

HIV Database Immunology Workshop

<https://www.hiv.lanl.gov/>

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seq-info@lanl.gov

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Database PI: Brian Foley

Additional database staff:

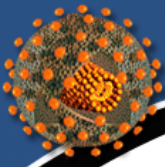
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Contract Office Representative: Anjali Singh, NIAID, NIH



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

LA-UR-22-31269



HIV DATABASES

<https://hiv.lanl.gov/>

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. AA12007-001-00000. Our content is reviewed by an [Editorial Board](#).

[SEQUENCE DATABASE ▶](#)

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[IEDB User Workshop 2022](#)

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[Web and Database Programmer Position](#)

We seek a motivated, skilled, and independent computer programmer with experience in web interfaces to develop and maintain database and bioinformatics tools and applications. The primary responsibility of the position will be improving the data entry system for the HIV Molecular Immunology Database. This meaningful work has already impacted the lives of tens of millions of people living with HIV. [Apply here](#). 23 August 2022

[N-Glycosite new function](#)

The [N-Glycosite](#) tool can highlight and tally N-linked glycosylation sites in an amino acid sequence. A new functionality can change O-marked glycosylation sites to N. 10 August 2022

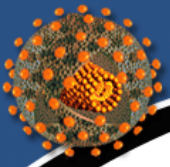
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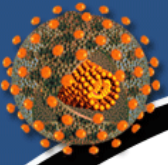
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Data and Tools

Pathogen

- Sequence
- Structure
- Modifications
- Ab Epitopes (linear or discontinuous)

Host

- CTL/HTL Epitopes
- Presenting HLA
- Immune Response
- Antibodies
- Ab Neutralizations
- Ab Features/Contacts
- Patient Database

Many “HIV Immunology” tools are broadly applicable

- **Tools list is color-coded by range of use**

HIV molecular immunology
database



HIV Molecular Immunology Database: Tools & Links

Tools Produced by the Los Alamos HIV Databases

- [CATNAP: Compile, Analyze and Tally NAb Panels](#) Download or analyze neutralization data
- [CombiNAber](#) Predict the neutralization of combinations of antibodies
- [HIV Genome Browser](#) Display HIV genome and proteome
- [QuickAlign](#) Align amino acids or nucleotides against our alignments
- [Analyze Align](#) Show weblogos, calculate frequency by position, and find variants in an alignment
- [Alignment Slicer](#) Cut vertical slices from sequence alignments
- [PeptGen](#) Generate overlapping peptides for any protein
- [PepMap](#) Generate peptide maps in Fasta, HTML and PDF formats
- [Motif Scan](#) Scan alignments for HLA binding motifs
 - [HLA genotype/serotype dictionary](#)
 - [HLA genotype/motif dictionary](#)
 - [HLA supertype dictionaries](#)
- [Hepitope](#) Search for hopeful epitopes based on HLA enrichment
- [HLA Frequency Analysis Tools](#) Calculate HLA frequencies or HLA linkage disequilibrium in a population
- [ELF](#) Epitope location finder
- [Sequence Locator Tool](#) Find the location of any HIV/SIV sequence
- [SeqPublish](#) Produce pretty alignments for publication
- [Heatmap](#) Display a table of numbers using colors to represent the numerical values
- [Epigraph Vaccine Suite](#) Design and assess Epigraphs for vaccine design
- [Mosaic Vaccine Suite](#) Design and assess polyvalent protein sequences for T-cell vaccines
- [N-Glycosite](#) Find N-linked glycosylation sites
- [Highlighter](#) Highlight matches and mismatches in a set of aligned sequences
- [Protein Feature Accent](#) View 3D graphics of HIV proteins
- [Variable Region Characteristics](#) analyzes Env variable loops and reports length, glycosolations, and net charge

- Tools specific for HIV/SIV
- General use tools with some HIV/SIV-specific features
- General use tools

HIV Immunology Database - 2022 Additions

Continuing Efforts

- Curated annotations
- Maintained and updated tools, maps and tables
- Updated Help pages
- Published annual compendium

Upgrades

- Expanded and searchable patient database, linked Seq and Immuno Patient Codes and Database IDs
- HLA nomenclature updated further, consistent with 2022 HLA update
- Somatic hypermutation data added to Neutralization DB (=CATNAP)
- API for JSON and CSV download capability expanded



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- Sequence DB
- Databases
- Immunology
- Neutralization DB
- T cell contacts DB
- HCV Databases
- HFV Databases

HIV Molecular Immunology Database

Immunology Database is an annotated, searchable collection of T-cell epitopes and antibodies.

Search Interfaces

- [CTL/CD8+ search](#)
- [T Helper/CD4+ search](#)
- [Antibody search](#)
- [CTL variant search](#)
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- [Patient search](#)

- [Search help](#)
- [Patient search help](#)
- [Variant search help](#)

Database Products

- [All database products and publications](#)
- [Epitope maps](#)
- [Epitope and antibody tables](#)
- [Epitope alignments](#)
- [Epitope density plots](#)
- [T cell epitope variants and escape mutations](#)
- [Neutralizing antibody resources / CATNAP](#)
- [The HIV Molecular Immunology Compendia](#)

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- [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](#).
- [HLA Typing and Epitope Mapping Data Sets](#)
- [Standardized Assessments of Neutralizing Antibodies for HIV/AIDS Vaccine Development](#) Assay protocols from Duke Central Reference Laboratory

Tools

- [Immunology database tools](#)
- [Sequence database tools](#)

Information

- [Tutorials and basic information](#)
- [Frequently-asked Questions \(FAQ\)](#)

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- [About the HIV Molecular Immunology Database](#)
- [Editorial board](#)
- [How to cite this database](#)

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Rapid Epitope Searches - and Sequential

- Linear Antibody Epitope Search
- Use of HIV Genome Browser Tool
- Find overlapping Helper/HTL Epitopes
- Overlapping CTL Epitope Search
- Discontinuous Antibody Epitope Searches



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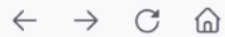
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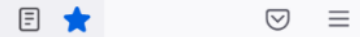
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Linear Antibody Epitope Search



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




Database

Databases Search Tools Products Info

HIV Molecular Immunology Database


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HIV Molecular Immunology Database Search

Antibody Search

[Search Help](#)

HIV protein	<input type="text" value="-ALL-"/> Gag p17 p24 p2p7p1p6	
HXB2 protein location	<input type="text"/> <input type="text"/>	Results overlap with query location
HXB2 DNA location	<input type="text"/> <input type="text"/>	Results overlap with query location
Epitope	<input type="text"/>	Results contain query sequence
Epitope name	<input type="text"/>	
MAb name	<input type="text" value="10E8"/>	<input type="checkbox"/> Exact Match (List by name) (List by type)
Record number	<input type="text"/>	
Subtype	<input type="text" value="-ALL-"/>	
Immunogen	<input type="text" value="anti-idiotyp
autoimmune disease
engineered
HIV-1 exposed seronegative
HIV-1 infection
HIV-2 infection
in vitro stimulation or selection"/>	
Vaccine details if Immunogen is Vaccine	Vaccine type <input type="text" value="-ALL-"/> Vaccine strain <input type="text" value="-ALL-"/> Vaccine component <input type="text" value="-ALL-"/> Adjuvant <input type="text" value="-ALL-"/>	
Ab type	<input type="text" value="-ALL-"/> Antisense protein (ASP) C-domain C-HR C-term flap region fusion peptide // near gp41-gp120 interface	
Species	<input type="text" value="-ALL-"/>	
Isotype	<input type="text" value="-ALL-"/>	
Author	<input type="text"/>	Search only for <input type="checkbox"/> First <input type="checkbox"/> Last <input checked="" type="radio"/> Show only this author's references <input type="radio"/> Show all references
Country	<input type="text" value="-ALL-"/>	
Keywords	<input type="text" value="-ALL-"/> acute/early infection ADCC adjuvant comparison antibody binding site antibody generation antibody gene transfer	<input checked="" type="radio"/> Show only notes containing selected keyword(s) <input type="radio"/> Show all notes
Notes	<input type="text"/>	<input checked="" type="radio"/> Show only notes matching this text <input type="radio"/> Show all notes

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

Displaying record number 2708

Download this epitope [record as JSON](#). [[Help](#)]

MAb name 10E8
HXB2 gp160(671-683)
location DNA(6235..8273)
Author location

Epitope NWFDISNWLWYIK

Subtype B
Ab type gp41 MPER (membrane proximal external region)
Neutralizing P (tier 2)
Contacts and Features [View contacts and features](#)
Species (isotype) human(IgG3)
Immunogen HIV-1 infection
Patient MHC/HLA [Donor N152:](#)

Keywords ADCC, antibody binding site, antibody generation, antibody interactions, assay or method development, autoantibody or autoimmunity, glycosylation, immunoprophylaxis, neutralization, vaccine antigen design, variant cross-reactivity, viral fitness and reversion, vaccine-induced immune responses, computational epitope prediction, acute/early infection, binding affinity, immunotherapy, mother-to-infant transmission, review, subtype comparisons, antibody sequence, structure, antibody gene transfer, antibody lineage, antibody polyreactivity, bispecific/trispecific, broad neutralizer, chimeric antibody, contact residues, transmission pair

Notes

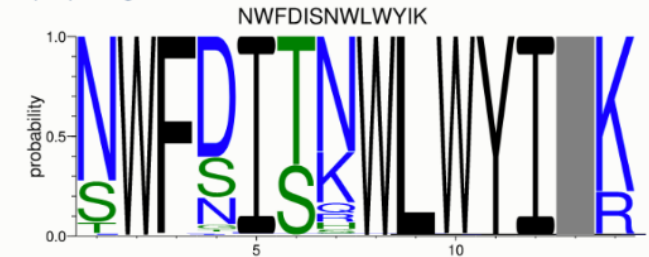
Showing 73 of 73 notes.

- 10E8: A novel antibody was isolated from donor CAP248, who first developed cross-neutralizing antibodies after about 1 year of infection. The neutralization breadth of CAP248-2B, isolated from a sample taken 3.5 years post-infection, largely recapitulates the donor's serum breadth, and was able to neutralize 22% of a panel of cross-clade viruses at IC₂₀. CAP248-2B was predicted to be derived from germline genes IGHV4-31*05, IGHD6-13*01, IGHJ3*01/02, IGLV2-14*01, and IGLJ1*01. The crystal structure suggested binding of the unusually long 19aa light chain of the paratope to both the C terminus of gp120 and to parts of gp41. The gp160 cleavage site was also the site of unusual escape mutations in the donor's viral

Genbank Accession K03455.1

[gp160 Epitope Map](#)

[Epitope Alignment](#)



[View neutralization details](#)

gp160 Ab Epitope Map

Interactive Epitope Maps

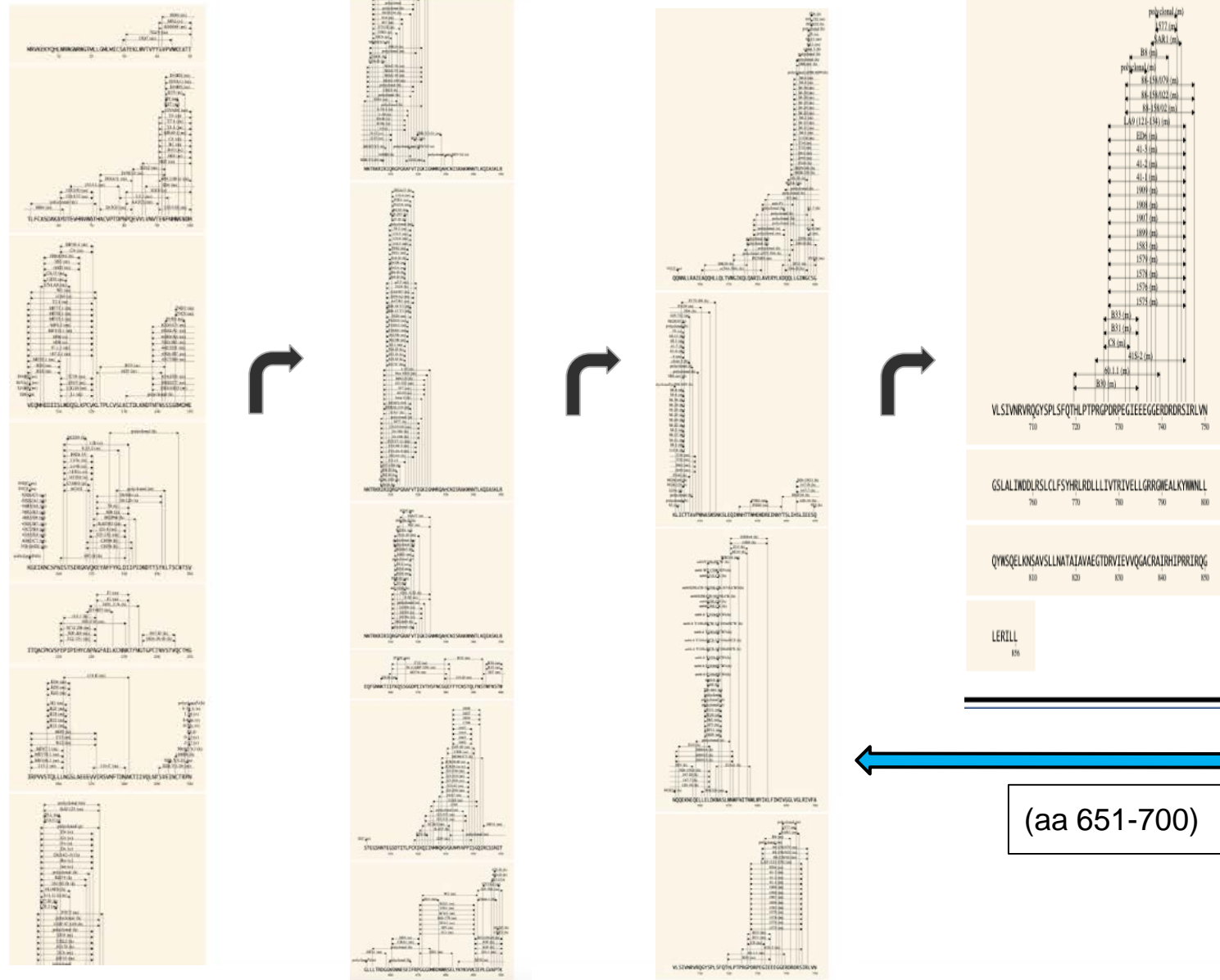
These interactive epitope maps are based on our database of human HIF-1 epitopes.

