trocha, L. Yang, G. P. Mazzara, D. L. Panicali, T. M. Buchanan, and B. D. Walker. HIV-1 Gag-Specific Cytotoxic T Lymphocytes Recognize Multiple Highly Conserved Epitopes. Fine Specificity of the Gag-Specific Response Defined by Using Unstimulated Peripheral Blood Mononuclear Cells and Cloned Effector Cells. *J. Immunol.*, 147:1512-1521, 1991. This study presented a detailed study of gag-specific CTL from HIV-1 seropositive individuals. Seven p24 and two p17 epitopes were described, that were recognized by class I-restricted CD3+CD8+ CTL. p17 epitopes: KIRLRPGGKKKYKLKHIVWASRELE and QTGSEELRSLYNTVATLYCVHQRIE; p24 epitopes: NPPIPVGEIYKRWIILGLNKIV, VHQAISPRTLNAWVKVVEEKAF, NAWVKVVEEKAFSPEVIPMFSA, SALSEGATPQDLNTMLNTVGGH, GHQAAMQMLKETINEEAAEWDR, and RAEQASQEVK. PubMed ID: 1715361. Show all entries for this paper.

Displaying record number 58923

Download this epitope record as JSON.

HXB2 Location	Gag(70-86) p17(70-86) DNA(997..1047)	Gag Epitope Map
Author Location	Gag(70-)	
Epitope	TGTEELRSLYNTVATLY	Epitope Alignment

Databases | Search | Tools | Products | Publications | search site | Search Site

Search CTL/CD8+ T-Cell Epitope

HIV protein	- ALL - Gag p17 p24 p2p7p1p6	
HXB2 protein location	—	Results contained within query location
HXB2 DNA location	—	Results overlap with query location
Epitope	SLYNTVATL	Results contain query sequence
Epitope name		
Record number		
Subtype	- ALL -	
Immunogen	- ALL - computer prediction engineered HIV-1 and HCV co-infection HIV-1 exposed seronegative HIV-1 infected monocyte-derived HIV-1 infection	
Vaccine details if Immunogen is Vaccine	Vaccine type: - ALL - Vaccine strain: - ALL - Vaccine component: - ALL - Adjuvant: - ALL -	
Species	- ALL -	
MHC/HLA	- ALL - A*01 A*01:01 A*01:23 A*02 A*02:01 A*02:02	
Author		First Last
Country	- ALL -	
Keywords	mother-to-infant transmission mutation acquisition naive T cells Nef-mediated down-regulation neutralization by CTL NK cells non-susceptible form	
Note		

Search | Reset | Click for Search Help

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Search CTL/CD8+ T-Cell Epitope Database

Found 5 matching records:

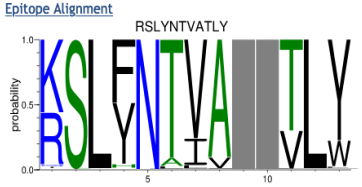
Displaying record number 62248

Download this epitope record as JSON.

HXB2 Location	Gag(76-86) p17(76-86) DNA(805..834)
Author Location	Gag(76-86)
Epitope	RSLYNTVATLY
Epitope Name	Gag-RY11
Subtype	C
Species (MHC/HLA)	human(A*30)
Immunogen	HIV-1 infection
Patient MHC/HLA	517-C: A*30:02, A*68:02, B*15:10, B*42:01, C*03:04, C*17:01; 517-M: A*30:02, A*30:04, B*42:01, B*58:02, C*06:02, C*17:01
Country	South Africa
Experimental methods	CD8 T-cell Elispot - IFN, Other
Keywords	responses in children, mother-to-infant transmission, rate of progression, escape

Gag Epitope Map

Epitope Alignment



Show epitope variants

Notes

- 11 perinatally infected pediatric slow progressors (PSPs) were followed longitudinally for a decade from birth to examine CTL responses to circulating and autologous HIV. It was found by ultra-deep sequencing that though, li develop variants early in infection; unlike adults, pediatric anti-variant CTL are generated

https://www.hiv.lanl.gov/content/immunology/ctl_search.html

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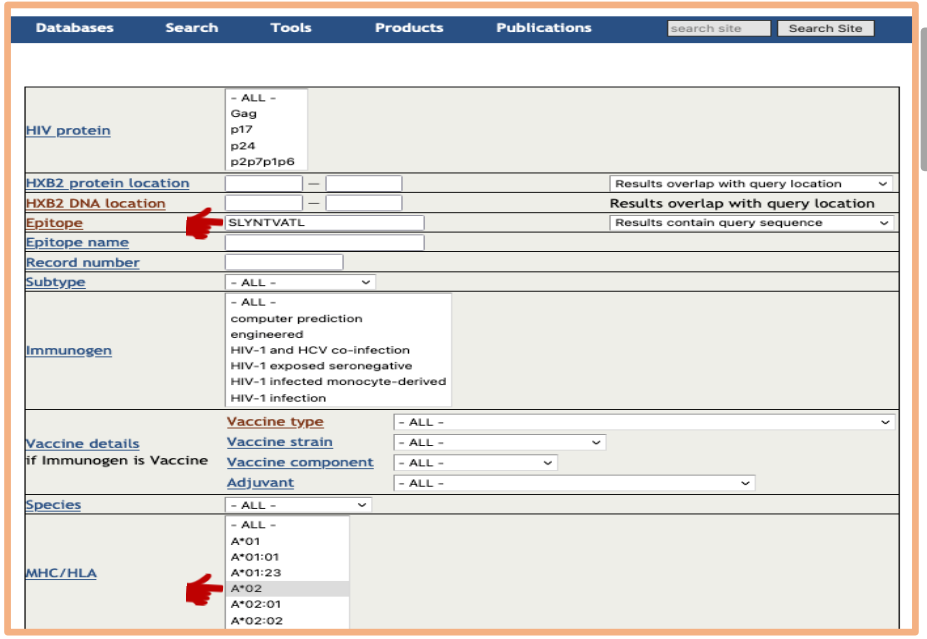
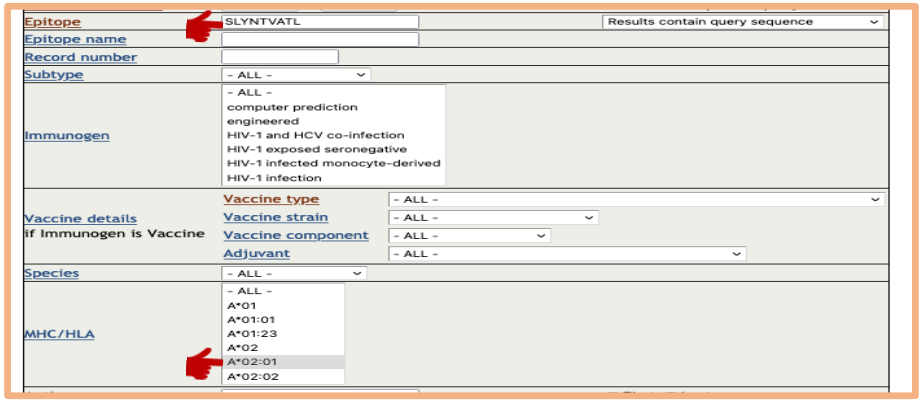
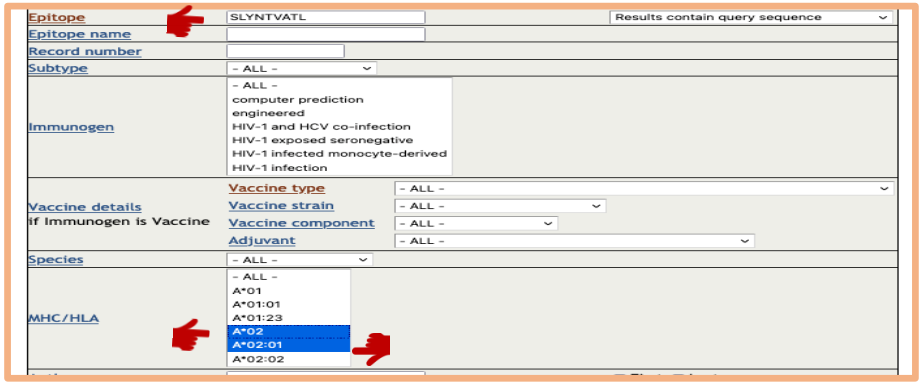
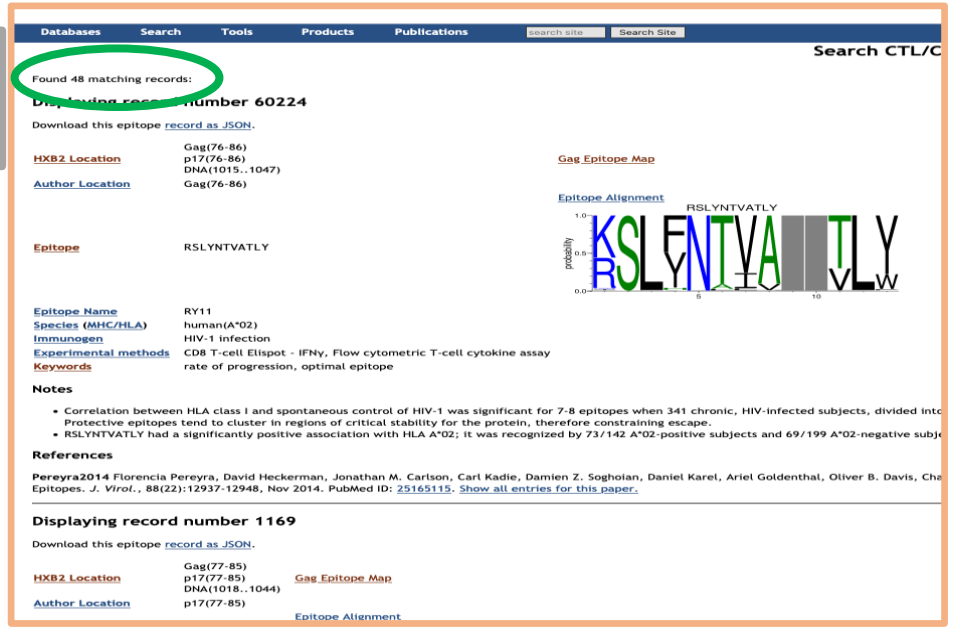
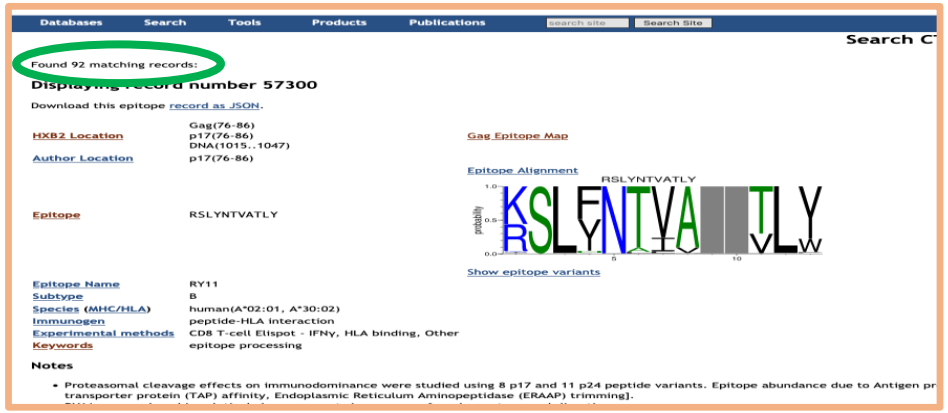
CUMULATIVE CTL SEARCHES











SLYNTVATL + A*02

48 records

SLYNTVATL + A*02:01

92 records

SLYNTVATL + (A*02+A*02:01)

140 records

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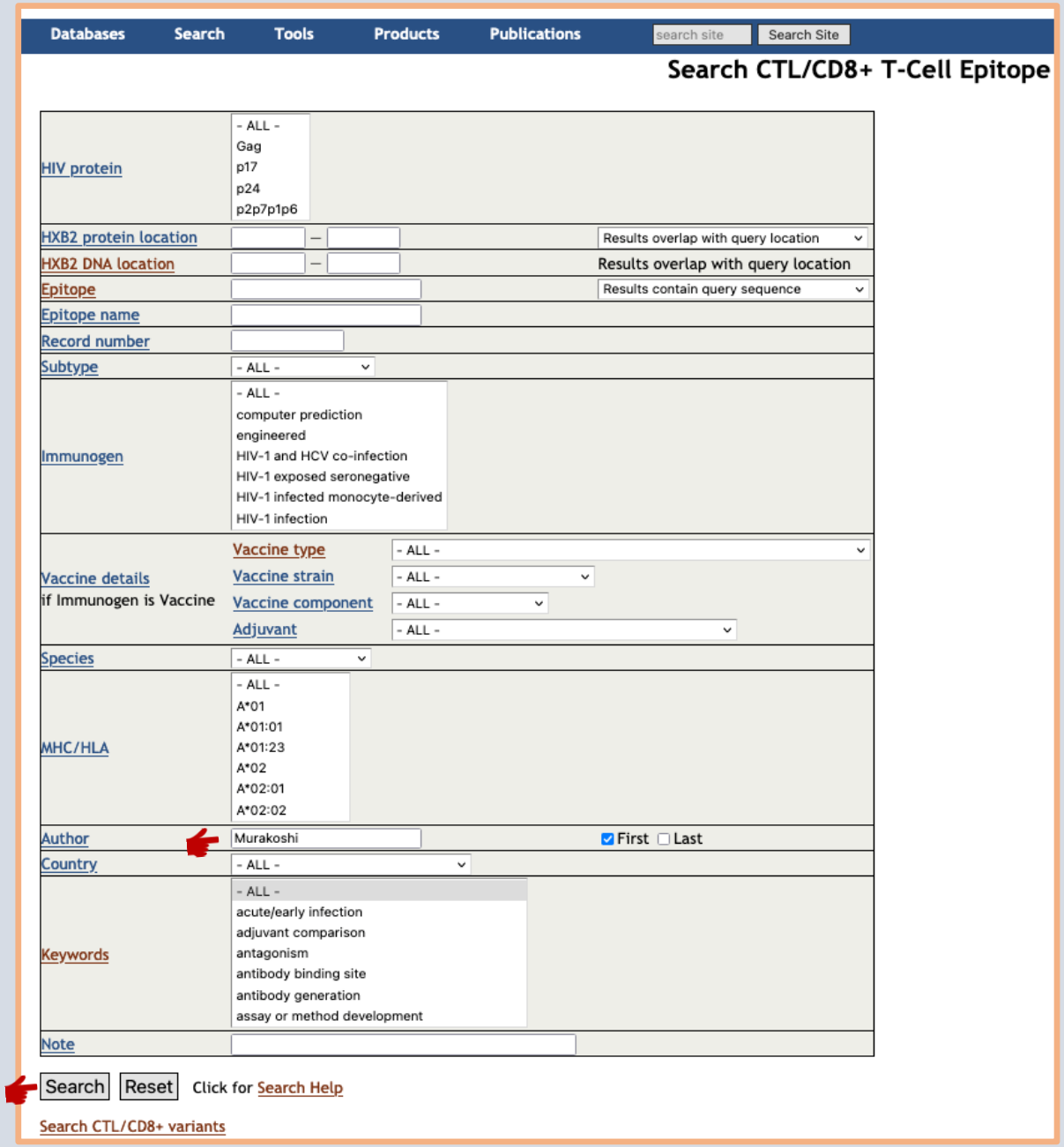
The next few slides show how to make full use of a simple epitope DB search

CTL Search on an Author of Interest

https://www.hiv.lanl.gov/content/immunology/ctl_search.html



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Search CTL/CD8+ T-Cell Epitope Database

Found 73 matching records:

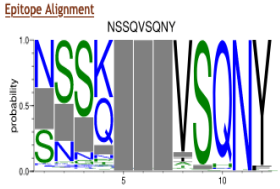
Displaying record number 61877

Download this epitope record as JSON.

HXB2 Location	Gag(124-132) p17(124-132) DNA(1159..1185)
Author Location	Gag(124-132)
Epitope	NSSQVSQNY

Gag Epitope Map

Epitope Alignment



Show epitope variants

Epitope Name	NY9, p17NY9
Subtype	B
Species (MHC/HLA)	human(B*35:01)
Immunogen	HIV-1 infection
Country	Japan
Experimental methods	CD8 T-cell Elispot - IFNγ, CTL suppression of replication, Intracellular cytokine staining, Tetramer binding
Keywords	escape, HLA associated polymorphism

Notes

- HLA-B*3501 is known to be a detrimental allele associated with rapid progression to AIDS. CTL responses to 16 known HLA-B*3501-restricted epitopes however, were studied in 63 B*3501+ ART-naive Japanese subjects, to find B*3501-epitope-specific CTLs which can suppress HIV-1 replication. The effect of viral protective-epitope mutations associated with B*3501 were also investigated and so one mechanism of the detrimental effect of HLA-B*3501 was clarified: the Y135F mutation within NefYF9, which is selected by HLA-A*2402-restricted CTL, impairs the ability of YF9-specific CTL to suppress HIV replication both in vivo and in vitro.
- Gag epitope NSSQVSQNY (NY9) elicited CTL response in 6/63 HLA-B*3501+ HIV-1-infected ART naive Japanese subjects, and a significant association was found with suppression of pVL (plasma viral load).
- The HLA-A*2402-associated polymorphism NefY135F which is seen in epitope YF9, fPLTFGWCF accumulates in B*3501+ Japanese individuals to 61% and is strongly associated with lower pVL and NY9-specific CTL responses. Thus NY9-specific CTL can suppress the replication of the Y135F mutant virus.