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

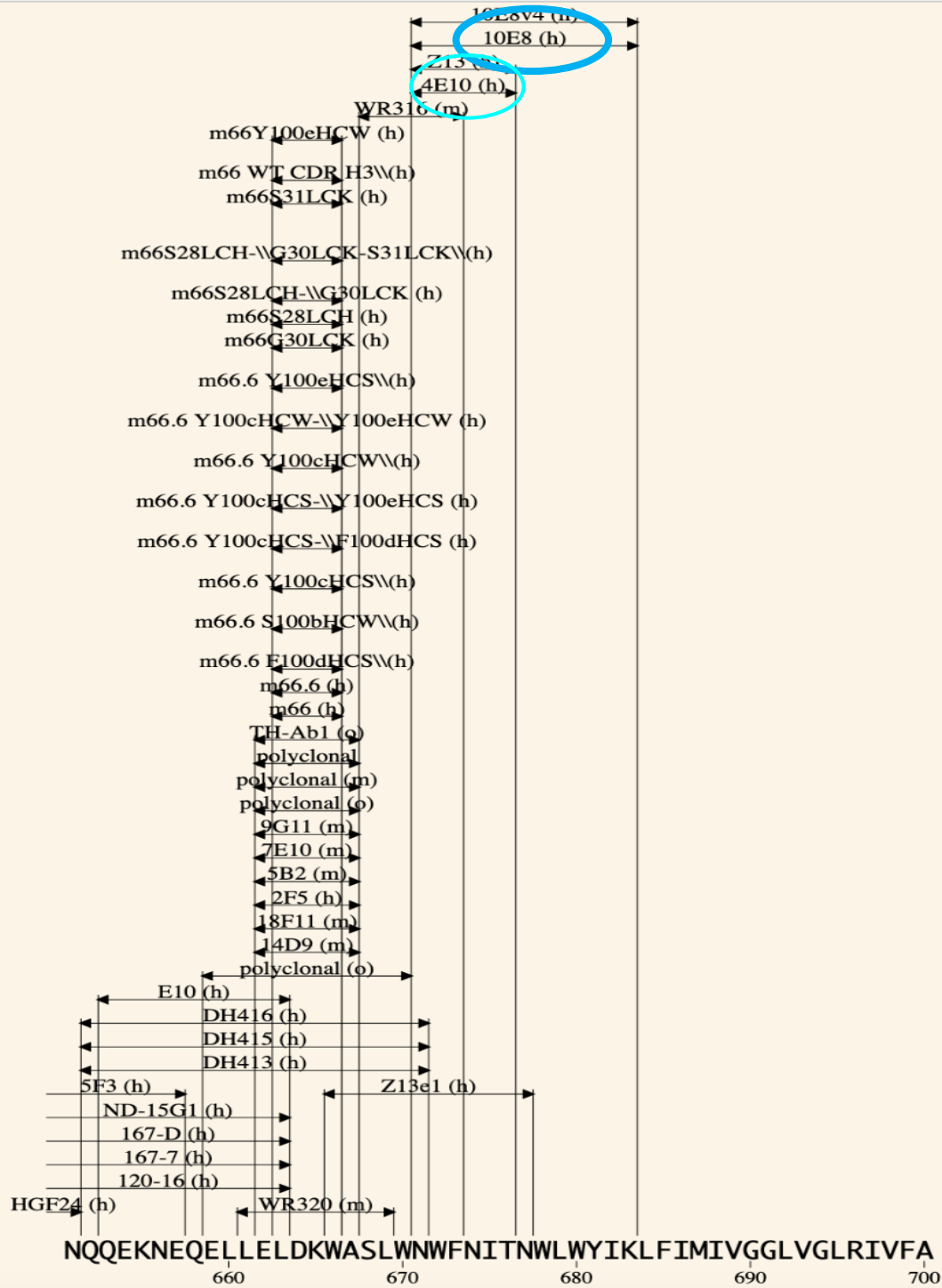
The names of MAb and the location of well characterized linear binding sites of 21 amino acids or less are indicated relative to the protein sequences of the gp160 clone. This map is meant to provide the relative location of epitopes on a given protein, but the HIF-2 sequence may not actually bind to the MAb of interest, as it may vary relative to the sequence for which the epitope was defined. Above each linear binding site, the MAb name is given followed by the species in parentheses. Human is represented by 'H', non-human primates by 'p', mouse by 'm', and others by 'x'. More precise species designations for any given MAb can be found using the web search interface.

Note: These epitopes only represent known linear antibody epitopes. Contact sites for non-linear epitopes can be viewed from our [3D feature search](#). [Genome Browser of Env sequences](#) is also available.

Data last updated at 2022-09-14 15:20:24-06



(aa 651-700)



gp160 Ab Epitope Map

Interactive Epitope Maps

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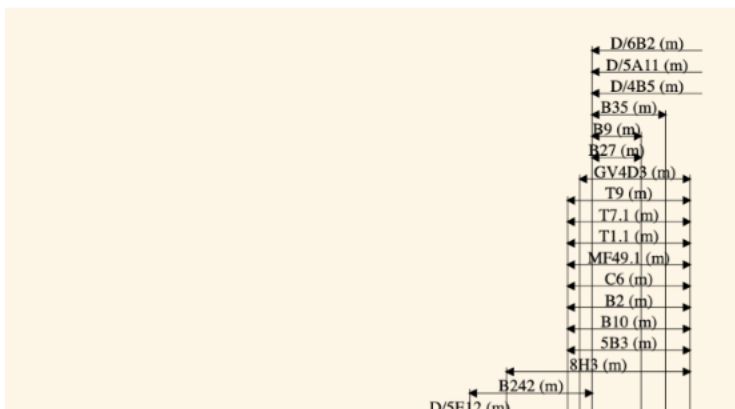
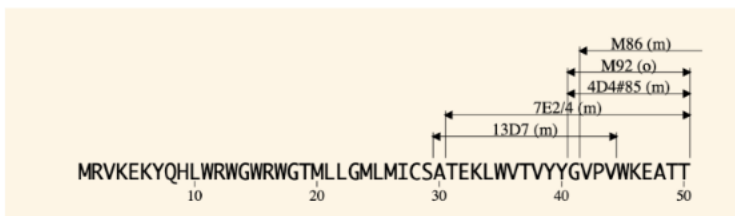
These maps are implemented with SVG (scalable vector graphics), which is supported by most, but not all, web browsers. The [static version of this page](#) is also available.

The names of MABs and the location of well characterized *linear* binding sites of 21 amino acids or less are indicated relative to the protein sequences of the HXB2 clone. This map is meant to provide the relative location of epitopes on a given protein, but the HXB2 sequence may not actually bind to the MAB of interest, as it may vary relative to the sequence for which the epitope was defined. Above each linear binding site, the MAB name is given followed by the species in parentheses. Human is represented by 'h', non-human primate by 'p', mouse by 'm', and others by 'o'. More precise species designations for any given MAB can be found using the web search interface.

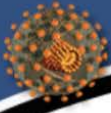
Note: These epitopes only represent known *linear* antibody epitopes. Contact sites for non-linear Env epitopes can be viewed from our [Env feature search](#), [Genome Browser](#), or [Env spreadsheet \(.xls\)](#).



Data last updated at 2022-09-14 15:20:24-06



From Linear Ab Epitope Search to HIV Genome Browser



HIV sequence database

- DATABASES
- SEARCH
- ALIGNMENTS
- TOOLS
- PUBLICATIONS
- INFO

HIV GENOME BROWSER
TOOL

HIV Genome Browser

Purpose: Interactive view of the HIV genome and proteome for juxtaposition and exploration of multiple types of data. [Help](#).

Starting Views

NOTE: These are just starting points! Within the genome browser, you can move among any of these views. Please read the quick tips and Help file before you start!

HIV-1 protein-level views:

- [Env](#) • [Gag](#) • [Nef](#) • [Pol](#) • [Rev](#) • [Tat](#) • [Vif](#) • [Vpr](#) • [Vpu](#)

HIV-1 protein-specific examples:

- [Env with CTL epitopes + entropy](#)
- [Pol with drug resistance sites + entropy](#)

Nucleotide-level views:

- [HIV-1 gene map](#)
- [SIV Mac239 gene map](#)
- [HIV-1 5' LTR](#)

Quick Tips

- **Mouseovers!** Look for mouseovers to guide you.
- **Click and right-click!** Features link to loads of information and analysis via click and right-click. If your mouse doesn't have right-click, use Ctrl-click.
- **Zoom!** There are several ways to zoom in/out. Some features can only be seen when zoomed-in or zoomed-out.
- For details about this interface, see [HIV Genome Browser Help](#).
- Watch the screencast video on the [JBrowse website](#).

References

- Skinner ME, Holmes IH. Setting up the JBrowse genome browser. Curr Protoc Bioinformatics. 2010 Dec;Chapter 9:Unit 9.13. PMID: 21154710
- Skinner ME, Uzilov AV, Stein LD, Mungall CJ, Holmes IH. JBrowse: a next-generation genome browser. Genome Res. 2009 Sep;19(9):1630-8. PMID: 19570905

https://www.hiv.lanl.gov/content/sequence/genome_browser/browser.html

filter by text 0 20 40 60 80 100 120 140 160 180 200 220 240 260 280 300 320 340 360 380 400 420 440 460 480 500 520 540 560 580 600 620 640 660 680 700 720 740 760 780 800 820 840

Env Env:1..856 (857 b) Go

intropy_M_group 125 250 375 500 625 750

intropy_B_clade

intropy_C_clade

.TL_epitopes

ib_epitopes 

helper_epitopes

neutralizing_Ab_context

IXB2_sites_of_interest

AA

Sub-protein_map gp120 gp41



JBrowse File View Help Share

0 50 100 150 200 250 300 350 400 450 500 550 600 650 700 750 800

Navigation: ← → 🔍 🔍 🔍 🔍 Env ▾ Env:593..831 (240 b) Go 📌

600 650 700 750 800

AA

Sub-protein_map

gp41

Ab_epitopes

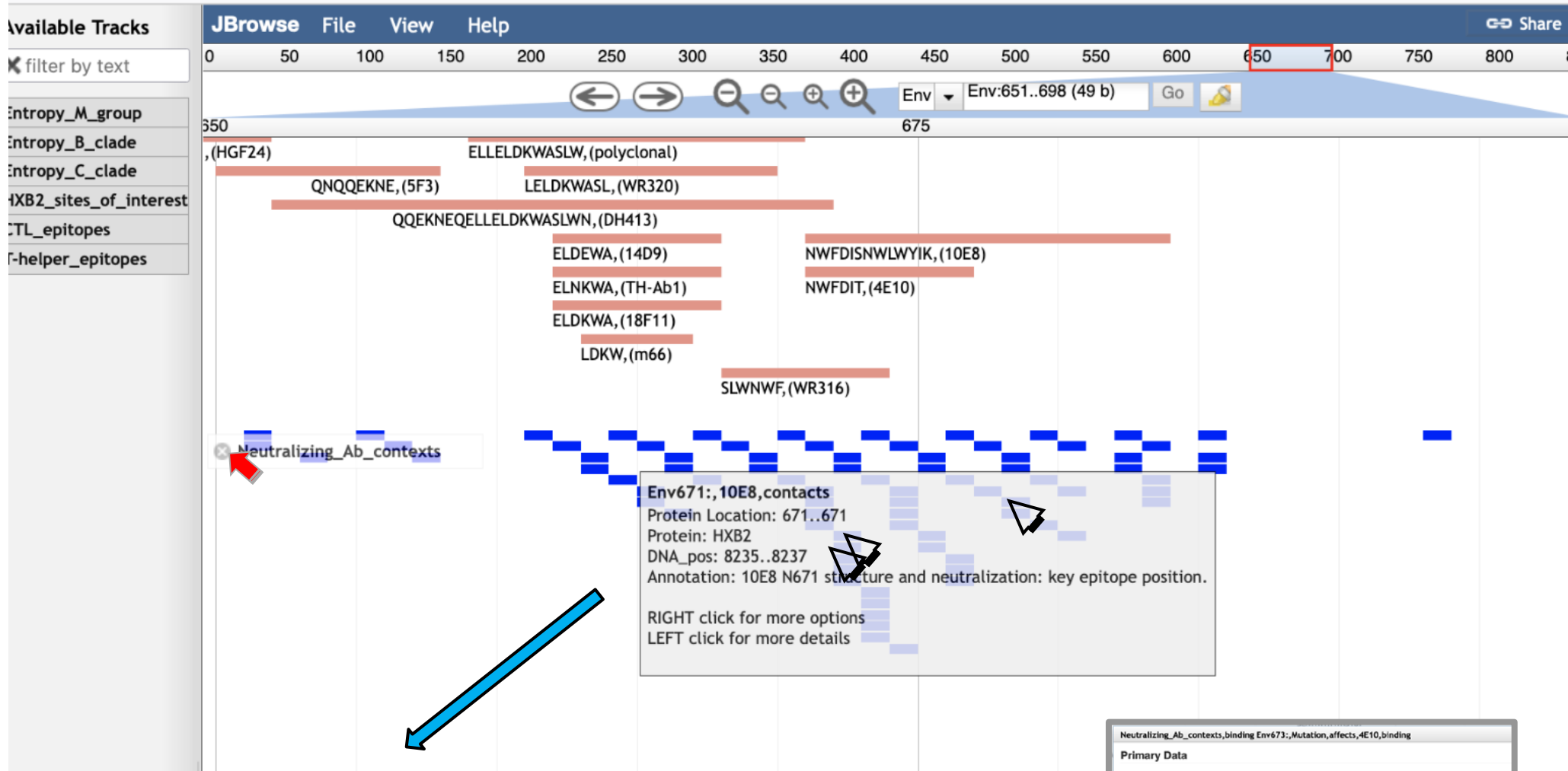
Neutralizing_Ab_contex (highlighted with red arrow)