References

Murakoshi2018a Hayato Murakoshi, Madoka Koyanagi, Tomohiro Akahoshi, Takayuki Chikata, Nozomi Kuse, Hiroyuki Gatanaga, Sarah L. Rowland-Jones, Shinichi Oka, and Masafumi Takiguchi. Impact of a Single HLA-A*24:02-Associated Escape Mutation on the Detrimental Effect of HLA-B*35:01 in HIV-1 Control. *EBioMedicine*, 36:103-112, Oct 2018. PubMed ID: 30249546. Show all entries for this paper.

RESULT of AUTHOR SEARCH in CTL Epitope DB (72 records)

scrolling down …

- B*5201-restricted protective epitope, SQYALGII, Gag SI8 was found in 92.7% chronically infected Japanese individuals and 91.3% of them who were B*5201+. Variants of this WT epitope were found too, SQYALGII, SI8-8L and SQYAIGII, SI8-5I. SI8-8L and SI8-5I were cross-recognized by SI8-specific CTL.

References

Murakoshi2019 Hayato Murakoshi, Nozomi Kuse, Tomohiro Akahoshi, Yu Zhang, Takayuki Chikata, Mohamed Ali Borghan, Hiroyuki Gatanaga, Shinichi Oka, Keiko Sakai, and Masafumi Takiguchi. Broad Recognition of Circulating HIV-1 by HIV-1-Specific Cytotoxic T-Lymphocytes with Strong Ability to Suppress HIV-1 Replication. *J. Virol.*, 93(1), 1 Jan 2019. PubMed ID: 30333175. Show all entries for this paper.

Displaying record number 62508

Download this epitope record as JSON.

HXB2 Location	Pol(709-717) RT(554)-Integrase(2)
Author Location	Pol(653-661)
Epitope	SGIRKVLFL

Pol Epitope Map

Epitope Alignment

Show epitope variants

Epitope Name	SL9, Pol SL9
Subtype	CRF01_AE
Species (MHC/HLA)	human(C*15:05)
Immunogen	HIV-1 infection
Patient MHC/HLA	VI-479: A*29:01, B*07:05, C*15:05; VI-003: ; VI-114: ; VI-231:
Country	Viet Nam
Experimental methods	CD8 T-cell Elispot - IFNγ, Intracellular cytokine staining, Other
Keywords	rate of progression, escape, novel epitope, chronic infection

Notes

- The detrimental haplotype A*29:01-B*07:05-C*15:05 is associated with 9 Pol and 3 Nef mutations, 2 of which are within a novel epitope described here, C*15:05-SGIRKVLFL (found within 17-mer peptide, Pol 17-118, VDKLVSSGIRKVLFLDG). Studies were performed in VI-479, a chronic HIV-patient homozygous for the detrimental haplotype.
- Three major mutations were found in Pol SL9 - S653A and S653T which increased pVL significantly as well as reduced CD4+ counts, and S653L which trended in the same direction.

References

Murakoshi2021 Hayato Murakoshi, Takayuki Chikata, Tomohiro Akahoshi, Chengcheng Zou, Mohamed Ali Borghan, Giang Van Tran, Trung Vu Nguyen, Kinh Van Nguyen, Nozomi Kuse, and Masafumi Takiguchi. Critical effect of Pol escape mutations associated with detrimental allele HLA-C*15: 05 on clinical outcome in HIV-1 subtype A/E infection. *AIDS*, 35(1):33-43 doi, Jan 2021. PubMed ID: 33031103 Show all entries for this paper.

choose the record from paper Murakoshi2021

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One of the searched Murakoshi records, Record# 62508 from Murakoshi2021

- B*5201-restricted protective epitope, SQYALGII, Gag SI8 was found in 92.7% chronically infected Japanese individuals and 91.3% of them who were B*5201+. Variants of this WT epitope were found too, SQYALGII, SI8-8L and SQYAiGII, SI8-5I. SI8-8L and SI8-5I were cross-recognized by SI8-specific CTL.

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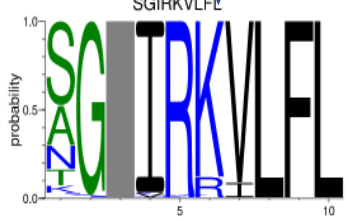
Author Location	Pol(653-661)
Epitope	SGIRKVLFL
Epitope Name	SL9, Pol SL9
Subtype	CRF01_AE
Species (MHC/HLA)	human(C*15:05)
Immunogen	HIV-1 infection
Patient MHC/HLA	VI-479: A*29:01, B*07:05, C*15:05; VI-003: ; VI-114: ; VI-231:
Country	Viet Nam
Experimental methods	CD8 T-cell Elispot - IFNγ, Intracellular cytokine staining, Other
Keywords	rate of progression, escape, novel epitope, chronic infection

Pol Epitope Map

Epitope Alignment



Show epitope variants

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Pol CTL/CD8+ Epitope Map

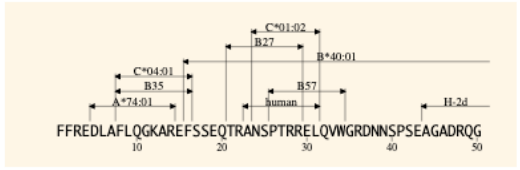
Interactive Epitope Maps

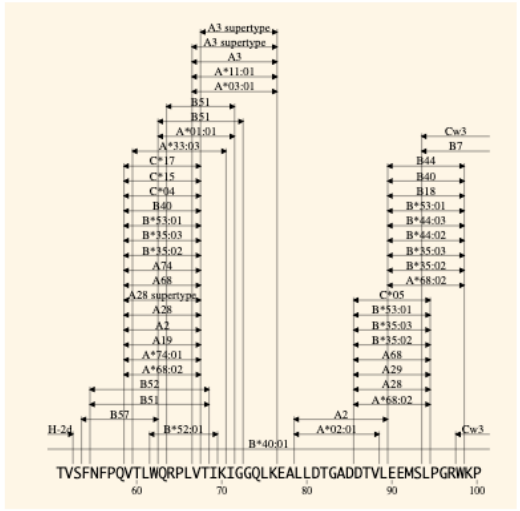
These interactive epitope maps are based on our database of human HIV-1 epitopes.

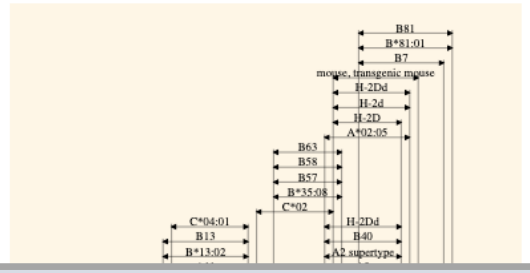
These maps are implemented with SVG (scalable vector graphics), which is supported by most, but not all, web browsers. The static version of this page is also available.

All HIV CTL, CD8+, epitopes mapped to within a region of 14 amino acids or less are indicated on the HIV protein epitope maps. The location and HLA restriction elements of CTL, CD8+, epitopes are indica
given protein, but the HXB2 sequence may not actually carry the epitope of interest, as it may vary relative to the sequence for which the epitope was defined. Epitopes with identical boundaries and HLA
level (example: A2) and another at the genotype level (example: A*0201) both will be included in the map. MHC specificities are indicative of the host species; when no MHC presenting molecule is define

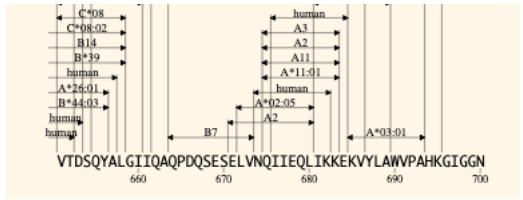
Data last updated at 2021-10-14 11:28:52-06

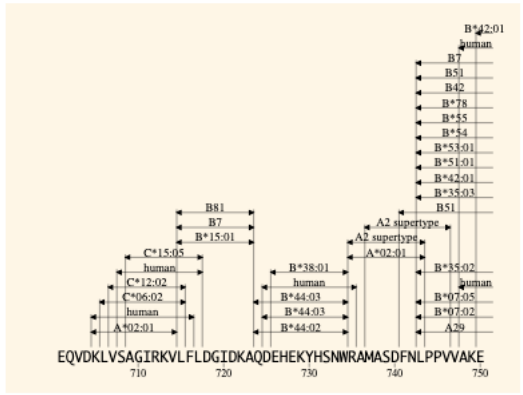


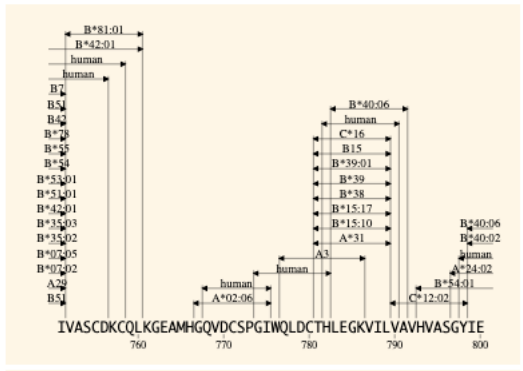




scroll through till epitope of interest

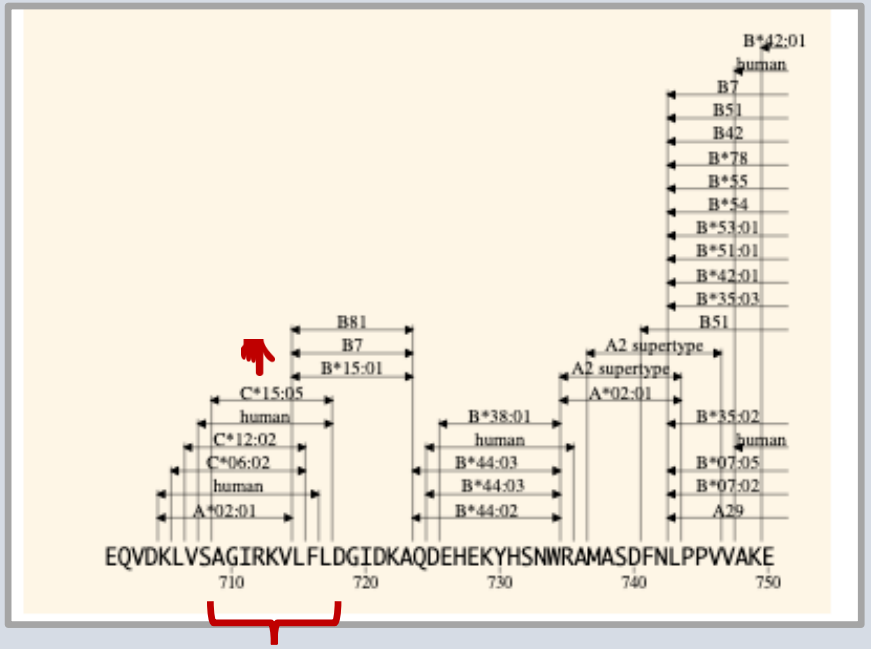






here,
Pol (709-717)

INTERACTIVE Pol EPITOPE MAP



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CLICKED BACK FROM MAP TO the CTL record of the EPITOPE SELECTED !

Databases Search Tools Products Publications search site Search Site

Search CTL/CD8+ T-Cell Epitope Database

Found 1 matching record:

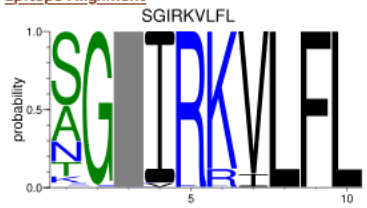
Displaying record number 62508

Download this epitope record as JSON.

HXB2 Location	Pol(709-717) RT(554)-Integrase(2)
Author Location	Pol(653-661)
Epitope	SGIRKVLFL

Pol Epitope Map

Epitope Alignment



Show epitope variants

Epitope Name	SL9, Pol SL9
Subtype	CRF01_AE
Species (MHC/HLA)	human(C*15:05)
Immunogen	HIV-1 infection
Patient MHC/HLA	VI-479: A*29:01, B*07:05, C*15:05; VI-003: ; VI-114: ; VI-231:
Country	Viet Nam
Experimental methods	CD8 T-cell Elispot - IFNγ, Intracellular cytokine staining, Other
Keywords	rate of progression, escape, novel epitope, chronic infection

Notes

- The detrimental haplotype A*29:01-B*07:05-C*15:05 is associated with 9 Pol and 3 Nef mutations, 2 of which are within a novel epitope described here, C*15:05-SGIRKVLFL (found within 17-mer peptide, Pol 17-118, VDKLVSSGIRKVLFLDG) detrimental haplotype.
- Three major mutations were found in Pol SL9 - S653A and S653T which increased pVL significantly as well as reduced CD4+ counts, and S653L which trended in the same direction.

References

Murakoshi2021 Hayato Murakoshi, Takayuki Chikata, Tomohiro Akahoshi, Chengcheng Zou, Mohamed Ali Borghan, Giang Van Tran, Trung Vu Nguyen, Kinh Van Nguyen, Nozomi Kuse, and Masafumi Takiguchi. Critical effect of Pol escape mutat HIV-1 subtype A/E infection. *AIDS*, 35(1):33-43 doi, Jan 2021. PubMed ID: 33031103 Show all entries for this paper.

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Search the Epitope Variant and Escape Mutation Database

Help

- Codes and Symbols in Variants
- Variant and Mutation Types
- Variants Database Help

Found 1 matching record:

Displaying record number 62508

HXB2 Location	Pol(709-717)	Pol Epitope Map View variants at this location
Epitope	SGIRKVLFL	Epitope Alignment
Variants	aGIRKVLFL	diminished response; escape documented in this paper; replicative capacity reduced
	tGIRKVLFL	diminished response; escape documented in this paper; replicative capacity reduced
	lGIRKVLFL	diminished response; escape documented in this paper
	kGIRKVLFL	HLA binding unchanged; observed variant; susceptible form
	qGIRKVLFL	HLA binding unchanged; observed variant; susceptible form
	nGIRKVLFL	observed variant; susceptible form
	fGIRKVLFL	observed variant; susceptible form
	hGIRKVLFL	observed variant; susceptible form
	iGIRKVLFL	observed variant; susceptible form
	yGIRKVLFL	observed variant; susceptible form
Epitope Name	SL9, Pol SL9	
Species (MHC/HLA)	human(C*15:05)	

Variant Details

Showing all: 10 variant(s).

Variant ID.	4460
Epitope Seq.	SGIRKVLFL
Variant Seq.	aGIRKVLFL
Mutations	S/A
Epitope Location	S1A
HXB2 Location	S653A
Mutation Type	**DR**: diminished response **E**: escape documented in this paper **RCR**: replicative capacity reduced
Epitope Subtype	CRF01_AE
Variant Subtype	CRF01_AE
Method	CD8 T-cell Elispot - IFNγ, CTL suppression of replication, Intracellular cytokine staining, Other
Note	aGIRKVLFL,mutation S653A or 1A, increases pVL, decreases recognition, but does not significantly change HLA-C*15:05 binding (increased binding to C*15:05 is seen in the 1A and 1L peptides only at high concentrations). Authors believe this shows a possible lower affinity to TCR by the mutant epitopes, thereby creating escape. S653fA's replication capacity was higher than the WT virus.

Variant ID.	4461
Epitope Seq.	SGIRKVLFL
Variant Seq.	tGIRKVLFL
Mutations	S/T
Epitope Location	S1T

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PART OF VARIANTS DATABASE HELP

https://www.hiv.lanl.gov/content/immunology/variants/variant_help.html

Symbols Used in Variants

Symbol	Meaning	Example
x	Lower case letters indicate a mutation.	Variant SLYNTVAvL indicates a mutation from T to V in the epitope SLYNTVATL.
(x)	Round brackets in the epitope variant designate an insertion.	Variant PLTF(a)GWCYKL has an A inserted between 4F and 5G (Nef 139F and 140G) in the epitope PLTFGWCYKL. Insertion position within the epitope is reported as (4.1)A, and insertion position in the protein is reported as Nef (139.1)A.
'-'	Dash in the epitope variant denotes a deletion.	Variant RAEQ-SQdV of epitope RAEQASQEV has lost amino acid A at position 5.
{xxx}	Curly brackets in the variant are used to designate a flanking region when there is a mutation upstream or downstream of the epitope.	Variant {p}ISPRTLNAW of epitope {A}ISPRTLNAW means that there is an A-to-P mutation upstream of the epitope N-terminus.
'+n'	Mutation in the downstream epitope flanking region.	Variant SPAIFQSSM{TKILd} of the epitope SPAIFQSSM{TKILE} has an E-to-D mutation 5 amino acids downstream of the epitope C-terminus.
'-n'	Mutation in the upstream epitope flanking region.	Variant {rWEKI}RLRPGGKKK of the epitope {KWEKI}RLRPGGKKK has a K-to-R mutation 5 amino acids upstream of the epitope N-terminus.
'*'	A non-mutated amino acid in the epitope flanking region either upstream or downstream of the epitope. Each '*' is one amino acid, and its sequence location is specific. This notation is used when the amino acids between the epitope and the mutation site are not reported in the original publication.	Variant KIRLRPGGK{*t} of epitope KIRLRPGGK has an R-to-T processing mutation 2 amino acids downstream. The intervening amino acid was not reported.
'...'	An unspecified number of amino acids were present between the mutation position in the flanking region and the epitope. This notation is used when the exact mutation position upstream or downstream is >5 amino acids away, or was not reported in the original publication. In the former case, the mutation position is reported.	Variant {q...}TSnLQEQIGW of epitope {H...}TSTLQEQIGW has an unspecified number of non-mutated amino acids between the N-terminus of the epitope and the upstream H-to-Q mutation.