HXB2_sites_of_interest

Ab_epitopes tooltip:

- NWFDISNWLWYIK,(10E8)
- HXB2 Location: 670..683
- Mab_name: 10E8
- Protein: HXB2
- RIGHT click for more options
- LEFT click for more details

<https://www.hiv.lanl.gov/content/sequence/jbrowse/>



Neutralizing_Ab_contexts, neutralization Env672; Sites, affecting, neutralization, of, 10E8

Neutralizing_Ab_contexts, neutralization
 Env672; Sites, affecting, neutralization, of, 10E8

Name	Env672; Sites, affecting, neutralization, of, 10E8
Type	function values() { [native code] }

Attributes

Annotation	Mutating both positions 672 and 673 to L affects neutralization
Dna_name	HXB2
Dna_pos	8238..8240
Protein_name	Env
Protein_pos	672..673
Pubmed	28076415
Reference	Witmer2017(Pubmed ID:28076415)
Seq_id	Env
Source	function values() { [native code] }

Region sequence

```
>Env Env:672..672
class=Neutralizing_Ab_contexts,neutralization length=1
W
```

mutating both positions 672 & 673 to L affects neutralization

Neutralizing_Ab_contexts, contacts Env672; 10E8, contacts

Neutralizing_Ab_contexts, contacts Env672; 10E8, contacts

Name	Env672; 10E8, contacts
Type	function values() { [native code] }

Attributes

Annotation	10E8 W672 structure and neutralization: key epitope position.
Dna_name	HXB2
Dna_pos	8238..8240
Protein_name	Env
Protein_pos	672..672
Pubmed	23151583
Reference	Huang2012a(Pubmed ID:23151583)
Seq_id	Env
Source	function values() { [native code] }

Region sequence

```
>Env Env:672..672 class=Neutralizing_Ab_contexts,contacts
length=1
W
```

W672: structure & neutralization key epitope position

Neutralizing_Ab_contexts, binding Env673; Mutation, affects, 4E10, binding

Primary Data

Name	Env673; Mutation, affects, 4E10, binding
Type	function values() { [native code] }

Attributes

Annotation	Mutation to Ala decreases binding of 4E10
Dna_name	HXB2
Dna_pos	8241..8243
Protein_name	Env
Protein_pos	673..673
Pubmed	22238313
Reference	Montero2012(Pubmed ID:22238313)
Seq_id	Env
Source	function values() { [native code] }

Region sequence

```
>Env Env:673..673 class=Neutralizing_Ab_contexts, binding
length=1
F
```

mutation affects binding for overlapping Ab 4E10 epitope

- Available Tracks**
- filter by text
 - Entropy_M_group
 - Entropy_B_clade
 - Entropy_C_clade
 - Neutralizing_Ab_contes
 - HXB2_sites_of_interest
 - CTL_epitopes
 - T-helper_epitopes

JBrowse File View Help Share

0 50 100 150 200 250 300 350 400 450 500 550 600 650 700 750 800

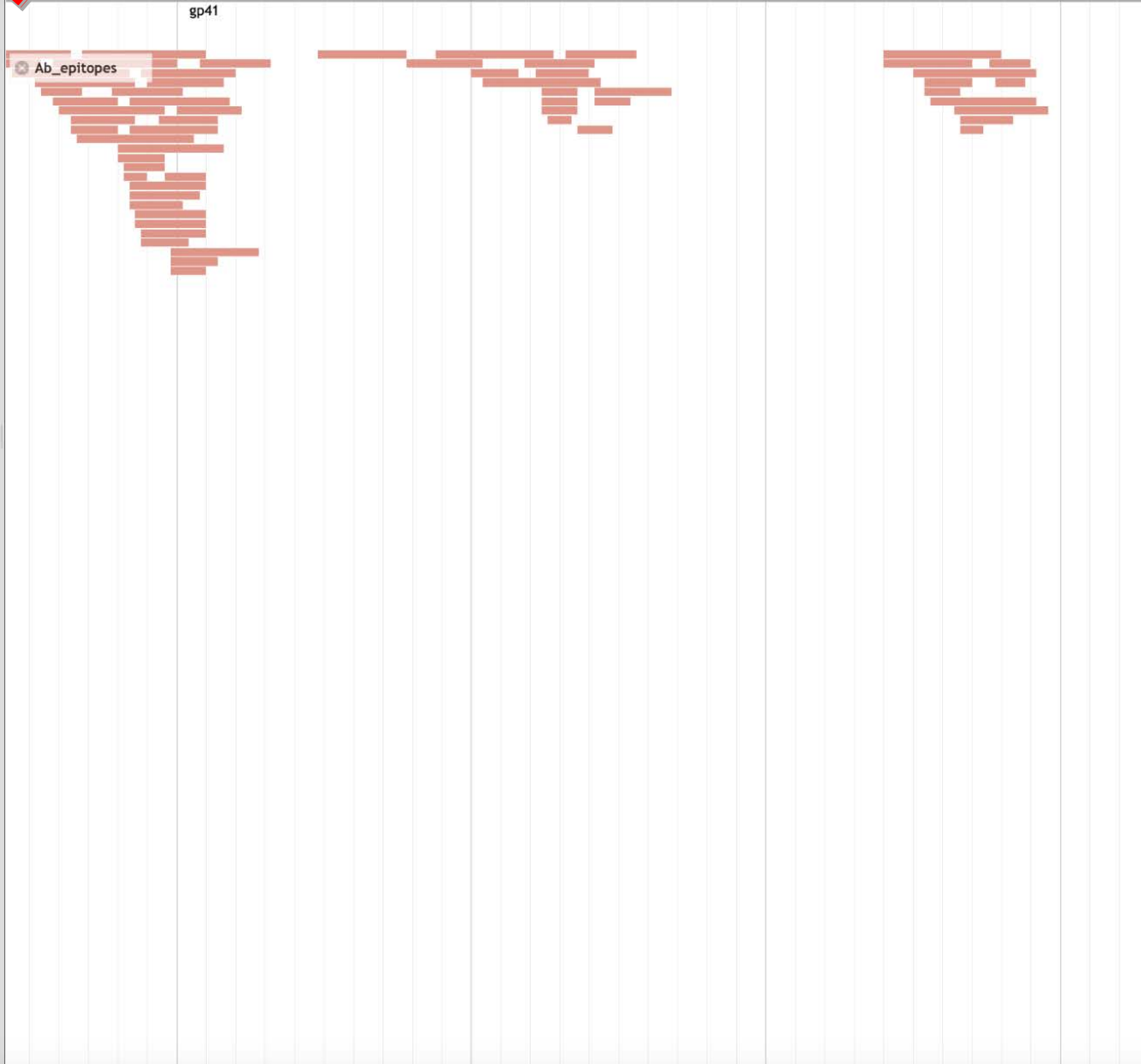
← → 🔍 🔍 🔍 🔍 🔍 Env Env:572..766 (195 b) Go 📄

600 650 700 750

AA

Sub-protein_map

gp41



<https://www.hiv.lanl.gov/content/sequence/jbrowse/>

Available Tracks

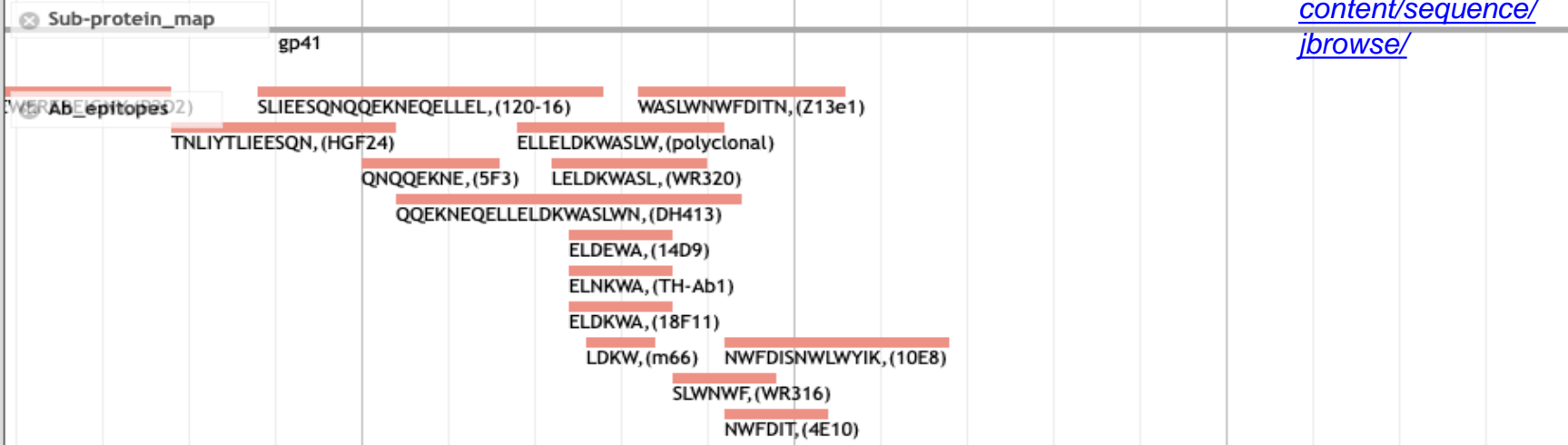
filter by text

- Entropy_M_group
- Entropy_B_clade
- Entropy_C_clade
- CTL_epitopes
- T-helper_epitopes
- Neutralizing_Ab_contes

0 20 40 60 80 100 120 140 160 180 200 220 240 260 280 300 320 340 360

650 675 700

AA...NYTSLIHS...LNW...LWYIK...VGLVGLR...VAVLS...VNRV...RQGYS...PLSFQT



<https://www.hiv.lanl.gov/content/sequence/jbrowse/>

HXB2_sites_of_interest:fusion,heptad,repeat,HR-2

Primary Data

Name: fusion,heptad,repeat,HR-2
Type: HXB2_sites_of_interest

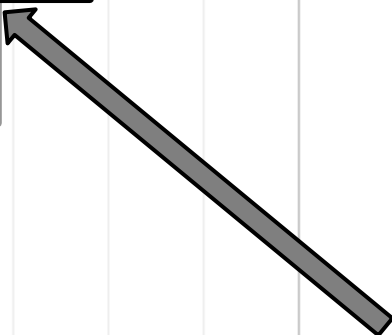
Attributes

Category: protein feature
Dna_name: HXB2
Dna_pos: 8136..8201
Parent_region: Env
Protein_name: Env
Protein_pos: 628..659
PubMed: 15219553
Reference: Cooper2004(15219553)
Seq_id: Env
Source: HIVdatabase
Style: protein structural feature

Region sequence

```
>Env Env1428..659 class=HXB2_sites_of_interest length=32
WNSMDFIINNYTSLIHSLSLIEESQNQQEKNEQELLELDKWASLWNWFDITN
```

fusion heptad-repeat, HR-2



HXB2_sites_of_interest:gp41,transmembrane,domain

Primary Data

Name: gp41,transmembrane,domain
Type: HXB2_sites_of_interest

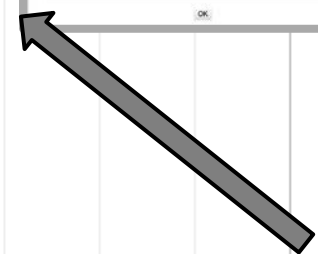
Attributes

Category: protein feature
Dna_name: HXB2
Dna_pos: 6277..6326
Parent_region: Env
Protein_name: Env
Protein_pos: 668..704
PubMed: 6627868
Reference: Guo1995(6627868)
Seq_id: Env
Source: HIVdatabase
Style: protein structural feature

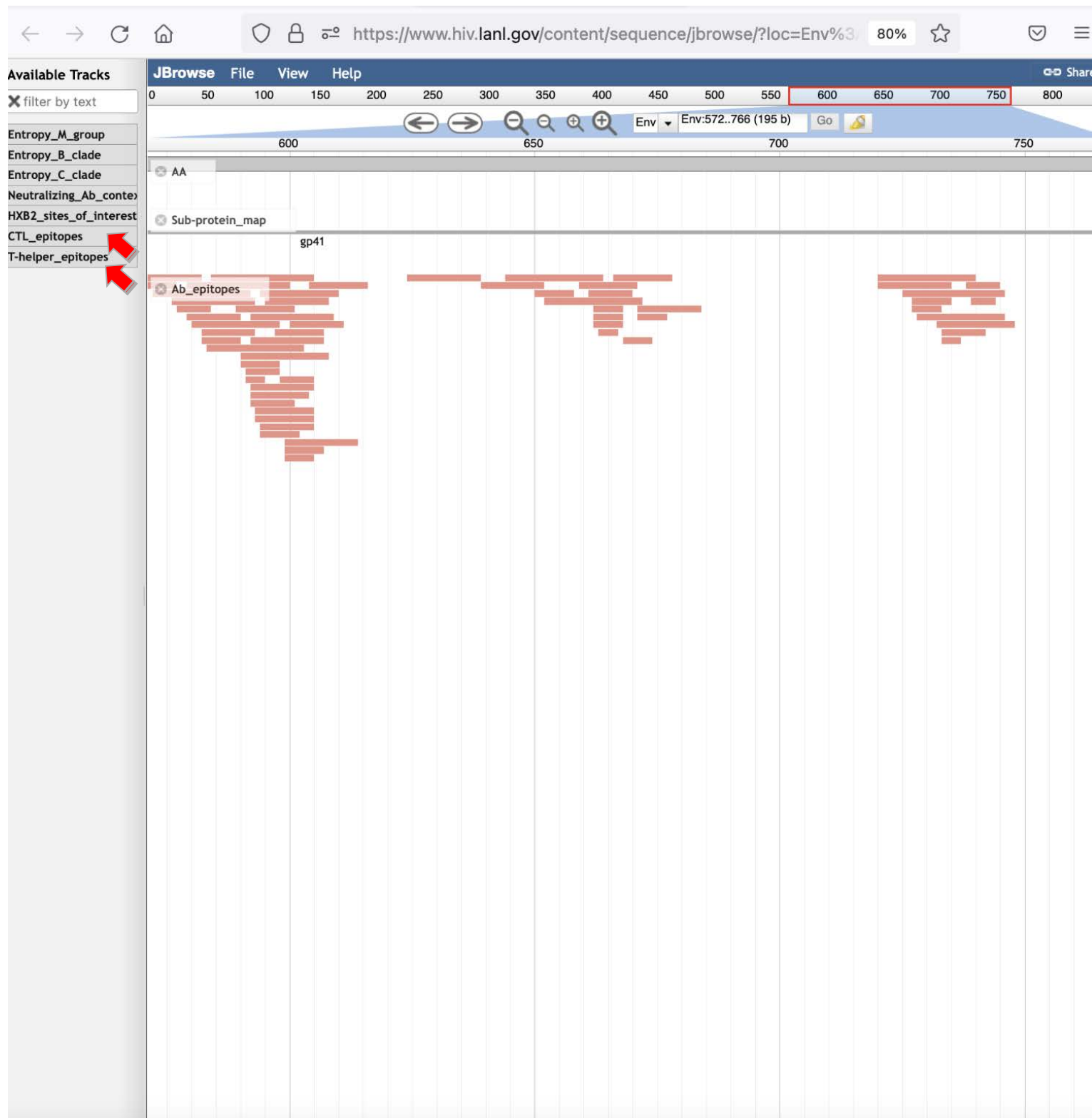
Region sequence

```
>Env Env1465..704 class=HXB2_sites_of_interest length=20
FIRLVGVLGLRIVAVLSI
```

gp41 transmembrane domain



- HXB2_sites_of_interest fusion,heptad,repeat,HR-2
- C-helix
- ct,with,gp120
- binding,site
- 524
- glycosite,637
- gp41,transmembrane,domain
- Gly-xxx-Gly,motif,(GGLVG),important,for,self-associatio
- GLRI,motif,associates,with,fusion,peptide
- gp41,cytoplasmic,tail
- YXXL,motif,inv

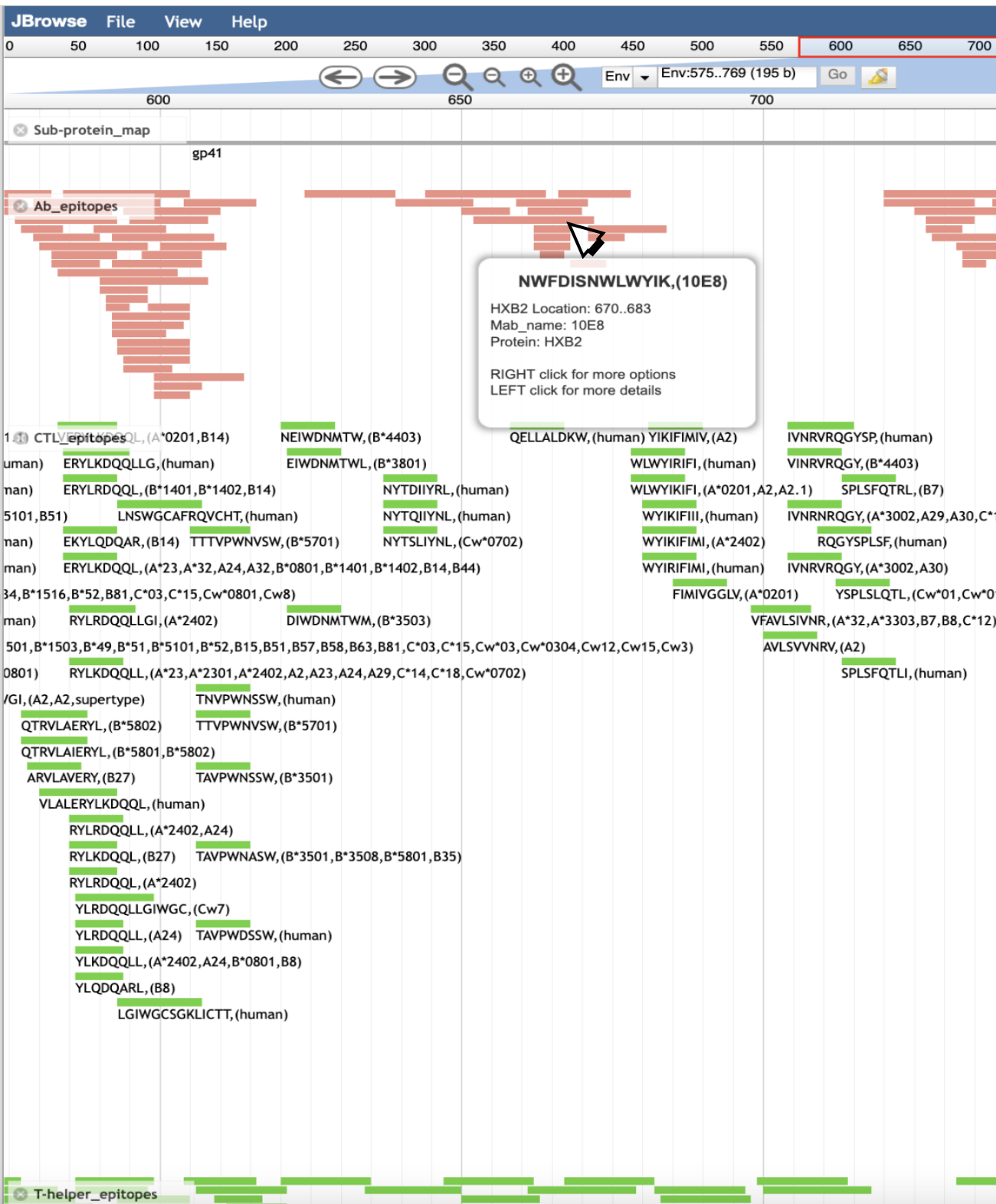


Overlapping
HTL and CTL
Epitopes ??

<https://www.hiv.lanl.gov/content/sequence/jbrowse/>

Available Tracks

- filter by text
- Entropy_M_group
- Entropy_B_clade
- Entropy_C_clade
- Neutralizing_Ab_contex
- HXB2_sites_of_interest



<https://www.hiv.lanl.gov/content/sequence/jbrowse/>

filter by text

- Entropy_M_group
- Entropy_B_clade
- Entropy_C_clade
- Neutralizing_Ab_contex
- HXB2_sites_of_interest



Overlapping HTL Epitope

T-helper epitopes LE LDKWASLWNWFNITNW, (human)

Primary Data

Name	LE LDKWASLWNWFNITNW, (human)
Type	T-helper epitopes
Position	Env 661..678
Species	human

Attributes

Dna_name	HXB2
Dna_pos	8205..8258
Epitope_seq	LE LDKWASLWNWFNITNW
Epitopes_len	18
Positions	Env 661..678
Protein_name	Env
Protein_pos	661..678
Seq_id	Env
Source	HIVdatabase
Species	human
Subtype	B

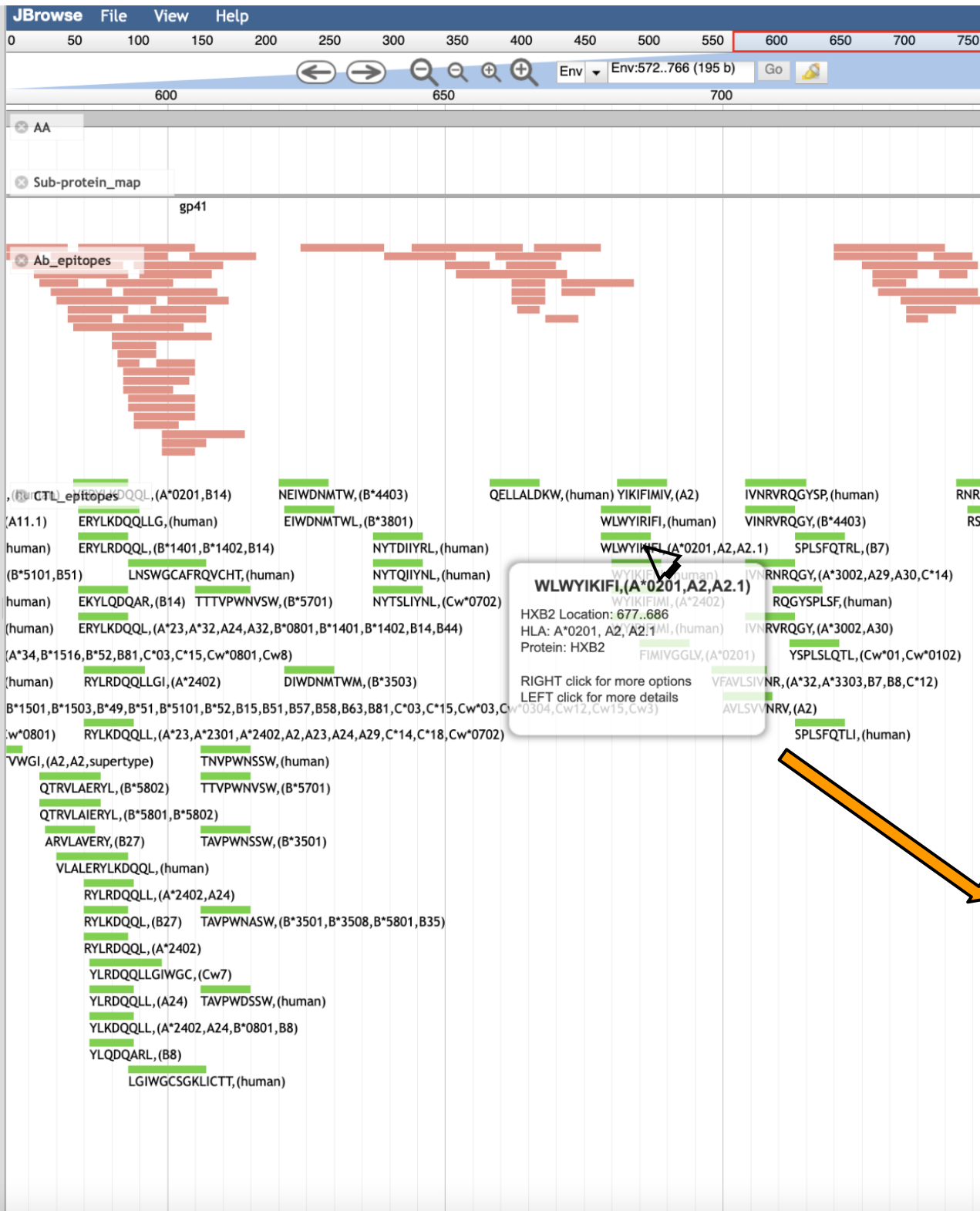
Region sequence

```
>Env Env:661..678 class=T-helper epitopes length=18
LE LDKWASLWNWFNITNW
```

OK

filter by text

- Entropy_M_group
- Entropy_B_clade
- Entropy_C_clade
- Neutralizing_Ab_contes
- HXB2_sites_of_interest
- T-helper_epitopes



Overlapping CTL Epitope

CTL_epitopes WLWYIKIFI, (A*0201, A2, A2.1)

CTL_epitopes WLWYIKIFI, (A*0201, A2, A2.1)

Name	WLWYIKIFI, (A*0201, A2, A2.1)
Type	CTL_epitopes
Position	Env 678..686
Species	human

Attributes

Dna_name	HXB2
Dna_pos	8256..8282
Epitope_seq	WLWYIKIFI
Epitopes_len	9
Hla	function values() ([native code])
Positions	Env 678..686
Protein_name	Env
Protein_pos	678..686
Seq_id	Env
Source	HIVdatabase
Species	human
Subtype	B

Region sequence

```
>Env Env:678..686 class=CTL_epitopes length=9
WLWYIKIFI
```

OK

filter by text

Entropy_M_group

Entropy_B_clade

Entropy_C_clade

Neutralizing_Ab_contes

0 50 100 150 200 250 300 350 400 450 500 550 600 650 700 750 800 8



Env Env:657..704 (49 b) Go

675

700

Sub-protein_map gp41

Ab epitopes
SONAEKEL, (120-16) WASLWNWFDITN, (Z13e1)

ELLELDKWASLW, (polyclonal)

LDKW, (5F3) LELDKWASL, (WR320)

QQEKNEQELLELDKWASLWN, (DH413)

ELDEWA, (14D9)

NWFDISNWLWYIK, (10E8)

ELNKWA, (TH-Ab1)

NWFDIT, (4E10)

ELDKWA, (18F11)

LDKW, (m66)

SLWNWF, (WR316)

HXB2_sites_of_interest C-helix

gp41, transmembrane, domain

repeat, HR-2

Gly-xxx-Gly, motif, (GGLVG), important, for, self-associati

GLRI, motif, associates, with, fusion, peptic

CTL_epitopes QELLALDKW, (human)

WLWYIRIFL, (human)