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List of Variant and Mutation Types

Code	Mutation type	Description
?	unclear	Not clear from the paper, for example "E ?" or "IE ?"
A	HLA association	Variant is statistically associated with a particular HLA molecule. *Since we focus on experimentally verified epitope variants, the variant with this mutation is entered only if it is already described as an experimentally determined mutation.*
AHE	altered HLA expression	the peptide or epitope increases or decreases cell surface expression of its restricting HLA molecule.
AKB	altered KIR binding or increased/decreased off-rate	Altered binding (or increased or decreased off-rate) of peptide-presenting HLA to either an inhibitory or stimulatory KIR NK-cell receptor, as compared to binding by original epitope-HLA.
CE	calculated escape	Predicted escape as shown by statistical correlation or other computational methods in a large cohort. *Since we focus on experimentally verified epitope variants, the variant with this mutation is entered only if it is already described as an experimentally determined mutation.*
CHB	calculated diminished HLA binding	Predicted decrease in binding to HLA as shown by algorithm(s). *Since we focus on experimentally verified epitope variants, the variant with this mutation is entered only if it is already described as an experimentally determined mutation.*
CM	compensatory mutation	Variant is associated with a compensatory mutation. This could be a compensatory mutation outside epitope boundaries, or a mutation within epitope boundaries, compensating for the same epitope or for a variant of another epitope. *Each particular entry is explained in the variant note.*
DHB	diminished HLA binding or increased off-rate	Decreased binding (or increased off-rate) to presenting HLA as compared to binding by original epitope.
DI	drug induced	Treatment with antiretroviral drugs induces this variant.
DR	diminished response	Experimental data suggests a partial escape by decreased CTL response, but authors do not call it an escape (judgment call of annotator).
E	escape documented in this paper	Same as NSF (non-susceptible form) but called an escape when dynamic changes seen in a longitudinal or transmission study or when author claims escape.
EL	epitope loss	Entire sequence of epitope lost in variant virus.
F	replicative capacity/ fitness enhanced	Variant is associated with an enhancement in replication of the virus as shown by replication assays.
HBOK	HLA binding unchanged	epitope or peptide variant does not alter binding to the restricting HLA molecule as compared to the WT epitope.
I	insertion	Insertion of one or more amino acids into epitope sequence
IE	inferred escape	Variant is predicted to be an escape by longitudinal study or transmission study (but the reactivity of the variant is not tested experimentally).
LE	literature escape	Escape previously documented in the literature (according to the authors).
NSF	non-susceptible form	No CTL response when patient cells are challenged with the variant peptide.
NSF-2	non-susceptible form-2	Neither index nor variant peptides are recognized by CTL, but the index peptide is a known epitope and, in most cases, there was a prior patient response to it.
OV	observed variant	variant sequence observed in longitudinal or transmission study.
P	processing	Variant escapes CTL detection by altering epitope processing in subcellular organelles, experimentally verified.
R	reversion	Variant reverts to wild type epitope sequence as documented by sequence, experimental studies or literature.
RCOK	replicative capacity is not abrogated	Variant does not cause loss of viral replication, as shown by replication assays.
RCR	replicative capacity reduced	Variant is associated with a reduction or loss (abrogation) of replication of the virus, as shown by replication assays.
SF	susceptible form	CTL response is elicited when patient cells are challenged with the variant peptide.
SNSF	subtype-specific non-susceptible form	No CTL response when patient cells are challenged with the variant peptide in the course of subtype comparative studies, however the same epitope from a different subtype does elicit CTL response.
SSF	subtype-specific susceptible form	CTL response is elicited when patient cells are challenged with the variant peptide in the course of subtype comparative studies, i.e. patient cells can recognize at least two different viral subtype variants.
TCR	TCR related mutation	Variant does not bind or shows decreased binding to TCR.

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Search the Epitope Variant and Escape Mutation Database

Help

- Codes and Symbols in Variants
- Variant and Mutation Types
- Variants Database Help

Found 1 matching record:

Displaying record number 62508

HXB2 Location	Pol(709-717)	Pol Epitope Map View variants at this location
Epitope	SGIRKVLFL	Epitope Alignment
Variants	aGIRKVLFL	diminished response; escape documented in this paper; replicative capacity reduced
	tGIRKVLFL	diminished response; escape documented in this paper; replicative capacity reduced
	lGIRKVLFL	diminished response; escape documented in this paper
	kGIRKVLFL	HLA binding unchanged; observed variant; susceptible form
	qGIRKVLFL	HLA binding unchanged; observed variant; susceptible form
	nGIRKVLFL	observed variant; susceptible form
	fGIRKVLFL	observed variant; susceptible form
	hGIRKVLFL	observed variant; susceptible form
	iGIRKVLFL	observed variant; susceptible form
	yGIRKVLFL	observed variant; susceptible form
Epitope Name	SL9, Pol SL9	
Species (MHC/HLA)	human(C*15:05)	

Variant Details

Showing all: 10 variant(s).

Variant ID.	4460
Epitope Seq.	SGIRKVLFL
Variant Seq.	aGIRKVLFL
Mutations	S/A
Epitope Location	S1A
HXB2 Location	S653A
Mutation Type	**DR**: diminished response **E**: escape documented in this paper **RCR**: replicative capacity reduced
Epitope Subtype	CRF01_AE
Variant Subtype	CRF01_AE
Method	CD8 T-cell Elispot - IFNy, CTL suppression of replication, Intracellular cytokine staining, Other
Note	aGIRKVLFL,mutation S653A or 1A, increases pVL, decreases recognition, but does not significantly change HLA-C*15:05 binding (increased binding to C*15:05 is seen in the 1A and 1L peptides only at high concentrations). Authors believe this shows a possible lower affinity to TCR by the mutant epitopes, thereby creating escape. S653fA's replication capacity was higher than the WT virus.

Variant ID.	4461
Epitope Seq.	SGIRKVLFL
Variant Seq.	tGIRKVLFL
Mutations	S/T
Epitope Location	S1T

SELECT ‘Variants at this location’

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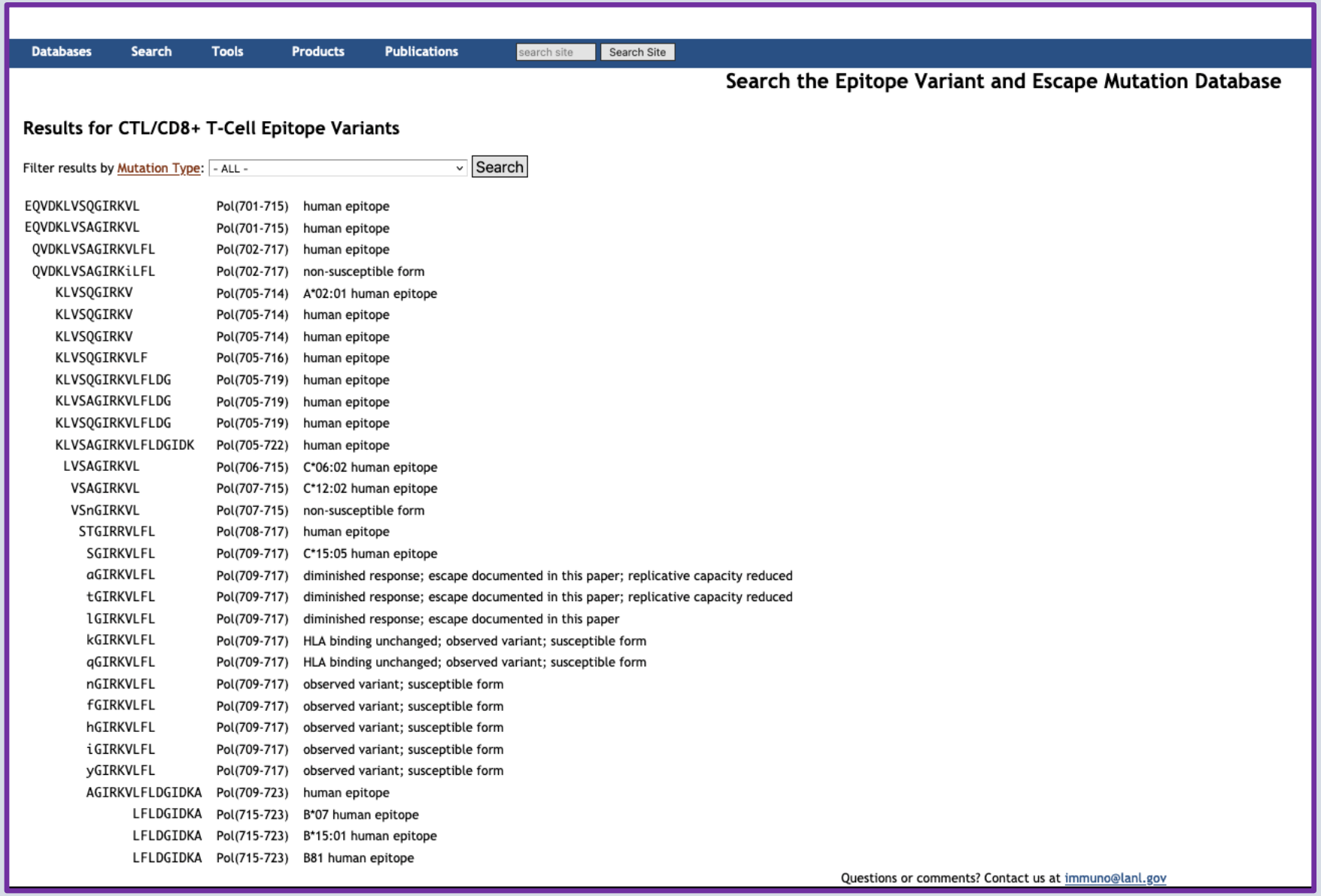
VARIANTS from several studies that overlap the Epitope of interest at Pol 709-717



Databases Search Tools Products Publications search site Search Site

Search the Epitope Variant and Escape Mutation Database

Results for CTL/CD8+ T-Cell Epitope Variants

Filter results by Mutation Type: - ALL - Search

EQVDKLVSQGIRKVL	Pol(701-715)	human epitope
EQVDKLVSAGIRKVL	Pol(701-715)	human epitope
QVDKLVSAGIRKVLFL	Pol(702-717)	human epitope
QVDKLVSAGIRKiLFL	Pol(702-717)	non-susceptible form
KLVSQGIRKV	Pol(705-714)	A*02:01 human epitope
KLVSQGIRKV	Pol(705-714)	human epitope
KLVSQGIRKV	Pol(705-714)	human epitope
KLVSQGIRKVLF	Pol(705-716)	human epitope
KLVSQGIRKVLFLDG	Pol(705-719)	human epitope
KLVSAGIRKVLFLDG	Pol(705-719)	human epitope
KLVSQGIRKVLFLDG	Pol(705-719)	human epitope
KLVSAGIRKVLFLDGIDK	Pol(705-722)	human epitope
LVSAGIRKVL	Pol(706-715)	C*06:02 human epitope
VSAGIRKVL	Pol(707-715)	C*12:02 human epitope
VSnGIRKVL	Pol(707-715)	non-susceptible form
STGIRRVLFL	Pol(708-717)	human epitope
SGIRKVLFL	Pol(709-717)	C*15:05 human epitope
aGIRKVLFL	Pol(709-717)	diminished response; escape documented in this paper; replicative capacity reduced
tGIRKVLFL	Pol(709-717)	diminished response; escape documented in this paper; replicative capacity reduced
lGIRKVLFL	Pol(709-717)	diminished response; escape documented in this paper
kGIRKVLFL	Pol(709-717)	HLA binding unchanged; observed variant; susceptible form
qGIRKVLFL	Pol(709-717)	HLA binding unchanged; observed variant; susceptible form
nGIRKVLFL	Pol(709-717)	observed variant; susceptible form
fGIRKVLFL	Pol(709-717)	observed variant; susceptible form
hGIRKVLFL	Pol(709-717)	observed variant; susceptible form
iGIRKVLFL	Pol(709-717)	observed variant; susceptible form
yGIRKVLFL	Pol(709-717)	observed variant; susceptible form
AGIRKVLFLDGIDKA	Pol(709-723)	human epitope
LFLDGIDKA	Pol(715-723)	B*07 human epitope
LFLDGIDKA	Pol(715-723)	B*15:01 human epitope
LFLDGIDKA	Pol(715-723)	B81 human epitope

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THE DIRECT METHOD OF FINDING A VARIANT is from the VARIANT DB's Search Page

https://www.hiv.lanl.gov/content/immunology/variants/variant_search.html?db=ctl

Search for CTL/CD8+ T-Cell Epitope Variants

HIV Protein	- ALL - Gag Pol Vif Vpr	
HXB2 location	-	Results overlap with query location
Epitope or Variant Sequence		Results contain query sequence
Epitope record number		
Variant record number	4461	Show only this variant Show all variants for the matching epitope
Mutation Type	- ALL -	Show only matching variants Show all variants for the matching epitopes
OR		
MHC/HLA	C*08:02 C*12 C*12:02 C*12:03 C*15:05 Cw1 Cw3	

Search Reset Click for Variant Search Help

Help

- Codes and Symbols in Variants
- Variant and Mutation Types
- Variants Database Help

Found 1 matching record:

Displaying record number 62508

HXB2 Location	Pol(709-717)	Pol Epitope Map View variants at this location
Epitope	SGIRKVLFL	Epitope Alignment
Variants	tGIRKVLFL	diminished response; escape documented in this paper; replicative capacity reduced
Epitope Name	SL9, Pol SL9	
Species (MHC/HLA)	human(C*15:05)	

Variant Details

Showing 1 of 10 variants.

Variant ID.	4461
Epitope Seq.	SGIRKVLFL
Variant Seq.	tGIRKVLFL
Mutations	S/T
Epitope Location	S1T
HXB2 Location	S653T
Mutation Type	**DR:** diminished response **E:** escape documented in this paper **RCR:** replicative capacity reduced
Epitope Subtype	CRF01_AE
Variant Subtype	CRF01_AE
Method	CD8 T-cell Elispot - IFNγ, CTL suppression of replication, Intracellular cytokine staining, Other
Note	tGIRKVLFL,mutation S653T or 1T, increases pVL, decreases recognition, but does not significantly change HLA-C*15:05 binding. Authors believe this shows a possible lower affinity to TCR by the mutant epitopes, thereby creating escape. S653T's replication capacity was similar to but lower than the WT virus.

References

Murakoshi2021 Hayato Murakoshi, Takayuki Chikata, Tomohiro Akahoshi, Chengcheng Zou, Mohamed Ali Borghan, Gia[illegible]n, Trung Vu Nguyen, Kinh Van Nguyen, Nozomi Kuse, and Masafumi Takiguchi. Critical effect of Pol escape mutations associated with detrimental allele HLA-C*15: 05 on clinical outcome in HIV-1 subtype A/E infection. *AIDS*, 35(1):33-43 doi, Jan 2021. PubMed ID: 33031103 Show all entries for this paper.

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FINDING PATIENTS/PARTICIPANTS who REACTED TO the EPITOPE OF INTEREST, Pol SL9

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Search CTL/CD8+ T-Cell Epitope Database

Found 1 matching record:

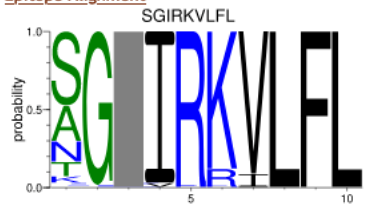
Displaying record number 62508

Download this epitope record as JSON.

HXB2 Location	Pol(709-717) RT(554)-Integrase(2)
Author Location	Pol(653-661)
Epitope	SGIRKVLFL
Epitope Name	SL9, Pol SL9
Subtype	CRF01_AE
Species (MHC/HLA)	human(C*15:05)
Immunogen	HIV-1 infection
Patient MHC/HLA	VI-479: A*29:01, B*07:05, C*15:05; VI-003: ; VI-114: ; VI-231:
Country	Viet Nam
Experimental methods	CD8 T-cell Elispot - IFNγ, Intracellular cytokine staining, Other
Keywords	rate of progression, escape, novel epitope, chronic infection

Pol Epitope Map

Epitope Alignment



Show epitope variants

Notes

- The detrimental haplotype A*29:01-B*07:05-C*15:05 is associated with 9 Pol and 3 Nef mutations, 2 of which are within a novel epitope described here, C*15:05-SGIRKVLFL (found within 17-mer peptide, Pol 17-118, VDKLVSSGIRKVLFLDG) detrimental haplotype.
- Three major mutations were found in Pol SL9 - S653A and S653T which increased pVL significantly as well as reduced CD4+ counts, and S653L which trended in the same direction.