VFAVLSIVNR, (A*32, A*3303,

WLWYIKIFI, (A*0201, A2, A2.1)

AVLSVNRV, (A2)

WYIKIFIMI, (human)

IVN

WYIKIFIMI, (A*2402)

VIN

WYIRIFIMI, (human)

IVN

YIKIFIMIV, (A2)

IVN

FIMIVGGLV, (A*0201)

T-helper_epitopes
LELDKWASLWNWENITNW, (human)

IKLFIMIVGGLVGLR, (human)

FVLSIVNRVRQGYS, (hu

QQEKNEQELL, (human)

FNITNWLWY, (human)

AVLSIVNRVRQGYS

NQEKNEQELLE, (human)

RTFIMIVGGLIGLRI, (human)

- About this track
- Pin to top
- Edit config
- Delete track
- Save track data
- Show labels

HIV Molecular Immunology Database Search

CTL/CD8+ Search

[Search Help](#)

HIV protein	<ul style="list-style-type: none">-ALL-Gagp17p24p2p7p1p6	
HXB2 protein location		Results overlap with query location ▾
HXB2 DNA location		Results overlap with query location ▾
Epitope	WLWYIKIFI	Results contain query sequence ▾
Epitope name		
Record number		
Subtype	-ALL-	
Immunogen	<ul style="list-style-type: none">-ALL-computer predictionengineeredHIV-1 and HCV co-infectionHIV-1 exposed seronegativeHIV-1 infected monocyte-derivedHIV-1 infection	
Vaccine details if Immunogen is Vaccine	Vaccine type -ALL- Vaccine strain -ALL- Vaccine component -ALL- Adjuvant -ALL-	
Species	-ALL-	
Restricting MHC/HLA	<ul style="list-style-type: none">-ALL-A*01A*01:01A*01:23A*02A*02:01A*02:02	
Experimental methods and outcome measured	<ul style="list-style-type: none">-ALL-CD4 T-cell Elispot - IFNγCD8 T-cell Elispot granzyme BCD8 T-cell Elispot - IFNγCD8 T-cell RecycleSpot - IFNγChromium-release assayCTL neutralization assay	
Author		<input type="checkbox"/> First <input type="checkbox"/> Last
Country	-ALL-	
Keywords	<ul style="list-style-type: none">-ALL-acute/early infectionadjuvant comparisonA-listantagonismantibody binding siteantibody generation	
Notes		

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

Search for
CTL Epitope

Displaying record number 55295

Download this epitope [record as JSON](#). [[Help](#)]

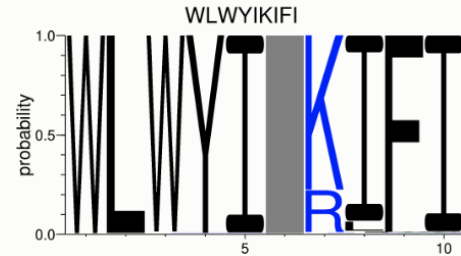
HXB2 location gp160(678–686)
gp41(167–175)
DNA(8256..8282)


Author location Env

[gp160 Epitope Map](#)

Epitope WLWYIKIFI

[Epitope Alignment](#)



Variants [WLWYIrIFI](#) observed variant 

Subtype B

Species (Restricting MHC/HLA) human(A*02:01)

Immunogen HIV-1 infection

Patient MHC/HLA [A1, A19, B*35:01, B44, C*16, Cw7; A*02:01, A19, B14, B44, C*16, Cw8](#)

Country United States

Experimental methods CD8 T-cell Elispot - IFN γ

Keywords co-receptor, escape, HAART, ART, HLA associated polymorphism, mother-to-infant transmission, mutation acquisition, rate of progression

[Show epitope variants](#)

Notes

- HIV-1 mother-to-child transmission is studied for LTNP by comparing entire genomes from 2 mother (M1, M2) and 2 daughter (D1, D2) RNA samples of a mother-child pair over 11 years. Genetic distance was 94% between subjects' strains. Divergence in sequences was attributed to distinct HLA selection pressures as ds/dn was larger for intra- rather than inter-person sequences. 10 new mutations in D2 were found related to unique daughter HLA alleles.
- Functional ELISpot studies using D2 and Nef peptides reveal strong associations between CTL responses and escape variants, contributing to delayed progression.
- LTNP status was not related to defective virus since all viral genes were intact and CTL response did not effectively control viral load. It is supposed that genetic HLA background and HIV-1 epitope-immune response interaction account for nonprogression of disease.
- All isolates contained R77Q in Vpr, a variation associated with reduction of cellular apoptosis.
- Epitope WLWYIKIFI was the only one mutated, to WLWYIrIFI in the mother M2 isolate. WLWYIKIFI was designated as being restricted to A2.1, a known alias for HLA-A*0201 which is expressed by daughter.

References

Reinis2007 Milan Reinis, Barbara Weiser, Carla Kuiken, Tao Dong, Dorothy Lang, Sharon Nachman, Yonghong Zhang, Sarah Rowland-Jones, and

Notes on
CTL Epitope

Discontinuous Antibody Epitope Search 1

Antibody Search

[Search Help](#)

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		
MAb name	32/5.8.42	<input type="checkbox"/> Exact Match (List by name) (List by type)
Record number		
Subtype	-ALL-	
Immunogen	-ALL- anti-idiotypic autoimmune disease engineered HIV-1 exposed seronegative HIV-1 infection HIV-2 infection	
Vaccine details	Vaccine type: -ALL- Vaccine strain: -ALL- if Immunogen is Vaccine: Vaccine component: -ALL- Adjuvant: -ALL-	
Ab type	-ALL- Antisense protein (ASP) C-domain C-HR C-term flap region fusion peptide // near gp41-gp120 interface	
Species	-ALL-	
Isotype	-ALL-	
Author		Search only for <input type="checkbox"/> First <input type="checkbox"/> Last <input checked="" type="radio"/> Show only this author's references <input type="radio"/> Show all references
Country	-ALL-	
Keywords	-ALL- acute/early infection ADCC adjuvant comparison antibody binding site antibody generation antibody gene transfer	<input checked="" type="radio"/> Show only notes containing selected keyword(s) <input type="radio"/> Show all notes
Notes		<input checked="" type="radio"/> Show only notes matching this text <input type="radio"/> Show all notes

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HIV Molecular Immunology Database Search

Antibody Search

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Found 1 matching record:

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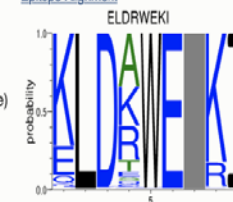
Displaying record number 1

Download this epitope record as JSON. ([Help](#))

MAb name: 32/5.8.42
HXB2 location: Gag(12-19 + 100-105)
DNA(823..846,1087..1104)
Author location: p17(12-19 IIIB)

[Gag Epitope Map](#)

[Epitope Alignment](#)



Epitope: ELDRWEKI + ALDKIE (Discontinuous epitope)

Ab type

Neutralizing

Species (isotype): mouse(IgG)

Immunogen: vaccine

Keywords

Vaccine Details

Vaccine type: viral lysate

Vaccine strain

Vaccine component

Adjuvant

Notes

Showing 1 of 1 note.

- 32/5.8.42: Binds to two discontinuous regions, positions 12-19 and 100-105, peptides ELDRWEKI and ALDKIE -- inhibited infectivity of cell free virus. [Papsidero1989](#)

References

Showing 1 of 1 reference.

[Papsidero1989](#) L. D. Papsidero, M. Sheu, and F. W. Ruscetti. Human immunodeficiency virus type 1-neutralizing monoclonal antibodies which react with p17 core protein:

<https://www.hiv.lanl.gov/mojo/immunology/search/ab/results>

Discontinuous Antibody Epitope Search 2

Antibody Search

[Search Help](#)

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	PG9	
MAb name		<input type="checkbox"/> Exact Match (List by name) (List by type)
Record number		
Subtype	-ALL-	
Immunogen	-ALL- anti-idiotypic autoimmune disease engineered HIV-1 exposed seronegative HIV-1 infection HIV-2 infection	
Vaccine details	Vaccine type: -ALL- Vaccine strain: -ALL- if Immunogen is Vaccine: Vaccine component: -ALL- Adjuvant: -ALL-	
Ab type	-ALL- Antisense protein (ASP) C-domain C-HR C-term flap region fusion peptide // near gp41-gp120 interface	
Species	-ALL-	
Isotype	-ALL-	
Author		Search only for <input type="checkbox"/> First <input type="checkbox"/> Last <input checked="" type="radio"/> Show only this author's references <input type="radio"/> Show all references
Country	-ALL-	
Keywords	-ALL- acute/early infection ADCC adjuvant comparison antibody binding site antibody generation antibody gene transfer	<input checked="" type="radio"/> Show only notes containing selected keyword(s) <input type="radio"/> Show all notes
Notes		<input checked="" type="radio"/> Show only notes matching this text <input type="radio"/> Show all notes

Search Reset

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

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HIV Molecular Immunology Database Search

Antibody Search

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Displaying record number 2124

Download this epitope record as JSON. [[Help](#)]

MAb name PG9
HXB2 location gp160
Author location gp120(126-196)
Epitope (Discontinuous epitope)
Subtype A
Ab type gp120 V2 // V2 glycan(V2g) // V2 apex, quaternary structure
Neutralizing P (tier 2)

[gp160 Epitope Map](#)

[View neutralization details](#)

Contacts and Features [View contacts and features](#)

Species (isotype) human(IgG1)

Immunogen HIV-1 infection

Patient MHC/HLA [Donor 24:](#)

ADCC, antibody binding site, antibody generation, antibody interactions, assay or method development, autoantibody or autoimmunity, elite controllers, genital and mucosal immunity, glycosylation, immunoprophylaxis, memory cells, neutralization, vaccine antigen design, variant cross-reactivity, vaccine-induced immune responses, computational epitope prediction, acute/early infection, escape, binding affinity, immunotherapy, mother-to-infant transmission, review, subtype comparisons, antibody sequence, structure, rate of progression, antibody gene transfer, antibody lineage, antibody polyreactivity, broad neutralizer, chimeric antibody, germline, junction or fusion peptide, polyclonal antibodies, transmission pair

Notes

Showing 175 of 175 notes.

- PG9: Since cross-reactive antibodies can interfere in immunoassays, HIV-1 Abs were tested for binding to the SARS-COV-2 spike protein (SARS-COV-2 S cross-reactivity). The following 9 gp120-epitope binding HIV-1 Abs are cross-reactive with COV-2 S: 2G12, PGT121, PGT126, PGT128, PGT145, PG9, PG16, 10-1074, 35O22. VRC01, VRC03 are HIV-1 gp120 CD4bs Abs that are not cross-reactive. Cross-reactivity of the 9 HIV-1 Abs was through glyco-epitopes. Glycan-dependent, V3-loop-binding PGT126 and PGT128 as well as 2G12 were the strongest binders of COV-2 S and were found to be immunoreactive but incapable of neutralization or antibody-dependent enhancement (ADE). [Mason2021 \(antibody interactions, neutralization\)](#)

<https://www.hiv.lanl.gov/mojo/immunology/search/ab/result>

S



HIV sequence database

DATABASES SEARCH ALIGNMENTS TOOLS PUBLICATIONS INFO

Env Feature Database

Neutralizing Antibody Contacts & Features

Purpose: to provide HIV-1 Env coordinates of contacts and other sites associated with neutralizing antibodies. Some of these data are also summarized in a [spreadsheet \(.xlsx\)](#). For details, see [Help](#).

New! [Download database](#)

Found 14 record(s).

	Env Feature ID	Title	Antibody class	Reference	Site type	Experimental method	MAB name
Details	4	Mutation affects neutralization	multiple	ORourke2009 ORourke2010 ORourke2012	neutralization	Neutralization assay	17b 4E10 b12 PG16 PG9 VRC01
Details	16	PG9-like contacts	V2-apex	McLellan2011	contacts		CH01 CH02 CH03 CH04 PG16 PG9 PGT141 PGT145
Details	17	Mutation affects PG9-like Ab sensitivity	V2-apex	Doria-RoseNA2012 Wang2018a	neutralization	Neutralization assay	CH01 CH02 CH03 CH04 PG16 PG9 PGT141 PGT145
Details	41	PG9 signature predictions	V2-apex	West2013	signature	Computational prediction	PG9
Details	62	PG9 residue prediction	V2-apex	Chuang2013 Chuang2014	signature		PG9
Details	75	PG9-like antibodies require N160 for neutralization	V2-apex	Doria-Rose2016	neutralization	Neutralization assay	CH01 PG16 PG9 PGT145
Details	96	PG9 escape mutations	V2-apex	Andrabi2015	resistance		PG9
Details	129	Mutation affects neutralization by V1V2 glycan mAbs	V2-apex	Cale2017	neutralization	Neutralization assay	CH01 PG9 PGT145 VRC38.01
Details	162	Disulfide bond introduced in V1V2 affects binding	multiple	deTaeye2019	binding	Binding assay	CH01 CH03 PG16 PG9 PGT121
Details	163	Disulfide bond introduced in V1V2 affects binding and neutralization	V2-apex	deTaeye2019	binding, neutralization	Binding assay	CH01 CH03 PG16 PG9 PGDM1400 PGT145 VRC26.09
Details	165	Mutations at the trimer apex that affect sensitivity	multiple	Guzzo2018	resistance	Neutralization assay	17b 2158 2F5 412d 447-52D 48d 4E10 697-D b13 CH103 F105 F425 B4e8 PG16 PG9 PGT121 PGT122 PGT123 PGT125 PGT126 PGT128 PGT130 PGT135 VRC24 VRC26.08 VRC38.01
		V2 Signature					

FROM Epitope Search TO Pathogen Attributes

- HIV protein maps
- HIV Genome Browser
- HIV sites of interest

~~~~~

# FROM Epitope Search TO Host Attributes

- Ab Contacts/Features
- Ab Neutralization

# HOST-PATHOGEN INTERACTION

- Vaccine Design

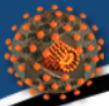
<https://hiv.lanl.gov/>

**We are happy to help with research questions on the use of our tools and database.**

**We appreciate ideas for further tool development!**

**Contact us:**

[immuno@lanl.gov](mailto:immuno@lanl.gov) or [seq-info@lanl.gov](mailto:seq-info@lanl.gov)



# HIV sequence database

Multiple paths to most tools

DATABASES SEARCH ALIGNMENTS TOOLS PUBLICATIONS INFO

- Search DB
- Advanced Search
- Intra-patient Search
- Next-gen Sequences
- Geography

## HIV Sequence Database

### Programs and Tools

- [Search Interface](#) retrieves HIV and SIV sequences, which can then be aligned and used to build trees
- [Geography Search Interface](#) retrieves HIV sequences based on geographical distribution
- [Genome Browser](#) uses jBrowse to display diverse data about the HIV-1 genome and proteome
- [Tools for working with sequences](#) lists all our online tools, organized by function

### Information

- [HIV Sequence Compendium](#) print or order our annual publication
- [Tutorials and other information](#) unpublished web-based content
- [Links](#) to other HIV/AIDS tools and information

### About this website

- [FAQ](#) general information about this website
- [How to Cite this Database](#)
- [Editorial Board](#)

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[HIV Premade Alignments](#) includes Consensus and Ancestral Sequences, Subtype Reference Alignments, and Complete Alignments

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[Archived News](#) ▶

#### [HIV Molecular Immunology 2020](#)

*HIV Molecular Immunology 2020* is now available online. The PDF version is hypertext enabled and features clickable table-of-contents, indexes, references and links to external web sites. 27 January 2022

#### [2020 Alignments](#)

The 2020 *Web*, *Filtered Web*, *Super Filtered Web*, and *Consensus Alignments* are now available [online](#). The curated web alignments contain a full range of sequences available through the end of 2020. New consensus sequences are available, described by [Linchangco et al. 2022](#). 24 January 2022

last modified: Tue Sep 7 15:54 2021

Questions or comments? Contact us at [seq-info@lanl.gov](mailto:seq-info@lanl.gov).

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## HIV Database Tools

- Tools specific for HIV/SIV
- General use tools with some HIV/SIV-specific features
- General use tools

### Analysis and Quality Control

- [Entropy](#) quantifies positional variation in an alignment using Shannon Entropy
- [GenSig](#) identifies genetic signatures. It can work on any phenotype file given in conjunction with a codon-aligned nucleotide alignment of a protein coding region
- [Glycan Shield Mapping](#) shows mapping absent hole-causing potential N-linked glycosylation sites (PNGS) on predicted glycan shields for an ENV sequence
- [HIV BLAST](#) finds sequences similar to yours in the HIV database
- [Hypermut](#) detects hypermutation
- [jpHMM at GOBICS](#) detects subtype recombination in HIV-1; hosted at GOBICS as a collaboration between the Department of Bioinformatics, University of Göttingen and the Los Alamos HIV Sequence Database
- [N-Glycosite](#) finds potential N-linked glycosylation sites
- [PCOORD](#) multidimensional analysis of sequence variation
- [Quality Control](#) runs several tools for quick troubleshooting of HIV-1 sequences; optional step prepares sequence submission for GenBank
- [RAPR](#) (Recombinant Analysis Program) uses the Wald-Wolfowitz Runs Test to check for recombination in every triplet in the alignment.
- [RIP](#) (Recombinant Identification Program) detects HIV-1 subtypes and recombination
- [SNAP](#) calculates synonymous/non-synonymous substitution rates
- [SUDI Subtyping](#) plots the distance of your sequence to established subtypes
- [Variable Region Characteristics](#) summarizes features of peptides from a protein alignment, reporting peptide characteristics such as length and N-linked glycosylation sites; particularly useful for characterizing variable regions of Env
- [VESPA](#) (Viral Epidemiology Signature Pattern Analysis) detects residues with different frequencies in two sequence sets

### Alignment and sequence manipulation

- [Align Multi-tool](#) manipulates sequence alignments, including sorting, pruning, and renaming
- [Alignment Slicer](#) cuts vertical slices from sequence alignments
- [Analyze Align](#) shows weblogos, calculates frequency by position, and finds variants in an alignment
- [Codon Alignment](#) takes a nucleotide alignment and returns a codon alignment and translation
- [Consensus Maker](#) computes a customizable consensus
- [ElimDupes](#) compares the sequences within an alignment and eliminates any duplicates
- [Gap Strip/Squeeze](#) removes columns with more than a given % of gaps

### Phylogenetics

- [AnnotateTree](#) creates a colored and weighted phylogenetic tree
- [Branchlength](#) calculates branch lengths between internal and end nodes; now included in the [TreeRate](#) tool
- [FindModel](#) finds which evolutionary model best fits your sequences
- [IQ-TREE](#) is a fast and effective stochastic algorithm for finding Maximum Likelihood trees, including site-specific rates of evolution at each alignment position
- [PhyloPlace](#) reports phylogenetic relatedness of an HIV-1 sequence with reference sequences
- [PhyML](#) generates much better trees than our simple TreeMaker tool
- [Poisson-Fitter](#) estimates time since MRCA and star-phylogeny. For use with acute (low diversity) samples
- [Rainbow Tree](#) Color code phylogenetic tree branches according to labels in the sequence names
- [TreeMaker](#) generates a Neighbor Joining phylogenetic tree
- [TreeRate](#) finds the phylogenetic root of a tree and calculates branch lengths and evolutionary rate

### Immunology

- [CATNAP](#) (Compile, Analyze, Tally NAb Panels) provides meta-analysis of published neutralization panel data
- [CombinAber](#) predicts and analyzes combination antibody neutralization scores using IC<sub>50</sub> and/or IC<sub>80</sub> for individual antibodies
- [ELF](#) (Epitope Location Finder) identifies known and potential epitopes within peptides
- [Epigraph Tool Suite](#) uses input of diverse sequences to generate Epigraph sequences for use in vaccine or reagent design
- [EpiAlign \(QuickAlign\)](#) aligns a protein sequence (e.g., epitope) to the appropriate protein alignment
- [Heatmap](#) displays a table of numbers by using colors to represent the numerical values
- [Hepitope](#) identifies potential epitopes based on HLA frequencies
- [Neutralization Index](#) computes a tier-like score for sera (using ID50 titers) or antibodies (using IC50 titers)
- [Mosaic Vaccine Tool Suite](#) designs and assesses polyvalent protein sequences for T-cell vaccines
- [Motif Scan](#) finds HLA anchor motifs in protein sequences for specified HLA serotypes, genotypes or supertypes
- [PeptGen](#) generates overlapping peptides from a protein sequence

### Database search interfaces

- [Advanced Search](#) creates a custom search interface
- [Antibodies](#) search for HIV antibodies by protein, immunogen, AB type, isotype, author, keywords

HIV Tools:  
>80% are  
NOT  
HIV-specific

# Feature and Contacts Database

## Env Feature Database

### Neutralizing Antibody Contacts & Features

**Purpose:** to provide HIV-1 Env coordinates of contacts and other sites associated with neutralizing antibodies. Some of these data are also summarized in a [spreadsheet \(.xlsx\)](#). For details, see [Help](#).

**New!** [Download database](#)

**MAb name**   
 10-1074  
 10-1074V  
 10-996  
 10E8  
 12A12  
 12A21  
 16A  
 16B  
 179NC75  
 17b  
 1B2530  
 2158  
 22A  
 27A  
 27B  
 27C  
 27D  
 2F5  
 2G12

**Reference**   
 Andrabi2015  
 Baia-Dal-Siborsingh2013  
 Barnes2018  
 Bhiman2015  
 Blattner2014  
 Bonsignori2016  
 Bricault2019  
 Brunel2006  
 Cale2017  
 Caskey2015  
 Chuang2013  
 Chuang2014  
 Chuang2019  
 Coetzer2006  
 deTaeye2015  
 deTaeye2019  
 Ding2015  
 Dings2017  
 Dings2018

**Antibody class**   
 CD4i  
 cluster A  
 glycan  
 gp120/gp41 interface  
 gp41 fusion domain  
 MPER  
 multiple  
 silent face  
 V2-apex  
 V3-glycan

**Site type**   
 binding  
 contacts  
 Env feature  
 immunotherapy  
 neutralization  
 resistance  
 signature

**Experimental method**   
 Binding assay  
 Computational prediction  
 Cryo-EM

**Env AA position**

**Env Feature ID**   
 2  
 3  
 4  
 5

Text search on Title and Annotation

Download all contact sites (and other features) in a single spreadsheet

Select "contacts" to get discontinuous antibody contacts

Almost all features are based on experimental data; any computational predictions are clearly delineated as such

# View Neutralizing Antibody Contacts & Features

Env Feature ID 8

Title VRC01 contacts

Antibody class CD4BS

Reference [Wu2011](#) [Zhou2010](#)

Site type contacts

Experimental method

MAB name VRC01 ([Immuno DB](#), [CATNAP](#))

Links to VRC01 information and IC50 data

| Env pos. | Feature                 | HXB2 AA | Entropy (0-3)                     |           |           | Annotation    |
|----------|-------------------------|---------|-----------------------------------|-----------|-----------|---------------|
|          |                         |         | Group M                           | Subtype B | Subtype C |               |
| 97       | gp120                   | K       | 0.433<br><a href="#">See Logo</a> | 0.421     | 0.511     | VRC01 contact |
| 123      | gp120                   | T       | 0.033<br><a href="#">See Logo</a> | 0.028     | 0.038     | VRC01 contact |
| 128      | gp120                   | S       | 0.188<br><a href="#">See Logo</a> | 0.339     | 0.088     | VRC01 contact |
| 129      | gp120                   | L       | 0.048<br><a href="#">See Logo</a> | 0.056     | 0.029     | VRC01 contact |
| 276      | gp120, Loop D           | N       | 0.120<br><a href="#">See Logo</a> | 0.063     | 0.169     | VRC01 contact |
| 278      | gp120, Loop D           | T       | 0.657<br><a href="#">See Logo</a> | 0.715     | 0.481     | VRC01 contact |
| 279      | gp120, Loop D           | D       | 0.860<br><a href="#">See Logo</a> | 0.850     | 0.898     | VRC01 contact |
| 280      | gp120, Loop D           | N       | 0.117<br><a href="#">See Logo</a> | 0.090     | 0.170     | VRC01 contact |
| 281      | gp120, Loop D           | A       | 1.081<br><a href="#">See Logo</a> | 0.814     | 1.357     | VRC01 contact |
| 282      | gp120, Loop D           | K       | 0.260<br><a href="#">See Logo</a> | 0.337     | 0.297     | VRC01 contact |
| 283      | gp120, Loop D           | T       | 0.992<br><a href="#">See Logo</a> | 1.091     | 0.474     | VRC01 contact |
| 365      | gp120, CD4 binding loop | S       | 0.574<br><a href="#">See Logo</a> | 0.489     | 0.619     | VRC01 contact |
| 366      | gp120, CD4 binding loop | G       | 0.034<br><a href="#">See Logo</a> | 0.012     | 0.028     | VRC01 contact |

Logo showing variability at this Env position

# AnalyzeAlign

# Sequence Alignment Analysis Tool

Purpose: Show weblogs, calculate frequency by position, and find variants in an alignment. [Explanation](#).

## Input

Alignment  Paste or upload alignment [?](#)  
[Sample Input]

HCV\_ALL\_2...\_PRO.fasta

Use LANL database alignment [?](#)

Alignment type  Filtered web  Web  Subtype reference  Compendium

Organism  HIV-1/SIVcpz  HIV-2/SIVsmm  Other SIV

Region

Subtypes  All  Major subtypes (A B C D F G CRF01 CRF02)

Sequence type  nucleotide  amino acid

Positions/range to analyze   
Total positions ≤ 200!

Range numbers refer to  alignment columns, including gaps  residues of 1<sup>st</sup> sequence  residues of HXB2 (K01755)

Group the sequences  Report results for all sequences as a single group  
 Report separate results for subsets of sequences (email results)

Group sequences by:

the characters in field  of names delimited by

first  character(s) in names

paste or upload grouped sequence names [\(example\)](#)

No file chosen

I am using a LANL alignment; group sequences by subtypes (the first field)

Provide an alignment representing the variability of the organism (e.g., HCV E2 protein alignment)

Choose the positions to analyze; possibly the location of your favorite epitope(s).

## Logo options

## Other options

Gap option  Delete gaps and shift alignment to C-terminus  
 yes  no (for amino acid sequences only, useful for T-cell epitopes)

Frequency calculation  Cut-off for calculating frequency by position  %

Master sequence for finding variants  consensus of alignment  consensus of seq group  
 1<sup>st</sup> seq of alignment  1<sup>st</sup> seq of seq group

user-specified

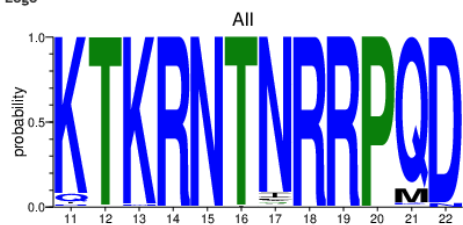
Choose a master sequence as the basis of comparison

## Output

Email results

Downloadable logo files  PDF  EPS  SVG

Combine logos for subsets into a page  Concatenate PDF or EPS logos as a  x  matrix (row x column)  
Orientation:  Portrait  Landscape  
Include logo of removed symbols, if option to remove symbols selected:



Download: [PNG](#)

Frequency by position

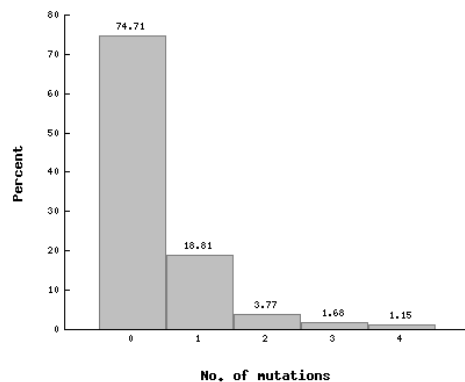
[See full raw counts](#)

cutoff: 95%

|    | Percentage and raw count of non-gap                          | Non-gap/total (percentage) | Gap/total (percentage) |
|----|--------------------------------------------------------------|----------------------------|------------------------|
| 11 | K: 92.08% (721) Q: 4.98% (39) other: 2.94% (23)              | 783/783 (100.00%)          | 0/783 (0.00%)          |
| 12 | T: 98.72% (773) other: 1.28% (10)                            | 783/783 (100.00%)          | 0/783 (0.00%)          |
| 13 | K: 98.08% (768) other: 1.92% (15)                            | 783/783 (100.00%)          | 0/783 (0.00%)          |
| 14 | R: 99.62% (780) other: 0.38% (3)                             | 783/783 (100.00%)          | 0/783 (0.00%)          |
| 15 | N: 99.62% (780) other: 0.38% (3)                             | 783/783 (100.00%)          | 0/783 (0.00%)          |
| 16 | T: 98.98% (775) I: 1.02% (8)                                 | 783/783 (100.00%)          | 0/783 (0.00%)          |
| 17 | N: 91.44% (716) I: 3.32% (26) Y: 1.15% (9) other: 4.09% (32) | 783/783 (100.00%)          | 0/783 (0.00%)          |
| 18 | R: 99.49% (779) other: 0.51% (4)                             | 783/783 (100.00%)          | 0/783 (0.00%)          |
| 19 | R: 99.87% (782) H: 0.13% (1)                                 | 783/783 (100.00%)          | 0/783 (0.00%)          |
| 20 | P: 99.87% (782) R: 0.13% (1)                                 | 783/783 (100.00%)          | 0/783 (0.00%)          |
| 21 | Q: 89.14% (698) M: 8.43% (66) other: 2.43% (19)              | 783/783 (100.00%)          | 0/783 (0.00%)          |
| 22 | D: 97.32% (762) N: 2.68% (21)                                | 783/783 (100.00%)          | 0/783 (0.00%)          |

Sequence variants

all



Variant Count Pct. No. of mutations

| Variant      | Count | Pct.  | No. of mutations |
|--------------|-------|-------|------------------|
| KTKRNTNRRPQD | 585   | 74.71 | 0                |
| -----M-      | 59    | 7.54  | 1                |
| -----I-----  | 24    | 3.07  | 1                |
| Q-----       | 16    | 2.04  | 1                |
| Q----L---KN  | 8     | 1.02  | 4                |
| R-----       | 7     | 0.89  | 1                |
| --N-----     | 5     | 0.64  | 1                |
| Q----P---H   | 5     | 0.64  | 3                |
| I-----       | 5     | 0.64  | 1                |
| -----Y-----  | 4     | 0.51  | 1                |
| -I-----      | 3     | 0.38  | 1                |
| -----T-----  | 3     | 0.38  | 1                |
| -----I-----  | 3     | 0.38  | 1                |
| I-----I----- | 2     | 0.26  | 2                |
| I-----Y----- | 2     | 0.26  | 2                |
| F-----K-     | 2     | 0.26  | 2                |

# AnalyzeAlign example output

A sequence logo showing the variability in the alignment.

A list of all variants present, relative to the selected master sequence.

A histogram of the number of positions with mutations, relative to the master sequence.

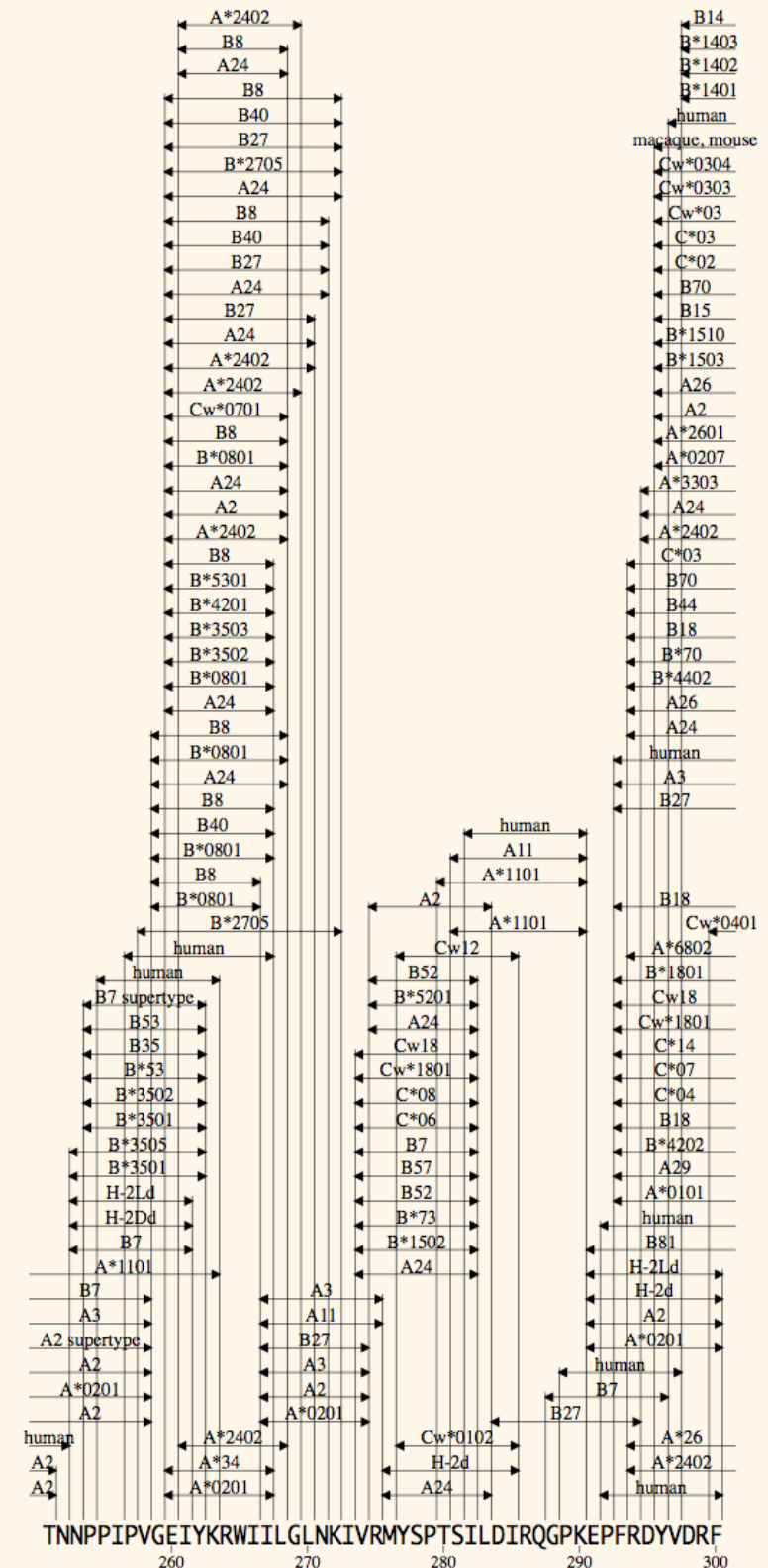
An alignment of all variants, relative to the master sequence chosen (including frequency of each).



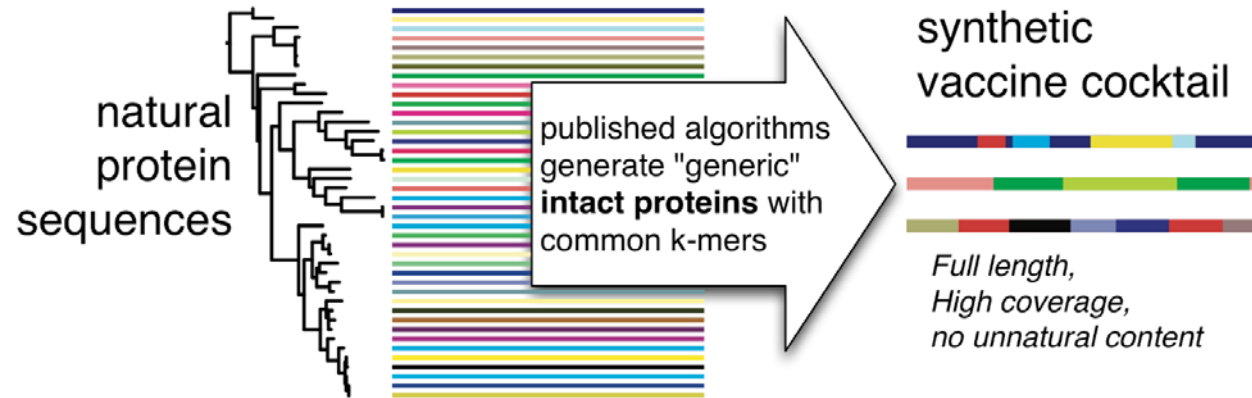
# Vaccine Design Tools

HIV epitopes are densely packed at the population level

- Vaccinating a diverse population with individual epitopes is infeasible
- Escape forms for one HLA are frequently sensitive for a different HLA
- It may not be necessary to **predict** epitopes — but only to **deliver** them
- Optimized immunogen cocktails could deliver most epitopes likely to be present in infecting virus



# Vaccine Design Tools: Mosaic/Epigraph



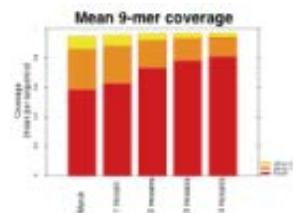
## Design Tools

Generate candidate vaccine protein cocktails that optimize coverage of potential T-cell epitopes based on frequencies in sets of natural pathogen sequences

**Mosaic Vaccine Designer** — genetic algorithm (Fischer et al. 2007)

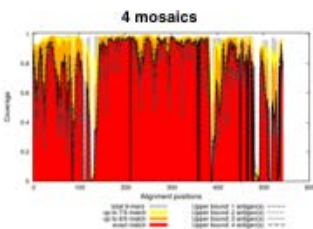
**Epigraph** — graph-theory approach (Theiler et al. 2016)

## Evaluation tools



### **Epitope Coverage Assessment (EPICOVER)**

Alignment-independent "k-mer" coverage by vaccines or peptides.



### **Positional Epitope Coverage Assessment (POSICOVER)**

Alignment-based coverage by vaccines or peptides.

# Mosaic Vaccine Designer

**Method:** genetic algorithm

**Target set:** natural protein sequences from a diverse pathogen population

**Cocktail size:** how many mosaic protein sequences to generate

**Epitope length:** default is 9 amino-acids

The screenshot shows the web interface for the Mosaic Vaccine Designer. At the top right, it says "HIV sequence database". A navigation bar contains "DATABASES", "SEARCH", "ALIGNMENTS", "TOOLS", "PUBLICATIONS", "GUIDES", and a "Search Site" input field. The main heading is "Mosaic Vaccine Designer".

**Purpose:** The Mosaic Vaccine Designer will generate candidate vaccine protein cocktails that optimize the coverage, by a small set of mosaic proteins that could be included in a vaccine cocktail, of potential T-cell epitopes in a large diverse set of proteins. The resulting 'mosaic' proteins in the proposed vaccine cocktail resemble real proteins from the input set of natural viral proteins (the 'training set'), but are assembled from fragments of the natural proteins using a genetic algorithm (a computational optimization method). This method was first applied to HIV, but is readily generalized and could be applied to other variable pathogens.

**Functions:**

- 'Create mosaic sequence cocktail' runs the genetic algorithm to generate a cocktail of synthetic sequences with near-optimal coverage
- 'Pick the best natural sequences' selects unmodified natural sequences from the training set in order of coverage
- 'See the coverage distribution of natural sequences' shows the coverages of a randomly selected set of natural sequence cocktails

**Usage:** Paste your protein sequences in the box below, or upload a file containing sequences. Most common [sequence formats](#) are accepted. As soon as your job is completed, a link to your results will be sent to your email address which you provided. To manage more detailed parameters, go to the Advanced Input. (Your job may take several hours or even days, according to your input.)

**Related Programs:**

- [Epitope Coverage Assessment Tool-Epicover](#)
- [Positional Epitope Coverage Assessment Tool-Posicover](#)

**Reference:** [Polyvalent vaccine design article](#) | [Pubmed version](#)

**Input**

Paste set of protein sequences  
 Sample Input