References

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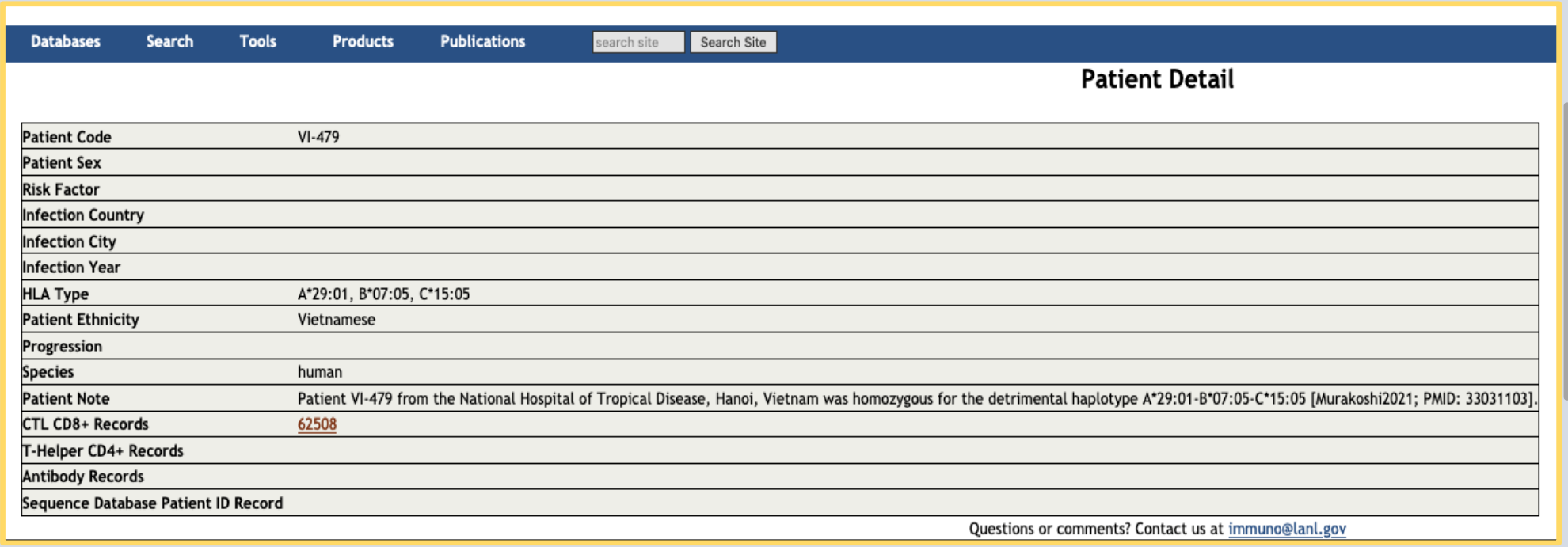
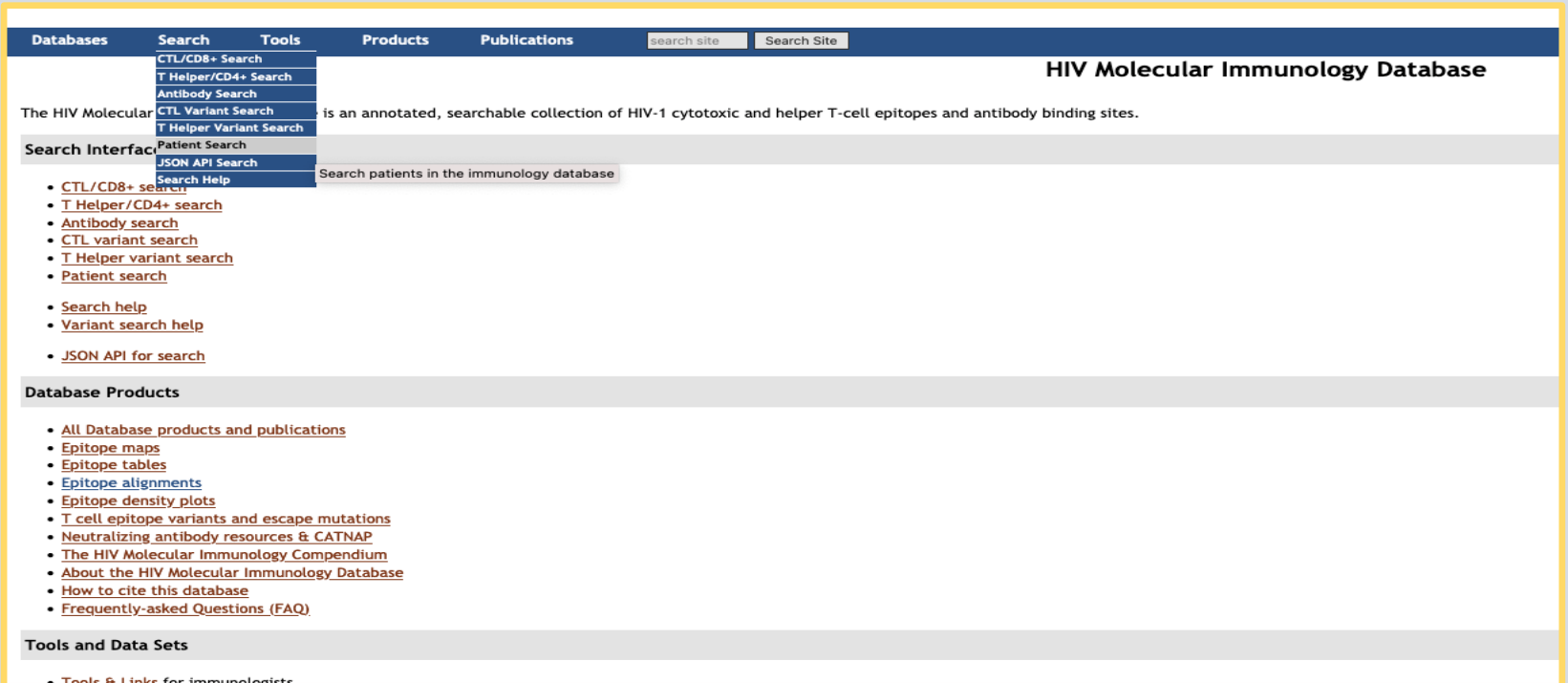


PATIENT DETAIL from the EPITOPE RECORD page
OR
from the PATIENT SEARCH FORM under SEARCH dropdown menus.

https://www.hiv.lanl.gov/mojo/immunology/patient/form



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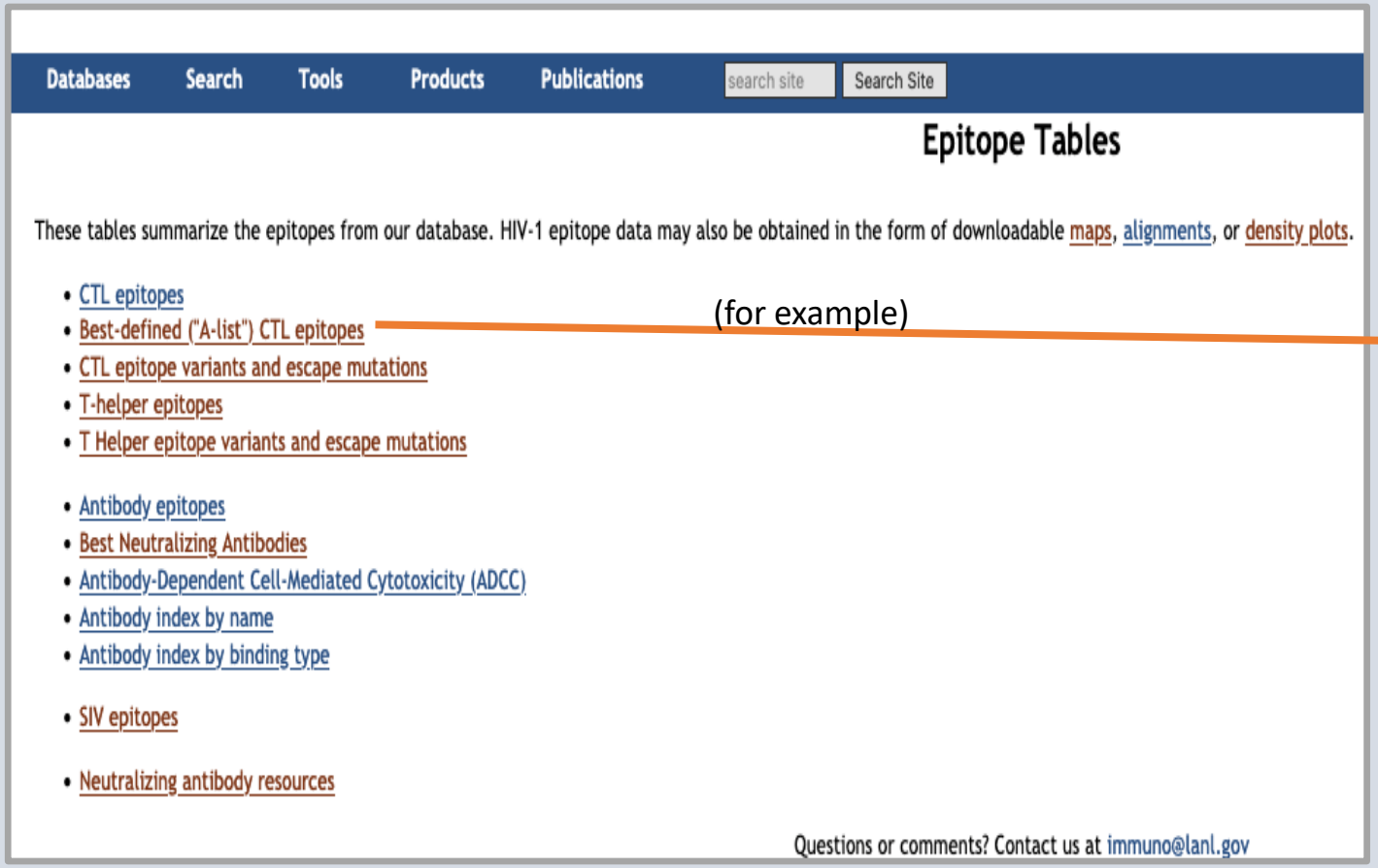
STATIC LISTS/TABLES OF INTEREST



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Epitope Tables

These tables summarize the epitopes from our database. HIV-1 epitope data may also be obtained in the form of downloadable maps, alignments, or density plots.

- CTL epitopes
- Best-defined ("A-list") CTL epitopes
- CTL epitope variants and escape mutations
- T-helper epitopes
- T Helper epitope variants and escape mutations

- Antibody epitopes
- Best Neutralizing Antibodies
- Antibody-Dependent Cell-Mediated Cytotoxicity (ADCC)
- Antibody index by name
- Antibody index by binding type

- SIV epitopes

- Neutralizing antibody resources

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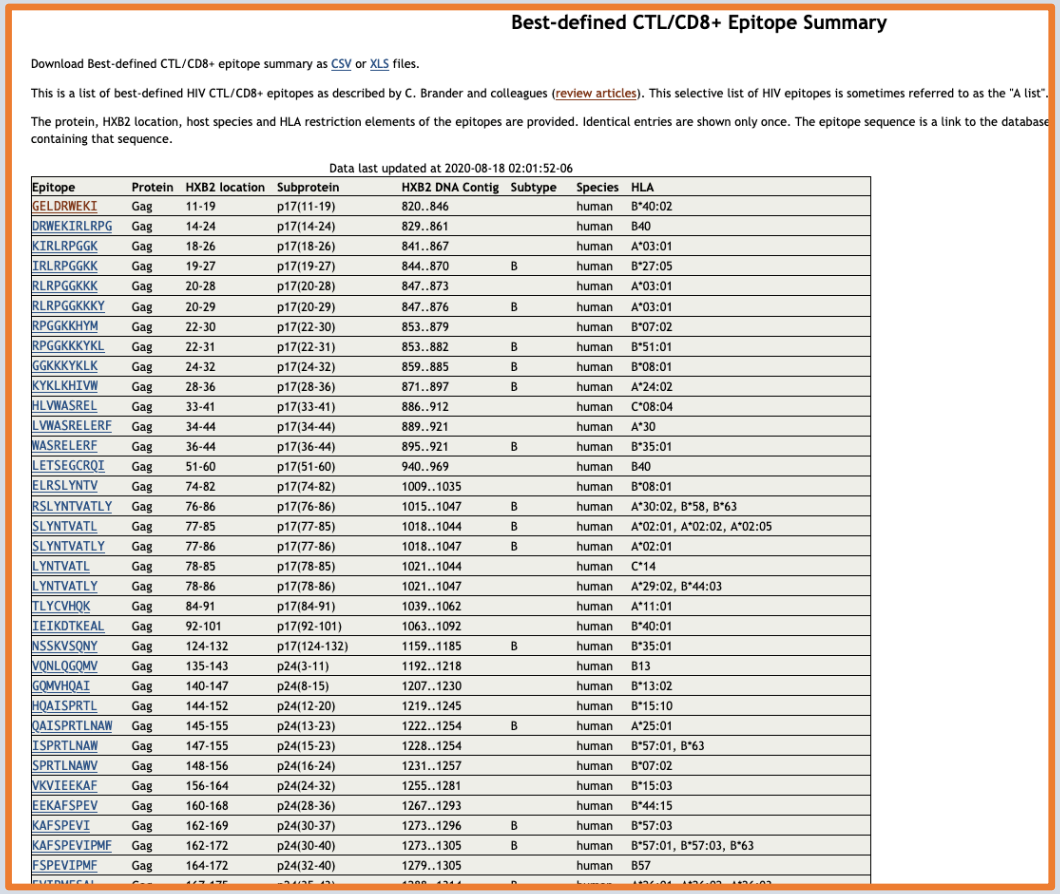
(for example)



Best-defined CTL/CD8+ Epitope Summary

Download Best-defined CTL/CD8+ epitope summary as CSV or XLS files.

This is a list of best-defined HIV CTL/CD8+ epitopes as described by C. Brander and colleagues (review articles). This selective list of HIV epitopes is sometimes referred to as the "A list".

The protein, HXB2 location, host species and HLA restriction elements of the epitopes are provided. Identical entries are shown only once. The epitope sequence is a link to the database containing that sequence.

Data last updated at 2020-08-18 02:01:52-06

Epitope	Protein	HXB2 location	Subprotein	HXB2 DNA Contig	Subtype	Species	HLA
GELDRWEKI	Gag	11-19	p17(11-19)	820..846		human	B*40:02
DRWEKIRLRPG	Gag	14-24	p17(14-24)	829..861		human	B40
KIRLRPGGK	Gag	18-26	p17(18-26)	841..867		human	A*03:01
IRLRPGGKK	Gag	19-27	p17(19-27)	844..870	B	human	B*27:05
RLRPGGKKK	Gag	20-28	p17(20-28)	847..873		human	A*03:01
RLRPGGKKKY	Gag	20-29	p17(20-29)	847..876	B	human	A*03:01
RPGGKKHYM	Gag	22-30	p17(22-30)	853..879		human	B*07:02
RPGGKKKYKL	Gag	22-31	p17(22-31)	853..882	B	human	B*51:01
GGKKKYKLK	Gag	24-32	p17(24-32)	859..885	B	human	B*08:01
KYKLKHIVW	Gag	28-36	p17(28-36)	871..897	B	human	A*24:02
HLVWASREL	Gag	33-41	p17(33-41)	886..912		human	C*08:04
LVWASRELERF	Gag	34-44	p17(34-44)	889..921		human	A*30
WASRELERF	Gag	36-44	p17(36-44)	895..921	B	human	B*35:01
LETSEGCRQI	Gag	51-60	p17(51-60)	940..969		human	B40
ELRSLYNTV	Gag	74-82	p17(74-82)	1009..1035		human	B*08:01
RSLYNTVATLY	Gag	76-86	p17(76-86)	1015..1047	B	human	A*30:02, B*58, B*63
SLYNTVATL	Gag	77-85	p17(77-85)	1018..1044	B	human	A*02:01, A*02:02, A*02:05
SLYNTVATLY	Gag	77-86	p17(77-86)	1018..1047	B	human	A*02:01
LYNTVATL	Gag	78-85	p17(78-85)	1021..1044		human	C*14
LYNTVATLY	Gag	78-86	p17(78-86)	1021..1047		human	A*29:02, B*44:03
TLYCVHQK	Gag	84-91	p17(84-91)	1039..1062		human	A*11:01
IEIKDTKEAL	Gag	92-101	p17(92-101)	1063..1092		human	B*40:01
NSSKVSQNY	Gag	124-132	p17(124-132)	1159..1185	B	human	B*35:01
VQNLQGQMV	Gag	135-143	p24(3-11)	1192..1218		human	B13
GQMVHQAI	Gag	140-147	p24(8-15)	1207..1230		human	B*13:02
HQAISPRTL	Gag	144-152	p24(12-20)	1219..1245		human	B*15:10
QAISPRTLNAW	Gag	145-155	p24(13-23)	1222..1254	B	human	A*25:01
ISPRTLNAW	Gag	147-155	p24(15-23)	1228..1254		human	B*57:01, B*63
SPRTLNAWV	Gag	148-156	p24(16-24)	1231..1257		human	B*07:02
VKVIEEKAF	Gag	156-164	p24(24-32)	1255..1281		human	B*15:03
EEKAFSPEV	Gag	160-168	p24(28-36)	1267..1293		human	B*44:15
KAFSPEVI	Gag	162-169	p24(30-37)	1273..1296	B	human	B*57:03
KAFSPEVIPMF	Gag	162-172	p24(30-40)	1273..1305	B	human	B*57:01, B*57:03, B*63
FSPEVIPMF	Gag	164-172	p24(32-40)	1279..1305		human	B57

https://www.hiv.lanl.gov/content/immunology/tables/optimal_ctl_summary.html

https://www.hiv.lanl.gov/content/immunology/tables/tables.html

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In addition to Annotations, tools and maps, and Compendia,
UPGRADES to
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Patient Data expanded and searchable

JSON and CSV Download

HLA Nomenclature updated

A^{+}-list (CTL epitopes) Upgrade, soon to be published at hiv.lanl.gov

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HIV sequence database

DATABASES SEARCH ALIGNMENTS TOOLS PUBLICATIONS GUIDES search site Search

News Archive

Note: news releases from the LANL HIV Databases are available as RSS feeds.