```
A1.CM. .a
MGGNWSKSSLVWPEIRERMRRAPPTPTTPAAKGVGAVSQDLAKHGAI
A1.KE.99a
MGGKWSKSSI VGVPEVRRRIQOTPPAARGVGAVSQDLEKHGAITSSNINHS
A1.KE.99b
MGGIWSKRSTRGWSEVRERIRQTPPTPPAARGVGAVSQDIARHGAVTSSNVN
```

Or upload protein sequence file

**Options**

Function  Create mosaic sequence cocktail  
 Pick the best natural sequences  
 See the coverage distribution of natural sequences

Cocktail Size (1-10)   
Epitope Length (8-12)   
Rare Threshold

Paste fixed sequences

Or upload fixed sequence file

# EPIGRAPH



DATABASES SEARCH ALIGNMENTS TOOLS PUBLICATIONS GUIDES Search Site

## Epigraph

Design ? Antigen Coverage Evaluation Coverage Distribution of Natural Sequences Exclude rare epitopes Characterize Potential T-cell Epitopes Design: Tailored Therapeutic Vaccine Evaluation: Tailored Therapeutic Vaccine

### Input

Protein sequences  
[Sample Input]

Choose File no file selected

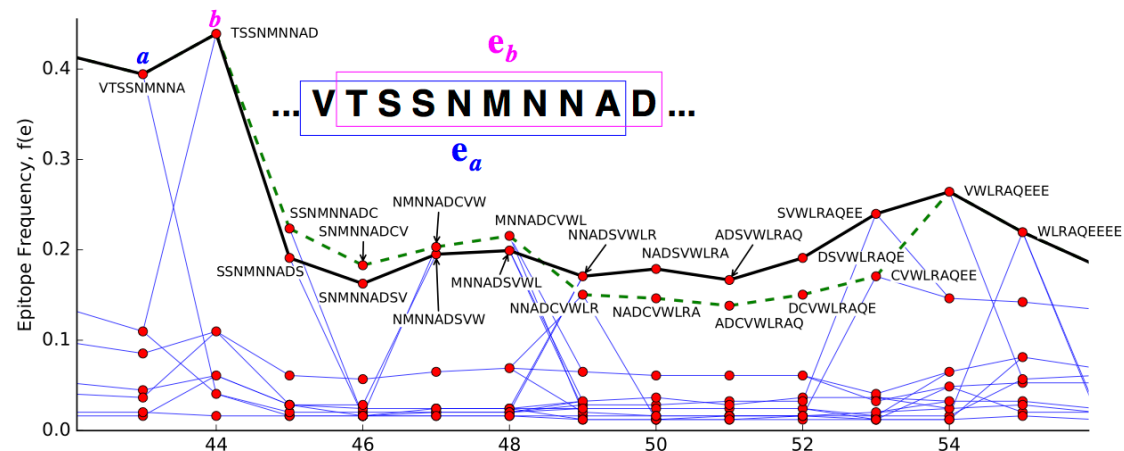
### Options

Algorithm  Unaligned sequence algorithm (Gaps will be removed before calculation if seqs are aligned)  Aligned sequence algorithm (Seqs must be the same length. If not, automatically "padded")

Epitope length 9

# of seqs in vaccine pool 2

Email results



**Method:** evaluation of acyclic graph

**Target set:** natural protein sequences for the pathogen population

**Cocktail size:** how many mosaic proteins in the output set.

**Epitope length:** default is 9 amino-acids.

## Advantages over Mosaic

**Essentially optimal** (fractionally better coverage)

**Much faster:** allows iteration and comparison of multiple input sets and alternate designs

# Vaccine Design Tools: Mosaic/Epigraph

## Mosaic/Epigraph vaccine designs have been applied to many pathogens

**Influenza** Kingstad-Bakke *et al* Vaccine, 2019 37:5051, PMID: 31300285; Florik *et al*, PLoS One, 2017 Aug 3;12(8):e0181738; Kamlangdee *et al*, J Virol. 2016 Jul 11;90(15):6771-6783 and J Virol. 2014 Nov;88(22):13300-9, PMID:25210173

**Dengue** Hou *et al* Front Immunol. 2019 Jun 20;10:1429, PMID: 31281322

**Rabies** Stading *et al*, Plos Negl Trop Dis, 2017, PMID: 28976983

**Pan-filoviruses** Theiler *et al*, Sci Rep. 2016, PMID: 27703185, Rahim *et al*, PLoS Pathog. 2019 Feb 28;15(2):e1007564 PMID: 30817809

**Chlamydia trachomatis** Badamchi-Zadeh *et al*, Front Immunol, 2016, PMID: 27199987

**Porcine Reproductive and Respiratory Syndrome Virus (PRRSV)** Cui *et al*, PLoS One. 2019 Jan 31;14(1), PMID: 30794703

**Dengue Fever** Hou *et al*, Front Immunol. 2019 Jun 20;10:1429, PMID: 31281322

**Hepatitis B** Bruening E, Douglas J, Yusim K, *et al.*, being experimentally tested

**Hepatitis C** Yusim *et al.*, Clin Vaccine Immunol, 2013, PMID: 23221002

**Lassa Virus** Alex Bukreyev, <https://apps.dtic.mil/sti/citations/AD1116972>

**HIV** Chen *et al*. J Virol. 2022 96(7):e0216121, PMID: 35297660; Barouch *et al*. 2018 392(10143):232-243, PMID: 30047376

# CATNAP (Compile, Analyze and Tally NAb Panels)

## What is CATNAP, *really*?

- A database of HIV antibody neutralization (IC50/80) data.
- A tool to analyze numerical data in association with variable sequences from any protein.

*(Coming soon: a database of SARS-CoV-2 neutralization data)*

<http://hiv.lanl.gov/catnap>

## CATNAP

### Compile, Analyze and Tally NAb Panels

The CATNAP family of tools has been designed to facilitate the analysis of neutralizing antibodies (NAbs) through the identification of potential genetic signatures resulting from a NAb's interaction with a protein. While interactions between NAbs and HIV-1 Env are the emphasis, the Custom Input version can accommodate other types of data, including other proteins and organisms.

#### CATNAP

**Purpose:** Analyze our database of HIV-1 IC<sub>50</sub> and IC<sub>80</sub> neutralization data from publicly-available sources, in conjunction with HIV-1 Envelope sequences. Access our extensive databases of information about neutralizing antibodies and viruses used in published neutralization studies. Alignments of Env sequences for these viruses are also provided.

**Help:** [CATNAP Help](#).

#### CATNAP: Custom Input

**Purpose:** Find potential genetic signatures based on your own numerical data in association with protein sequences. In addition to neutralization data, this tool is flexible enough to accommodate almost any kind of data in conjunction with almost any protein sequence.

**Help:** [Custom CATNAP Help](#).

#### CATNAP: Hybrid

**Purpose:** Compare and analyze your HIV-1 IC<sub>50</sub> and IC<sub>80</sub> neutralization data with published data. This tool will display your data side-by-side with data from our database of published HIV-1 neutralization data.

**Help:** [Hybrid CATNAP Help](#).

Download and analyze built-in HIV antibody IC50/80 data

Analysis of **your data** for any organism: numerical data linked to aligned sequences

Analysis of built-in IC50/80 data together with your own HIV antibody IC50/80 data

# CUSTOM CATNAP

SARS-COV-2 data from Wang et al.  
Nature 2022 Aug;608(7923):603-608

## CATNAP: Custom Input

● ≤0.01275(Q<sub>1</sub>) ● ≤0.321(Q<sub>2</sub>) ● ≤1.03175(Q<sub>3</sub>) ● >1.03175 ○ Undetected: UD  
(A value occurring many times in the data set and ranging more than two color groups will take the most intense color which the value can be.)

[More virus info in HIV Seq DB](#)

| Virus name                           | Tier |
|--------------------------------------|------|
| Omicron_BA.1.1__EPI_ISL_10000001     |      |
| Omicron_BA.1__EPI_ISL_10000028       |      |
| Omicron_BA.2.12.1__EPI_ISL_10783322  |      |
| Omicron_BA.2_L452M__EPI_ISL_10696425 |      |
| Omicron_BA.2_L452R__EPI_ISL_10242829 |      |
| Omicron_BA.2__EPI_ISL_10000005       |      |
| Omicron_BA.4__EPI_ISL_11207535       |      |

Spike  
sequence  
names

| AA (NxST) | 5-7   | ADG-2 | Brii-196 | Brii-198 | CAB- |
|-----------|-------|-------|----------|----------|------|
| N (+)     | 0.534 | 0.295 | 1.792    | UD       | 0.01 |
| N (+)     | 0.347 | 0.181 | 2.385    | 0.078    | 0.01 |
| N         | UD    | UD    | 1.171    | UD       | 0.02 |
| N         | UD    | UD    | 0.907    | UD       | 0.03 |
| N         | UD    | UD    | 6.815    | UD       | 0.04 |
| N         | UD    | UD    | 1.346    | 0.782    | 0.03 |
| N         | UD    | UD    | 0.978    | UD       | 0.02 |

IC50 values  
UD=undetected

Rseq