Variant Visualizer

Variant Visualizer is a new tool that provides new options and output styles for visualizing variants in an alignment of nucleotide or protein sequences. The tool is similar to Highlighter, but the Variant Visualizer has more options for refining the graphical output. The output can be refined interactively without rerunning the tool. *21 July 2021*

HIV Immunology Database JSON API

A *JSON API* (JavaScript Object Notation - Application Programming Interface) is now available for the HIV Molecular Immunology Database to retrieve curated epitope and related data from the database in JSON format, as an alternative to the existing HTML format. It is fully documented via OpenAPI and allows the contents of the HIV Immunology Database to be queried and extracted. Data extraction may be automated for multiple searches and extracted data may then be manipulated with the user's choice of programming language. *19 March 2021*

HIV Molecular Immunology 2018-19

HIV Molecular Immunology 2018-19 is now available online. The PDF version is hypertext enabled and features clickable table-of-contents, indexes, references and links to external web sites. *14 September 2020*

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HIV Molecular Immunology Database

The HIV Molecular Immunology Database is an annotated, searchable collection of HIV-1 cytotoxic and helper T-cell epitopes and antibody binding sites.

Search Interfaces

- CTL/CD8+ search
- T Helper/CD4+ search
- Antibody search
- CTL variant search
- T Helper variant search
- Patient search

- Search help
- Variant search help

- JSON API for search

Database Products

- All Database products and publications
- Epitope maps
- Epitope tables
- Epitope alignments
- Epitope density plots
- T cell epitope variants and escape mutations
- Neutralizing antibody resources & CATNAP
- The HIV Molecular Immunology Compendium
- About the HIV Molecular Immunology Database
- How to cite this database
- Frequently-asked Questions (FAQ)

Tools and Data Sets

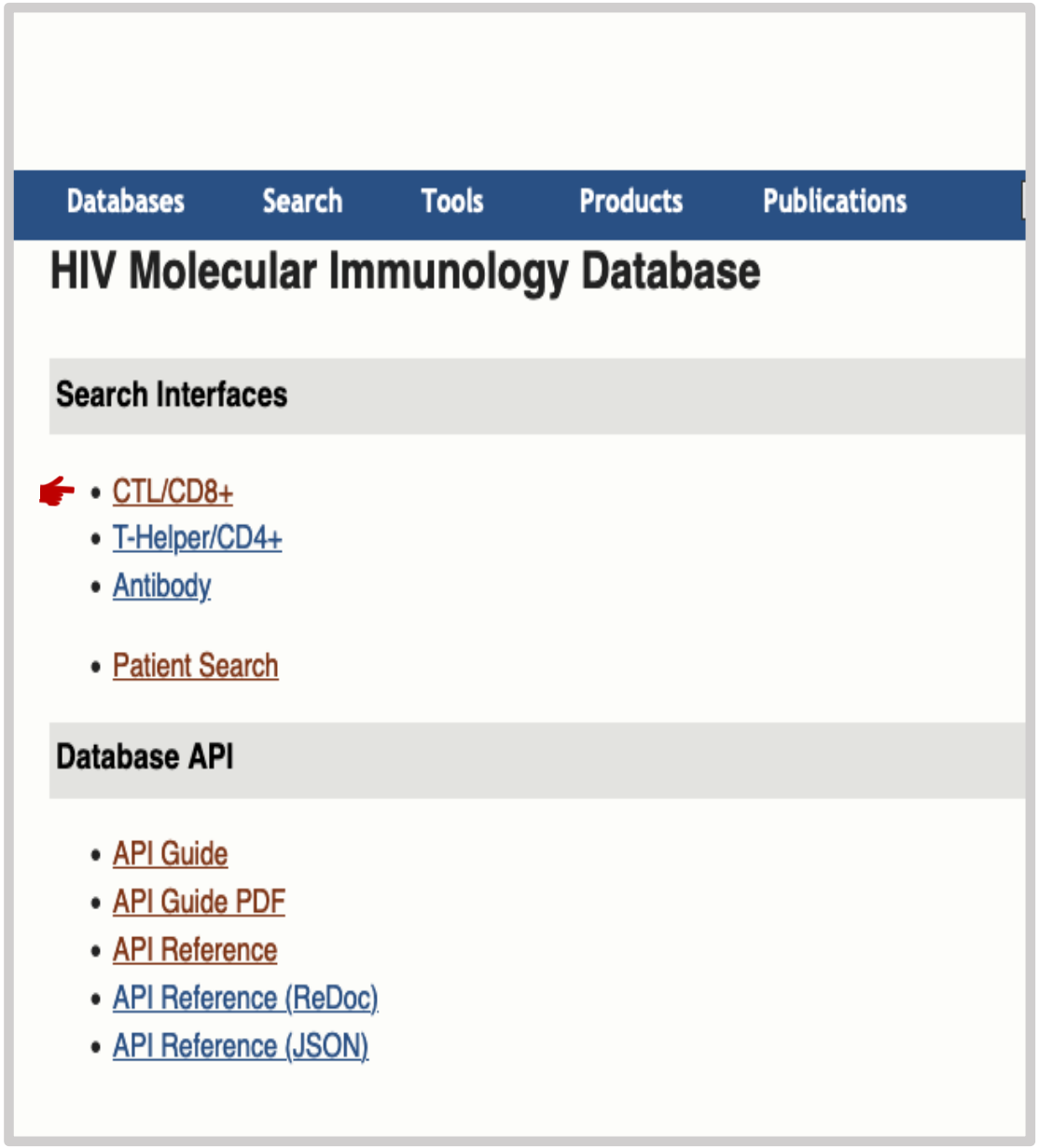
- Tools & Links for immunologists
- SIV Epitopes (PDF) review article summarizing known SIV epitopes
- Identifying HLA-Associated Polymorphisms in HIV-1 (PDF) review article summarizing HIV polymorphism associated with escape mutations. Also a table of polymorphisms.
- HLATEM HLA Typing and Epitope Mapping Data Sets
- Standardized Assessments of Neutralizing Antibodies for HIV/AIDS Vaccine Development Assay protocols from Duke Central Reference Laboratory

News

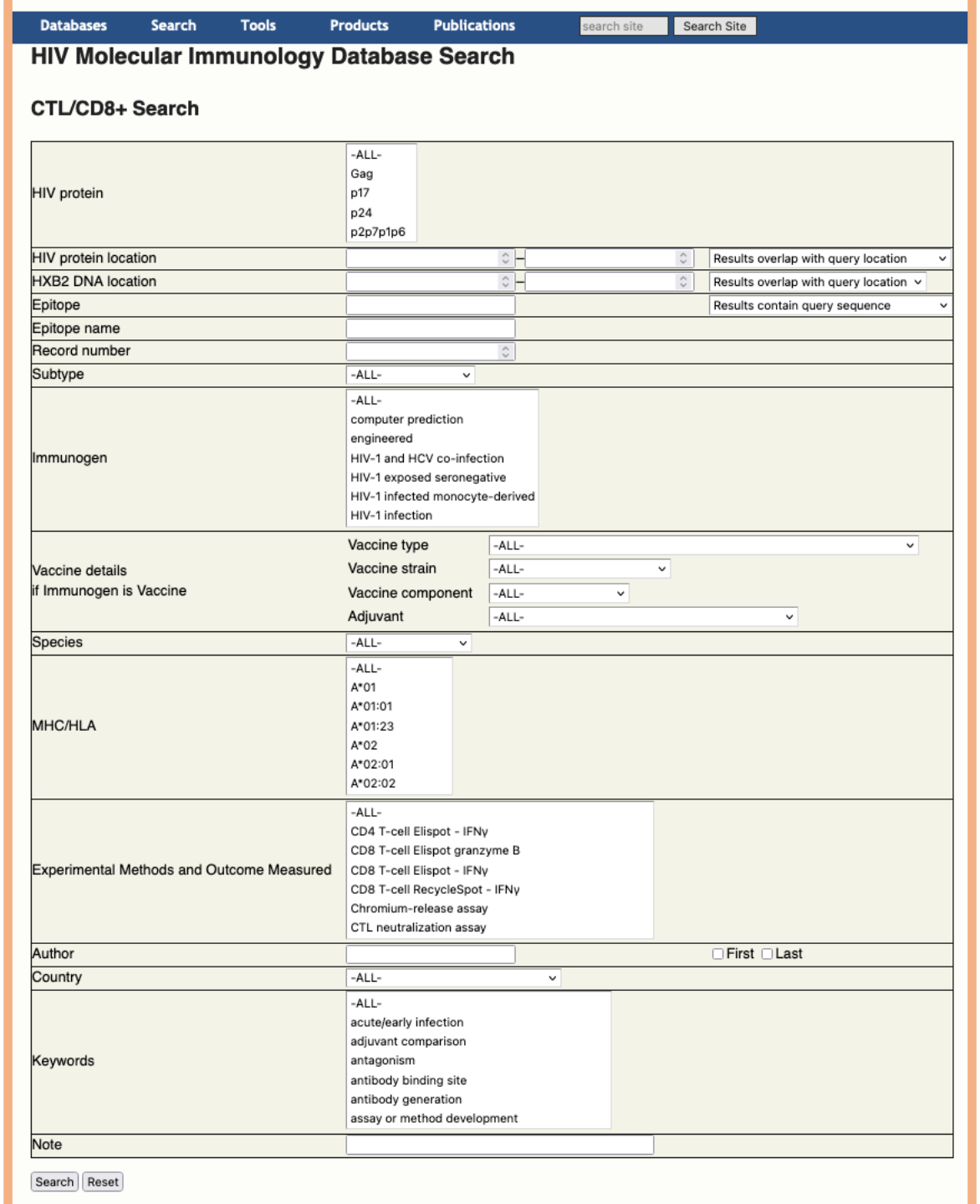
News Archive

No new news.

Questions or comments? Contact us at immuno@lanl.gov



https://www.hiv.lanl.gov/mojo/immunology/index



Databases | Search | Tools | Products | Publications | search site | Search Site

HIV Molecular Immunology Database Search

CTL/CD8+ Search

HIV protein	-ALL- Gag p17 p24 p2p7p1p6	
HIV protein location	–	Results overlap with query location
HXB2 DNA location	–	Results overlap with query location
Epitope		Results contain query sequence
Epitope name		
Record number		
Subtype	-ALL-	
Immunogen	-ALL- computer prediction engineered HIV-1 and HCV co-infection HIV-1 exposed seronegative HIV-1 infected monocyte-derived HIV-1 infection	
Vaccine details if Immunogen is Vaccine	Vaccine type: -ALL- Vaccine strain: -ALL- Vaccine component: -ALL- Adjuvant: -ALL-	
Species	-ALL-	
MHC/HLA	-ALL- A*01 A*01:01 A*01:23 A*02 A*02:01 A*02:02	
Experimental Methods and Outcome Measured	-ALL- CD4 T-cell Elispot - IFNγ CD8 T-cell Elispot granzyme B CD8 T-cell Elispot - IFNγ CD8 T-cell RecycleSpot - IFNγ Chromium-release assay CTL neutralization assay	
Author	Murakoshi	☑ First ☐ Last
Country	-ALL-	
Keywords	-ALL- acute/early infection adjuvant comparison antagonism antibody binding site antibody generation assay or method development	
Note		

Search | Reset

Databases | Search | Tools | Products | Publications | search site | Search Site

HIV Molecular Immunology Database Search

CTL/CD8+ Search

Found 73 matching records:

Download these results as CSV or download as JSON

Displaying record number 61877

Download this epitope record as JSON.

HXB2 Location	Gag(124–132) p17(124–132) DNA(1159..1185)	Gag Epitope Map
Author Location	Gag(124–132)	
Epitope	NSSQVSQNY	Epitope Alignment
Variants	NSgQVSQNY observed variant, replicative capacity is not abrogated	Show epitope variants
Epitope Name	NY9, p17NY9	
Subtype	B	
Species (MHC/HLA)	human(B*35:01)	
Immunogen	HIV-1 infection	
Country	Japan	
Experimental methods	CD8 T-cell Elispot - IFNγ, CTL suppression of replication, Intracellular cytokine staining, Tetramer binding	
Keywords	escape, HLA associated polymorphism	

Notes

- HLA-B*3501 is known to be a detrimental allele associated with rapid progression to AIDS. CTL responses to 16 known HLA-B*3501-restricted epitopes however, were studied in 63 B*3501+ ART-nai protective-epitope mutations associated with B*3501 were also investigated and so one mechanism of the detrimental effect of HLA-B*3501 was clarified: the Y135F mutation within NefYF9, which is and in vitro.
- Gag epitope NSSQVSQNY (NY9) elicited CTL response in 6/63 HLA-B*3501+ HIV-1-infected ART naive Japanese subjects, and a significant association was found with suppression of pVL (plasma
- The HLA-A*2402-associated polymorphism NefY135F which is seen in epitope YF9, fPLTFGWCF accumulates in B*3501+ Japanese individuals to 61% and is strongly associated with lower pVL and

References

Murakoshi2018a Hayato Murakoshi, Madoka Koyanagi, Tomohiro Akahoshi, Takayuki Chikata, Nozomi Kuse, Hiroyuki Gatanaga, Sarah L. Rowland-Jones, Shinichi Oka, and Masafumi Takiguchi. Impact *EBioMedicine*, 36:103-112, Oct 2018. PubMed ID: 30249546. Show all entries for this paper.

Displaying record number 61881

Download this epitope record as JSON.

HXB2 Location	Gag(180–188) p24(48–56) DNA(1327..1353)	Gag Epitope Map
Author Location		
Epitope	TPQDLNTML	Epitope Alignment

https://www.hiv.lanl.gov/mojo/immunology/search/ctl/form

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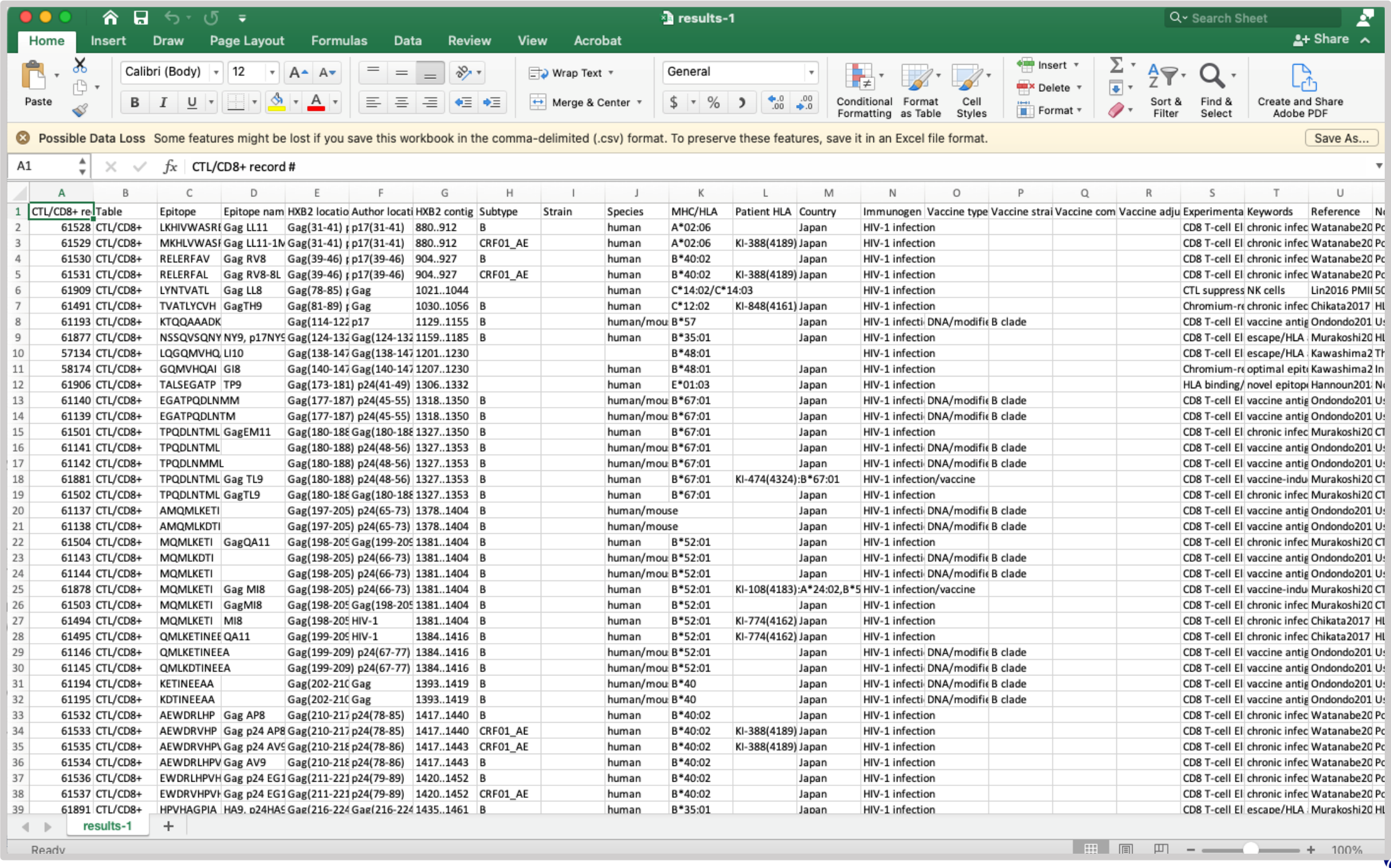

73 “Murakoshi” CTL records, downloaded to a spreadsheet

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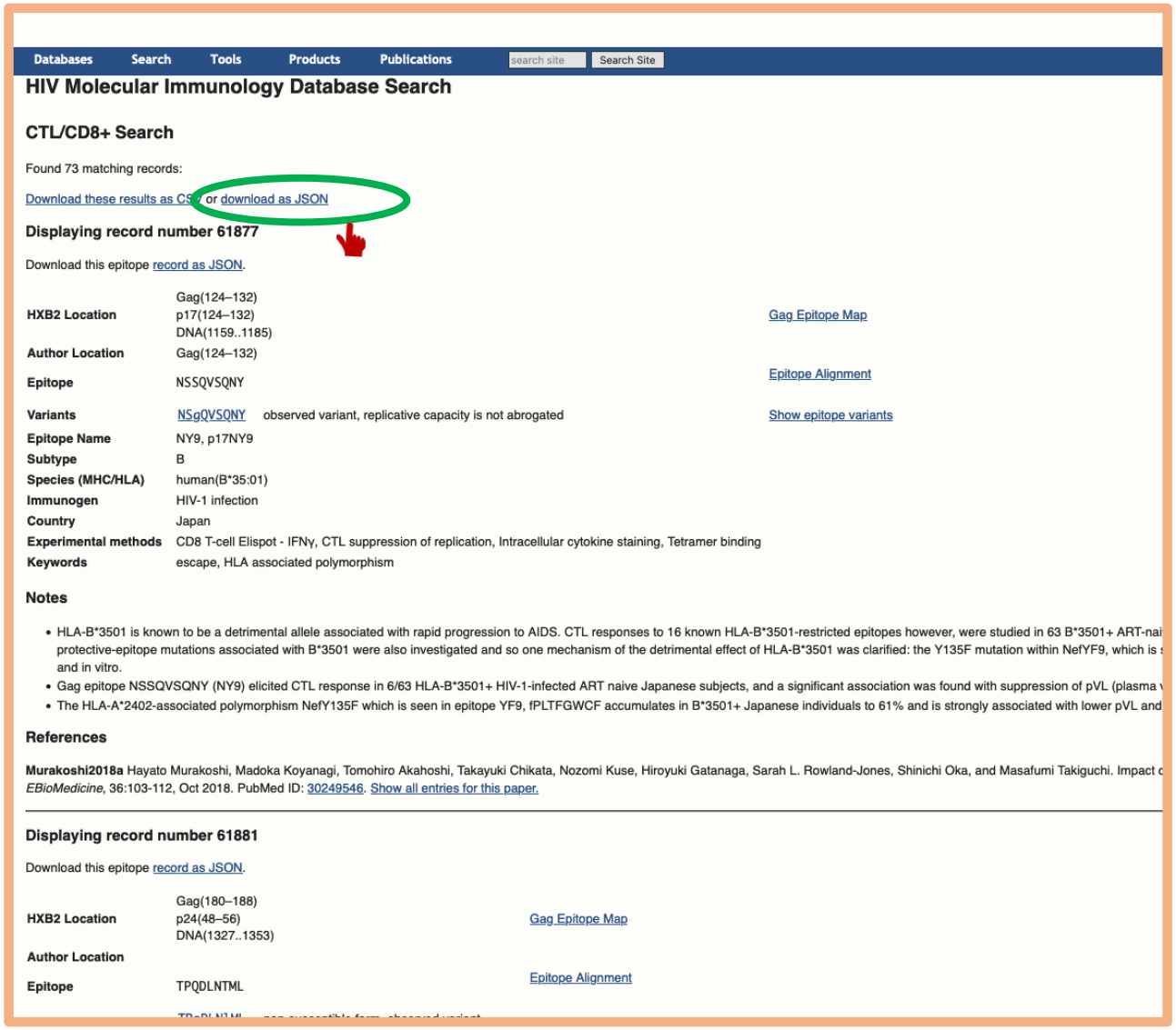

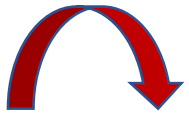

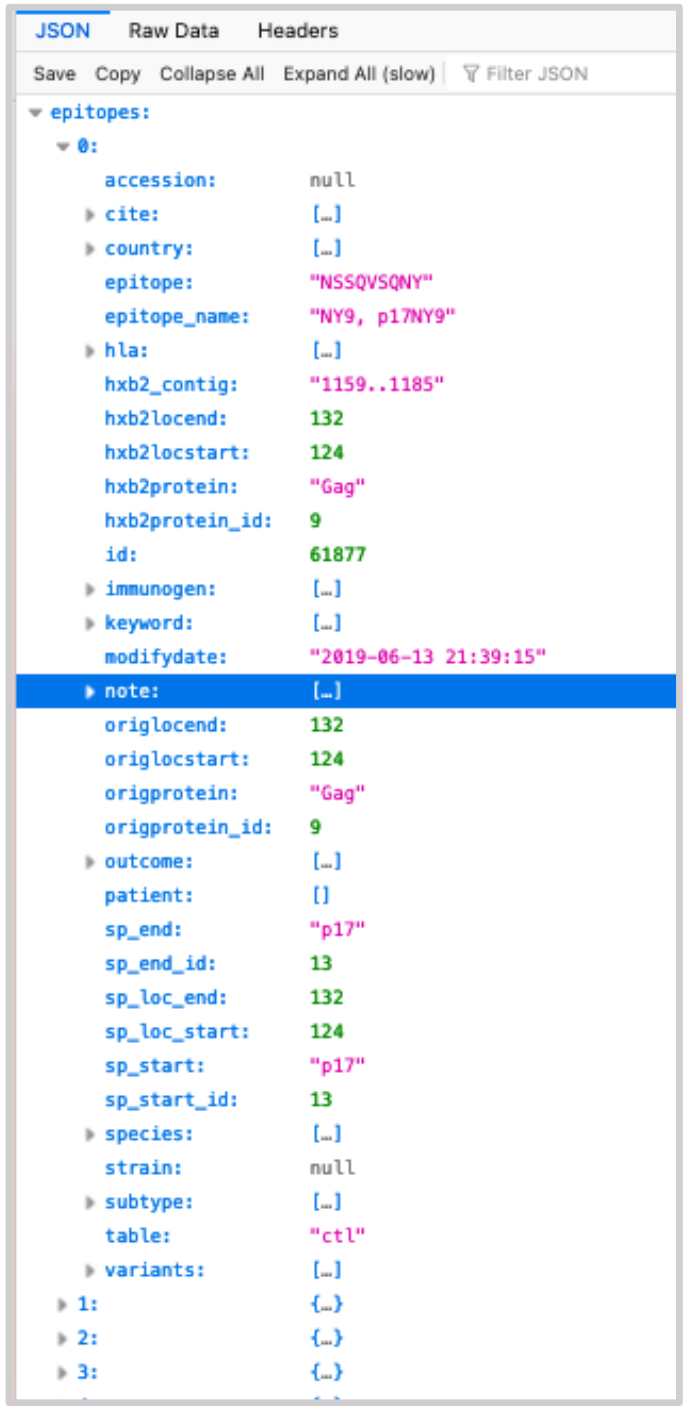

73 “Murakoshi” CTL records, downloaded in JSON

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In addition to Annotations, tools and maps, and Compendia, UPGRADES to Immunology Database include:

Patient Data expanded and searchable

JSON and CSV download

HLA Nomenclature updated

A^+-list (CTL epitopes) Upgrade, soon to be published at hiv.lanl.gov

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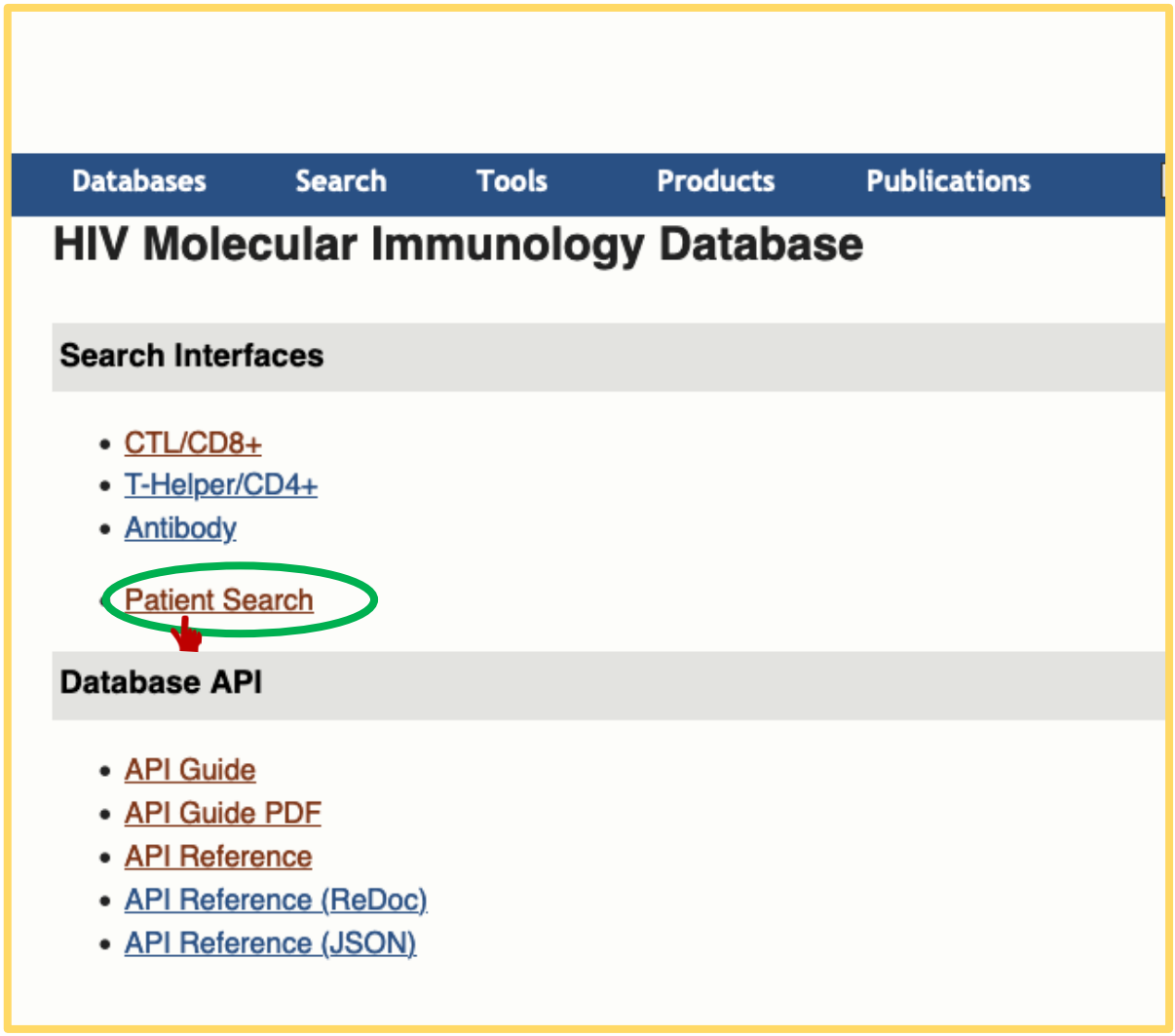
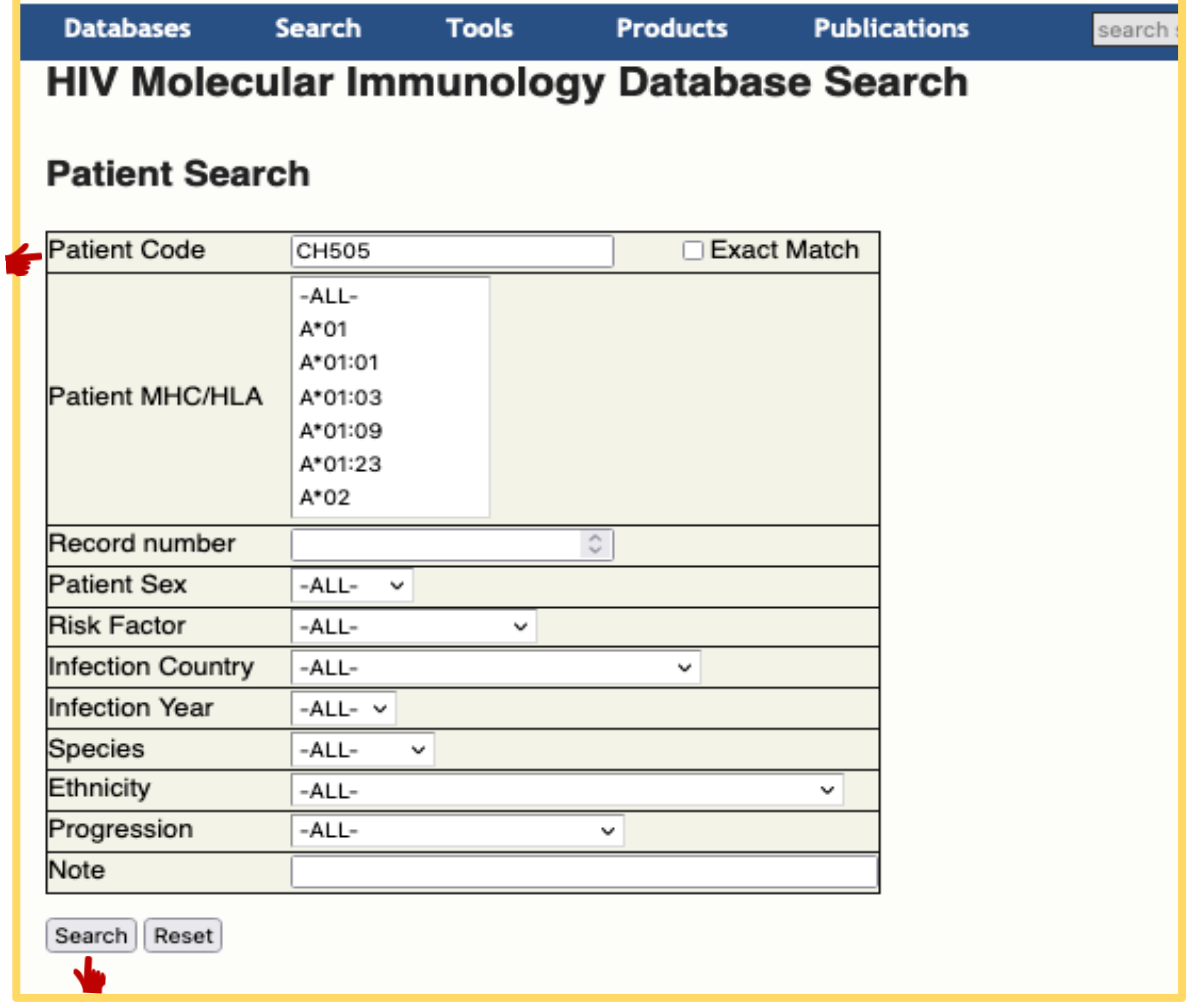
PATIENT SEARCHES EXPANDED





https://www.hiv.lanl.gov/mojo/immunology/patient/form

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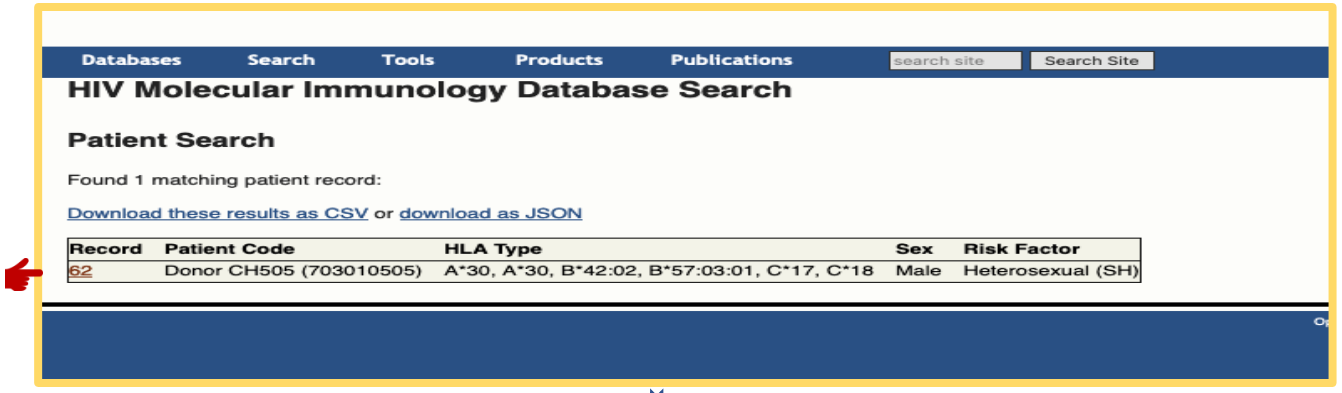

HIV Molecular Immunology Database Search

Patient Detail

Patient Record	62
Patient Code	Donor CH505 (703010505)
Patient Sex	Male
Risk Factor	Heterosexual (SH)
Infection Country	MW
Infection City	
Infection Year	2008
HLA Type	A*30, A*30, B*42:02, B*57:03:01, C*17, C*18
Patient Ethnicity	African
Progression	
Species	human
Patient Note	African donor enrolled approximately 4 weeks after infection and followed for over 6 years. During this time viral load ranged from 14,460 to 847,279 copies/ml (median = 173,667 copies/ml), and CD4 counts ranged from 69 to 431 cells/mm3 (median = 294 cells/ mm3). A single founder virus is estimated to have established HIV-1 clade C with development of autologous neutralizing antibodies at 14 weeks; Abs CH103,CH104,CH105,CH106 isolated 136 weeks post-infection. Antibody CH235 was isolated from the patient's week 41-peripheral blood memory B cells in culture.
CTL CD8+ Records	59059, 59060
T-Helper CD4+ Records	
Antibody Records	CH103 (2861), CH104 (2862), CH105 (2863), CH106 (2864), IA1 (3176), IA2 (3177), IA3 (3178), IA4 (3179), IA5 (3180), IA6 (3181), IA7 (3182), IA8 (3183), CH103 UCA (3184), CH235 (3185), CH236 (3186), CH239 (3187), CH240 (3188), CH241 (3189), CH186 (3190), CH187 (3191), CH188 (3192), CH200 (3193), DH151 (3234), DH228 (3235), CH235.9 (3291), CH235.12 (3292), CH243 (3374), CH244 (3375), CH245 (3376), CH247 (3377), CH248 (3378), 1AH92U (3380), CH235.7 (3381), CH235.10 (3382), CH235.11 (3383), CH235.13 (3384)
Sequence Database Patient ID Record	56552

In addition to Annotations, tools and maps, and Compendia, UPGRADES to Immunology Database include:

Patient DB expanded and searchable

JSON and CSV download

HLA Nomenclature updated

A^+-list (CTL epitopes) Upgrade, soon to be published at hiv.lanl.gov

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HLA UPGRADE to ‘HLA Informatics Group’ designations

Databases Search Tools Products Publications search site Search Site

HIV protein	- ALL - Gag p17 p24 p2p7p1p6	
HXB2 protein location	—	Results overlap with query location
HXB2 DNA location	—	Results overlap with query location
Epitope		Results contain query sequence
Epitope name		
Record number		
Subtype	- ALL -	
Immunogen	- ALL - computer prediction engineered HIV-1 and HCV co-infection HIV-1 exposed seronegative HIV-1 infected monocyte-derived HIV-1 infection	
Vaccine details if Immunogen is Vaccine	Vaccine type	- ALL -
	Vaccine strain	- ALL -
	Vaccine component	- ALL -
	Adjuvant	- ALL -
Species	- ALL -	
MHC/HLA	A*03:01 A03 supertype A1 A*11 A11 A*11:01 A*11:03	
Author		First Last
Country	- ALL -	
Keywords	- ALL - acute/early infection adjuvant comparison antagonism antibody binding site antibody generation assay or method development	
Note	A0301	

Search Reset Click for Search Help

Search CTL/CD8+ variants

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Search CTL/CD8+ T-Cell Epitope Database

Found 2 matching records:

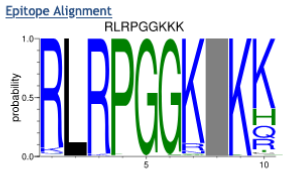
Displaying record number 52892

Download this epitope record as JSON.

HXB2 Location	Gag(20-28) p17(20-28) DNA(847..873)
Author Location	Gag
Epitope	RLRPGGKKK
Epitope Name	1332
Subtype	multiple
Species (MHC/HLA)	human(A*03:01, A3, B42, B62)
Immunogen	HIV-1 infection
Patient MHC/HLA	A23, A3, B49, B57; A24, A3, B27, B57, C*18; A26, A3, B52, B8
Country	United States
Experimental methods	T-cell Elispot
Keywords	binding affinity, computational epitope prediction, immunodominance, HLA cross-presentation

Gag Epitope Map

Epitope Alignment



Notes

- Epitopes defined using sequence parsing and matching algorithm Conservatrix, and epitope prediction tool EpiMatrix, were shown to be conserved in a broad range of HIV-1 sequences derived from different parts of the recognized as promiscuous epitopes and five as MHC supertypes.
- Estimated binding probability for RLRPGGKKK: 34% Promiscuous epitope binding to A03, A0301, B62, Bw62, B42. Immunodominant epitope.

References

DeGroot2003 Anne S. De Groot, Bill Jesdale, William Martin, Caitlin Saint Aubin, Hakima Sbai, Andrew Bosma, Judy Lieberman, Gail Skowron, Fadi Mansourati, and Kenneth H. Mayer. Mapping Cross-Clade HIV-1 Vaccine Epito 14505932. Show all entries for this paper.

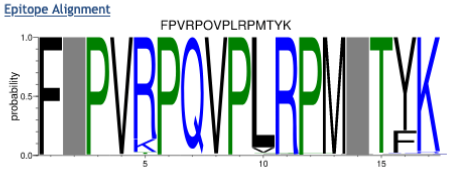
Displaying record number 53618

Download this epitope record as JSON.

HXB2 Location	Nef(68-82) DNA(8998..9042)
Author Location	Nef(73-82)
Epitope	FPVRPQVPLRPMTYK
Subtype	A, D

Nef Epitope Map

Epitope Alignment



https://www.hiv.lanl.gov/mojo/immunology/search/ctl/form

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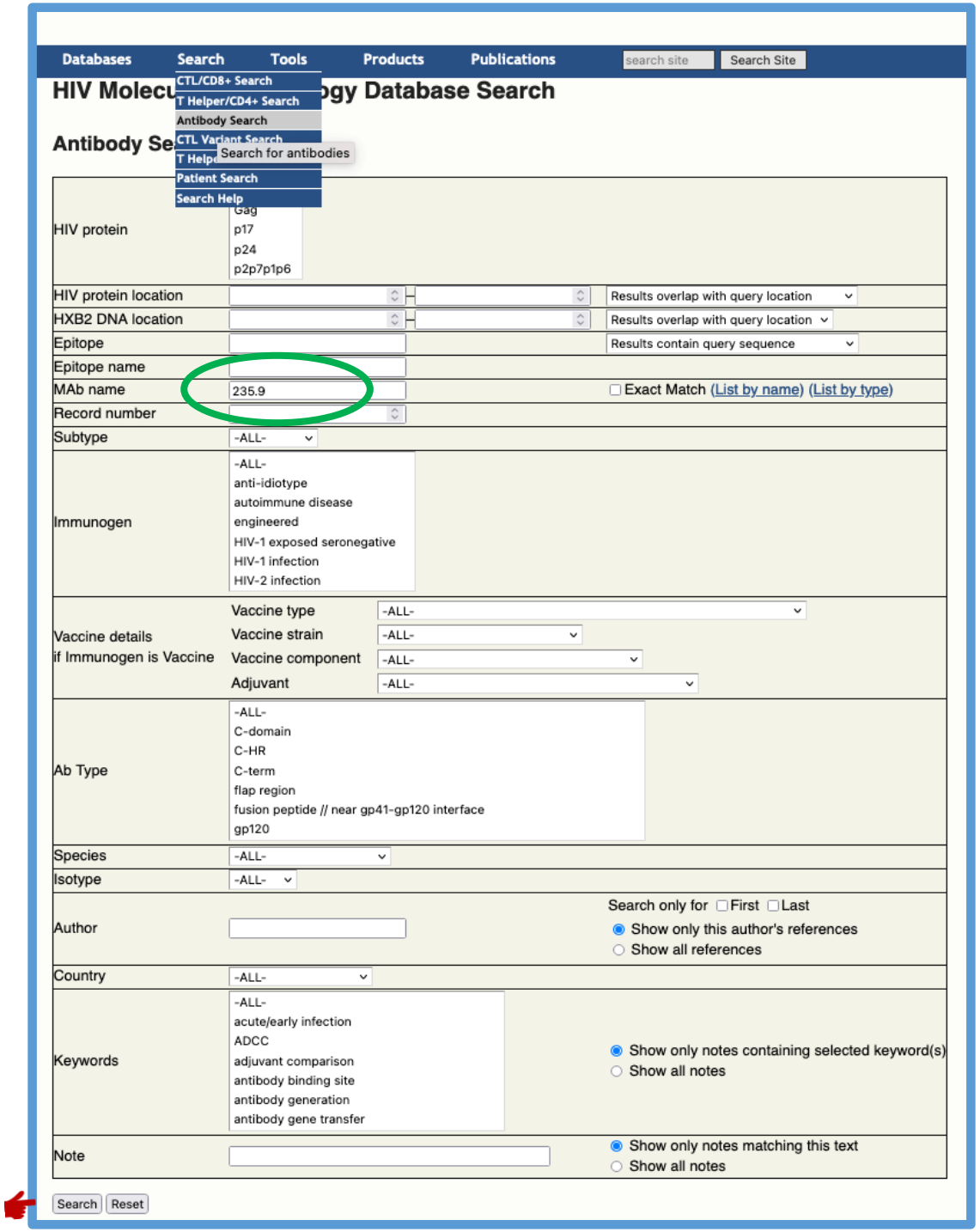
ANTIBODY SEARCHES



https://www.hiv.lanl.gov/mojo/immunology/search/ab/form

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Search Antibody Database

Found 1 matching record:

Displaying record number 3291

Link to Epitope Alignment

Link to Epitope Map

Env Epitope Map

MAb ID	CH235.9 (CH493)
HXB2 Location	Env
Author Location	Env
Epitope	
Subtype	C
Ab Type	gp120 CD4BS
Neutralizing	P (tier 2) View neutralization details
Contacts and Features	View contacts and features
Species (Isotype)	human
Patient	Donor CH505
Immunogen	HIV-1 infection
Keywords	antibody generation, antibody lineage, antibody sequence, binding affinity, escape, mutation acquisition, neutralization, review

Link to CATNAP

Link to Antibody Features Database
(Ab contact positions and related protein features)

Link to Patient Donor detail

Notes

Showing 3 of 3 notes. **Notes from papers**

- CH235.9: This review discussed antibody-virus coevolution and lineage development as a path to elicit broadly neutralizing Abs. CD4bs mAbs from donor CH505 (lineages CH103 and CH235) were used as main examples. *Bonsignori2017a* (**review**, **antibody lineage**)
- This patent application states that CH493 is also referred to as CH235.9. *Lam2017*
- CH235.9: In 5 years additional members of the CH235 clonal lineage were isolated based on deep sequencing of donor CH505's V_L and V_H chains at 17 timepoints in the donor's infection. Two of these had greater neutralization potency, CH235.9 and CH235.12. Study of crystal structures indicated a site of vulnerability near the Env CD4 binding site. The lineages of CH103 and CH235, both derived from Donor CH505 were compared - CH103 lineage K_d increased an order of magnitude each step of maturation but maintained a fast association rate; CH235 lineage however, had slower K_ds and K_as over maturation. This mAb was autoreactive, at the cytoplasmic level. CH235.9 CDRL3 interacts with HIV-1 N280 in gp120, forming 3 H-bonds which are proposed to be disrupted due to autologous virus escape mutations in patient CH505, N280S and N280T. CH235.9 was produced as a recombinant mAb of V_H and V_L sequences found at week 152. CH235.9 neutralized 44% of a 75-autologous virus panel, 77% of a 202-multiclade Env-psuedovirus panel and 58% of an 113-patient CH505-derived autologous pseudoviral panel as part of CH235 lineages, all at potencies of <50 µg/ml. It also acquired the ability to neutralize all loop D mutants that were resistant to early members of the CH235 lineage. *Bonsignori2016* (**antibody generation**, **mutation acquisition**, **neutralization**, **escape**, **binding affinity**, **antibody sequence**, **antibody lineage**)

References

Showing 3 of 3 references.

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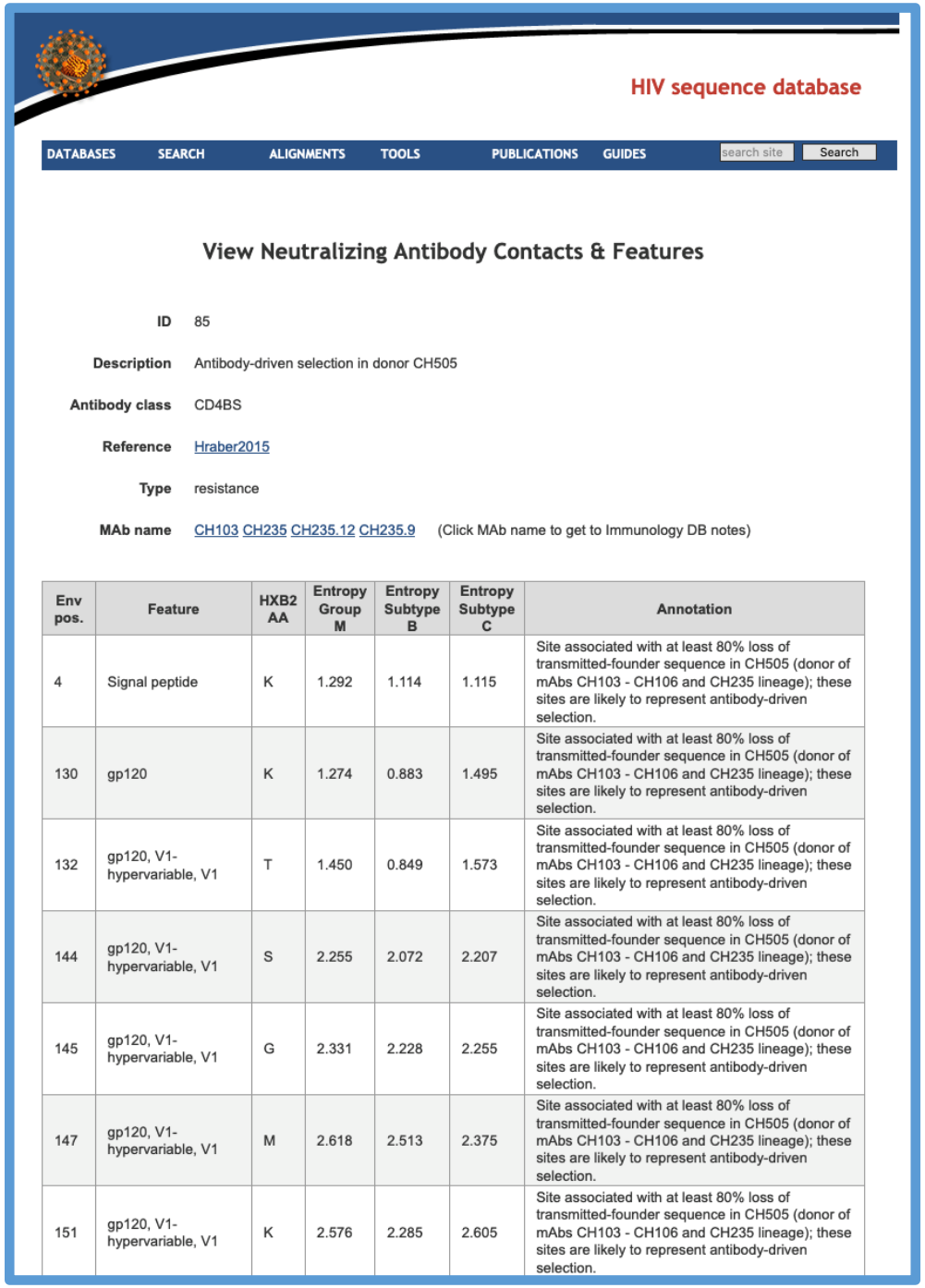

HIV sequence database

DATABASES SEARCH ALIGNMENTS TOOLS PUBLICATIONS GUIDES search site Search

View Neutralizing Antibody Contacts & Features

ID 85

Description Antibody-driven selection in donor CH505

Antibody class CD4BS

Reference Hraber2015

Type resistance

MAb name CH103 CH235 CH235.12 CH235.9 (Click MAb name to get to Immunology DB notes)

Env pos.	Feature	HXB2 AA	Entropy Group M	Entropy Subtype B	Entropy Subtype C	Annotation
4	Signal peptide	K	1.292	1.114	1.115	Site associated with at least 80% loss of transmitted-founder sequence in CH505 (donor of mAbs CH103 - CH106 and CH235 lineage); these sites are likely to represent antibody-driven selection.
130	gp120	K	1.274	0.883	1.495	Site associated with at least 80% loss of transmitted-founder sequence in CH505 (donor of mAbs CH103 - CH106 and CH235 lineage); these sites are likely to represent antibody-driven selection.
132	gp120, V1-hypervariable, V1	T	1.450	0.849	1.573	Site associated with at least 80% loss of transmitted-founder sequence in CH505 (donor of mAbs CH103 - CH106 and CH235 lineage); these sites are likely to represent antibody-driven selection.
144	gp120, V1-hypervariable, V1	S	2.255	2.072	2.207	Site associated with at least 80% loss of transmitted-founder sequence in CH505 (donor of mAbs CH103 - CH106 and CH235 lineage); these sites are likely to represent antibody-driven selection.
145	gp120, V1-hypervariable, V1	G	2.331	2.228	2.255	Site associated with at least 80% loss of transmitted-founder sequence in CH505 (donor of mAbs CH103 - CH106 and CH235 lineage); these sites are likely to represent antibody-driven selection.
147	gp120, V1-hypervariable, V1	M	2.618	2.513	2.375	Site associated with at least 80% loss of transmitted-founder sequence in CH505 (donor of mAbs CH103 - CH106 and CH235 lineage); these sites are likely to represent antibody-driven selection.
151	gp120, V1-hypervariable, V1	K	2.576	2.285	2.605	Site associated with at least 80% loss of transmitted-founder sequence in CH505 (donor of mAbs CH103 - CH106 and CH235 lineage); these sites are likely to represent antibody-driven selection.

Antibody Contacts and Features DB

ID 84

Description Electrostatic interactions with D368

Antibody class CD4BS

Reference Bonsignori2016

Type binding

MAb name CH235.12 CH235.9 VRC01 (Click MAb name to get to Immunology DB notes)

Env pos.	Feature	HXB2 AA	Entropy Group M	Entropy Subtype B	Entropy Subtype C	Annotation
368	gp120, CD4 binding loop	D	0.024	0.023	0.029	D368 contacts the CDR H2 loop of VRC01, CH235.9, and CH235.12 by electrostatic interactions.

Important position(s) with Hxb2 amino acid: D368

https://www.hiv.lanl.gov/components/sequence/HIV/featuredb/search/env_ab_view_pub.comp?ac_id=85

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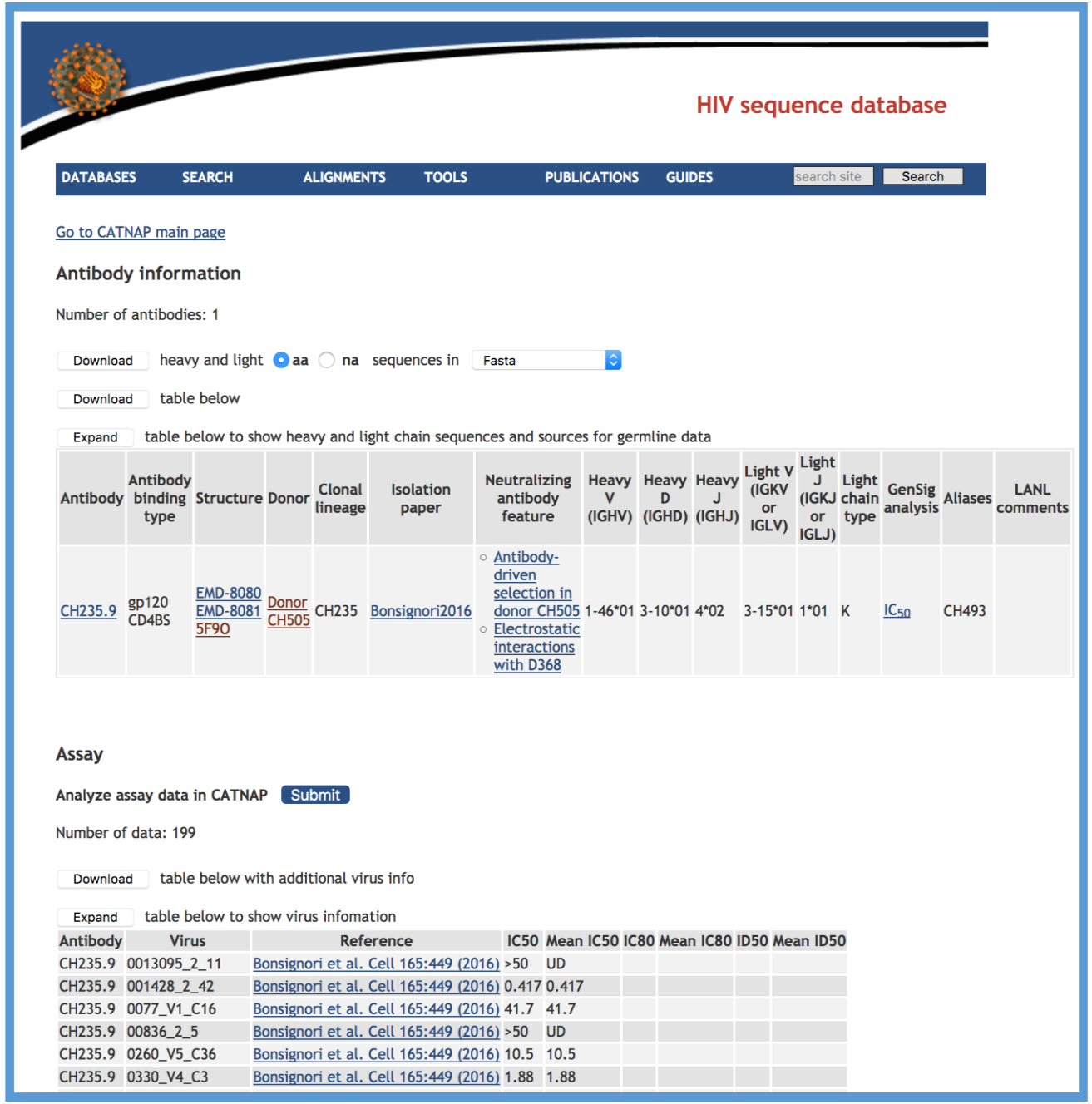

HIV sequence database

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Antibody information

Number of antibodies: 1

Download heavy and light aa na sequences in Fasta

Download table below

Expand table below to show heavy and light chain sequences and sources for germline data

Antibody	Antibody binding type	Structure	Donor	Clonal lineage	Isolation paper	Neutralizing antibody feature	Heavy V (IGHV)	Heavy D (IGHD)	Heavy J (IGHJ)	Light V (IGKV or IGLV)	Light J (IGKJ or IGLJ)	Light chain type	GenSig analysis	Aliases	LANL comments
CH235.9	gp120 CD4BS	EMD-8080 EMD-8081 5F9O	Donor CH505	CH235	Bonsignori2016	○ Antibody-driven selection in donor CH505 ○ Electrostatic interactions with D368	1-46*01	3-10*01	4*02	3-15*01	1*01	K	IC_{50}	CH493	

Assay

Analyze assay data in CATNAP Submit

Number of data: 199

Download table below with additional virus info

Expand table below to show virus infomation

Antibody	Virus	Reference	IC50	Mean IC50	IC80	Mean IC80	ID50	Mean ID50
CH235.9	0013095_2_11	Bonsignori et al. Cell 165:449 (2016)	>50	UD				
CH235.9	001428_2_42	Bonsignori et al. Cell 165:449 (2016)	0.417	0.417				
CH235.9	0077_V1_C16	Bonsignori et al. Cell 165:449 (2016)	41.7	41.7				
CH235.9	00836_2_5	Bonsignori et al. Cell 165:449 (2016)	>50	UD				
CH235.9	0260_V5_C36	Bonsignori et al. Cell 165:449 (2016)	10.5	10.5				
CH235.9	0330_V4_C3	Bonsignori et al. Cell 165:449 (2016)	1.88	1.88				

CATNAP and Sequence DB: CH235.9

https://www.hiv.lanl.gov/components/sequence/HIV/neutralization/main_immuno.comp?immuno_ab_id=3291

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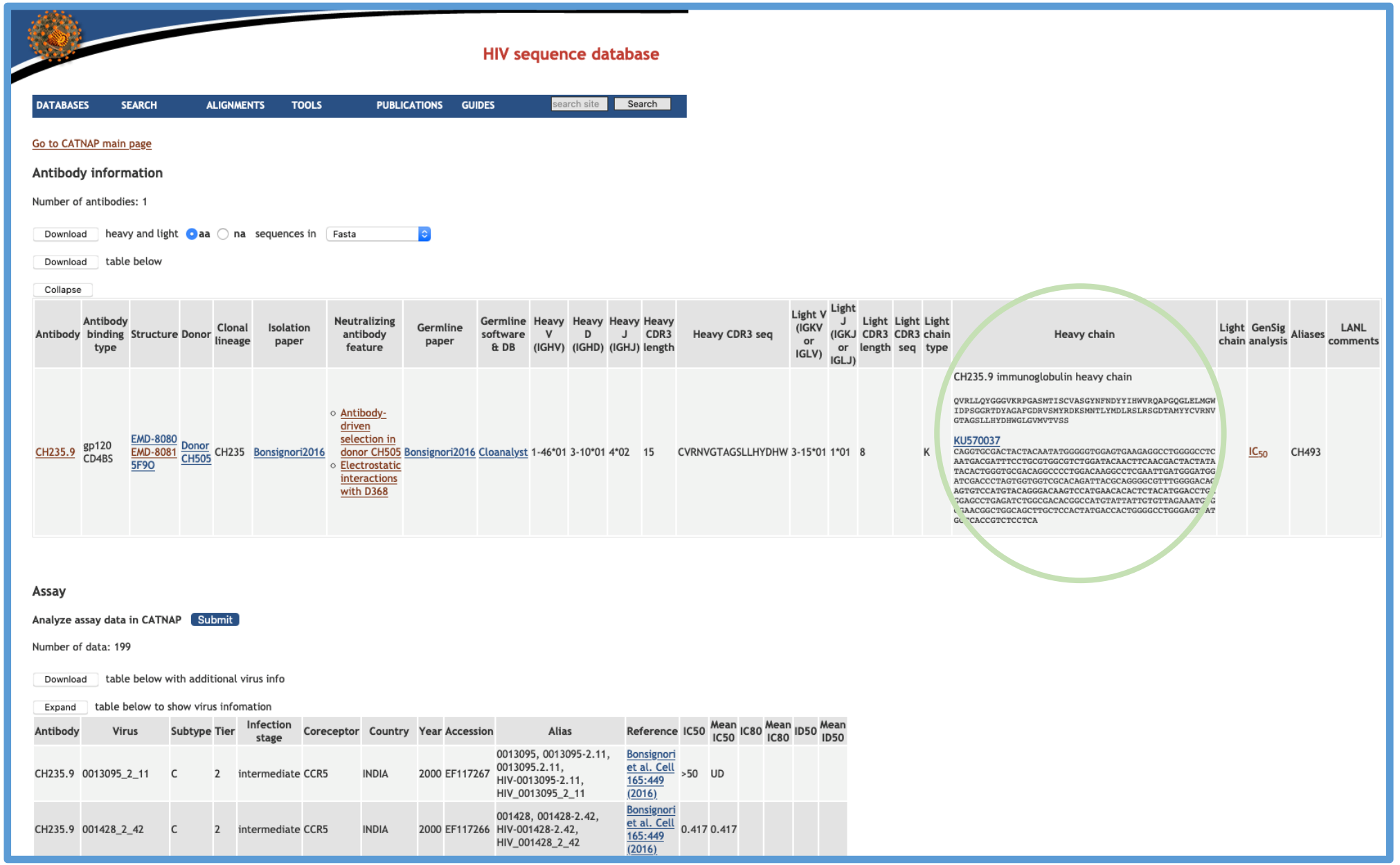
CATNAP and Sequence DB expanded view: CH235.9



HIV sequence database

DATABASES SEARCH ALIGNMENTS TOOLS PUBLICATIONS GUIDES search site Search

Go to CATNAP main page

Antibody information

Number of antibodies: 1

Download heavy and light aa na sequences in Fasta

Download table below

Collapse

Antibody	Antibody binding type	Structure	Donor	Clonal lineage	Isolation paper	Neutralizing antibody feature	Germline paper	Germline software & DB	Heavy V (IGHV)	Heavy D (IGHD)	Heavy J (IGHJ)	Heavy CDR3 length	Heavy CDR3 seq	Light V (IGKV or IGLV)	Light J (IGKJ or IGLJ)	Light CDR3 length	Light CDR3 seq	Light chain type	Heavy chain	Light chain	GenSig analysis	Aliases	LANL comments
CH235.9	gp120 CD4BS	EMD-8080 EMD-8081 5F9O	Donor CH505	CH235	Bonsignori2016	○ Antibody-driven selection in donor CH505 ○ Electrostatic interactions with D368	Bonsignori2016	Cloanalyst	1-46*01	3-10*01	4*02	15	CVRNVGTAGSLLHYDHW	3-15*01	1*01	8		K	CH235.9 immunoglobulin heavy chain QVRLLQYGGGVKRPGASMTISCVASGYNFNDYYIHWVRQAPGQGLELMGW IDPSGGRTDYAGAFGDRVSMYRDKSMNTLYMDLRSLRSGDTAMYYCVRNV GTAGSLLHYDHWGLGVMVTVSS KU570037 CAGGTGCGACTACTACAATATGGGGGTGGAGTGAAGAGGCCTGGGGCCTC AATGACGATTTCCTGCGTGGCGTCTGGATACAACTTCAACGACTACTATA TACACTGGGTGCGACAGGCCCCTGGACAAGGCCTCGAATTGATGGGATCG ATCGACCCTAGTGGTGGTCGCACAGATTACGCAGGGCGTTTGGGGACAC AGTGTCCATGTACAGGGACAAGTCCATGAACACACTCTACATGGACCTG TGGAGCCTGAGATCTGGCGACACGGCCATGTATTATTGTGTTAGAAATG G GAACGGCTGGCAGCTTGCTCCACTATGACCACTGGGGCCTGGGAGT AT GC CACCGTCTCCTCA		IC_{50}	CH493	

Assay

Analyze assay data in CATNAP Submit

Number of data: 199

Download table below with additional virus info

Expand table below to show virus infomation

Antibody	Virus	Subtype	Tier	Infection stage	Coreceptor	Country	Year	Accession	Alias	Reference	IC50	Mean IC50	IC80	Mean IC80	ID50	Mean ID50
CH235.9	0013095_2_11	C	2	intermediate	CCR5	INDIA	2000	EF117267	0013095, 0013095-2.11, 0013095.2.11, HIV-0013095-2.11, HIV_0013095_2_11	Bonsignori et al. Cell 165:449 (2016)	>50	UD				
CH235.9	001428_2_42	C	2	intermediate	CCR5	INDIA	2000	EF117266	001428, 001428-2.42, HIV-001428-2.42, HIV_001428_2_42	Bonsignori et al. Cell 165:449 (2016)	0.417	0.417				

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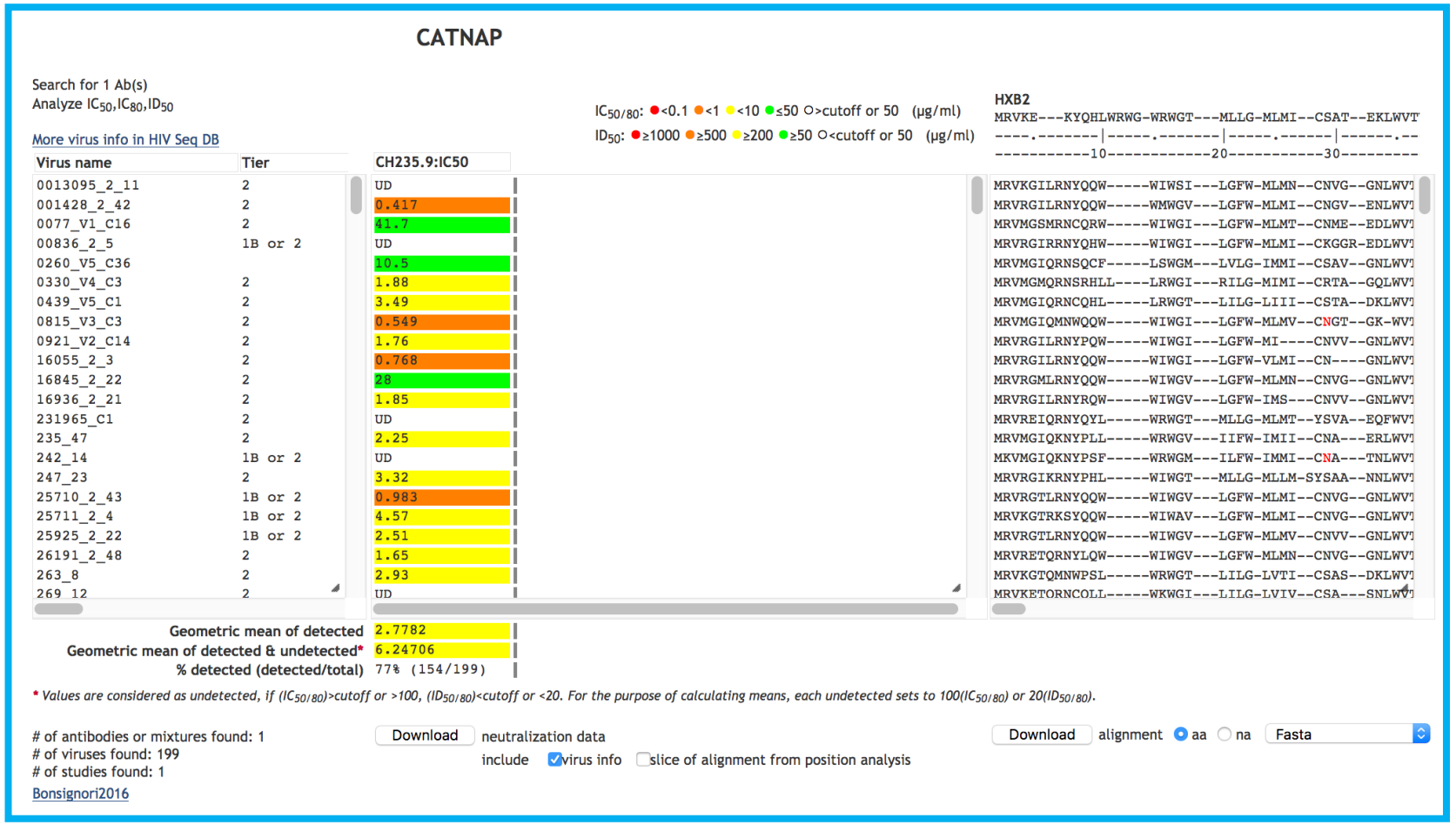
Neutralization Data: CH235.9

- Antibodies with neutralization data are linked to CATNAP
  - Detailed antibody information including Ab sequences and germlines
  - Inhibition assay results against virus panels
  - Genetic signatures associated with antibody sensitivity or resistance



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Thank you

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seq-info@lanl.gov