```

MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLH
-----|-----|-----|-----|-----
-----10-----20-----30-----40-----5
MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLH
MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLH
MFVFLVLLPLVSSQCVNLTTRTQ---SYTNSFTRGVYYPDKVFRSSVLH
MFVFLVLLPLVSSQCVNLTTRTQ---SYTNSFTRGVYYPDKVFRSSVLH
MFVFLVLLPLVSSQCVNLTTRTQ---SYTNSFTRGVYYPDKVFRSSVLH
MFVFLVLLPLVSSQCVNLTTRTQ---SYTNSFTRGVYYPDKVFRSSVLH
MFVFLVLLPLVSSQCVNLTTRTQ---SYTNSFTRGVYYPDKVFRSSVLH
MFVFLVLLPLVSSQCVNLTTRTQ---SYTNSFTRGVYYPDKVFRSSVLH
    
```

Spike sequence  
alignment; red N's  
have predicted  
glycosylation

|                                          |           |           |            |           |      |
|------------------------------------------|-----------|-----------|------------|-----------|------|
| Geometric mean of detected               | 0.43046   | 0.23107   | 1.69815    | 0.24697   | 0.02 |
| Geometric mean of detected & undetected* | 21.0854   | 17.6517   | 1.69815    | 17.9905   | 0.02 |
| % detected (detected/total)              | 29% (2/7) | 29% (2/7) | 100% (7/7) | 29% (2/7) | 100% |

\* Values are considered as undetected, if (IC<sub>50/80</sub>)>cutoff or >100, (ID<sub>50/80</sub>)<cutoff or <20. For the purpose of calculating means, each undetected sets to 100/(IC<sub>50/80</sub>) or 20/(ID<sub>50/80</sub>).

# of antibodies or mixtures found: 21  
# of viruses found: 7

Download neutralization data  
include  virus info  slice of alignment from position analysis

### Position analysis

Analyze Rseq position 17 5-7

Analysis at position 17 for Ab 5-7

Amino Acid Counts

| AA    | Count | # for detected | # for undetected | Fisher test p-value | Odds ratio |
|-------|-------|----------------|------------------|---------------------|------------|
| N     | 7     | 2              | 5                | 1                   | 0          |
| Total | 7     | 2              | 5                |                     |            |

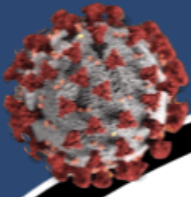
N-linked Glycosylation Motif Counts

| NxST  | Count | # for detected | # for undetected | Fisher test p-value | Odds ratio |
|-------|-------|----------------|------------------|---------------------|------------|
| g+    | 2     | 2              | 0                | 0.04762             | Inf        |
| g-    | 5     | 0              | 5                | 0.04762             | 0          |
| -     | 0     | 0              | 0                | 1                   | 0          |
| Total | 7     | 2              | 5                |                     |            |

Position analysis of antibody 5-7 at position 17 of the alignment...

...shows a statistical difference in neutralization between glycosylated and non-glycosylated N.





# COVID-19 Viral Genome Analysis Pipeline

Enabled by data from

<http://cov.lanl.gov>

- [Home](#)
- [Variants](#)
- [Resources](#)
- [Tools](#)
- 
- 

This website provides analyses and tools for exploring accruing mutations in hCoV-19 (SARS-CoV-2) geographically and over time, with an emphasis on the Spike protein, using data from GISAID.

The SARS-CoV-2 sequence data used for these analyses was updated from GISAID on Sep 22, 2022.

With the ever growing database of sequences in GISAID, sometimes the web connection times out before the analysis is complete. If you have this problem, please check "email results" and an email with a link will be sent to you when the job is complete.

## News

Oct 3, 2022

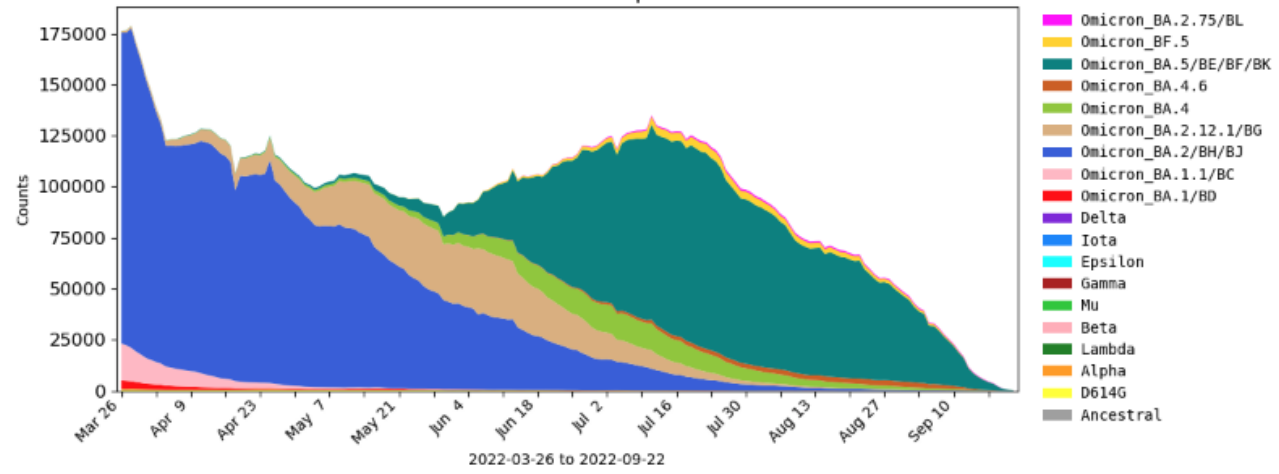
We have released a new update to our listings of SARS-CoV-2 [Spike Variants](#).

Aug 15, 2022

We have released a new update to our listings of SARS-CoV-2 [Spike Variants](#).

[See more](#)

Global: 2543178 sequences



[Embers plot, See data](#)

## AnalyzeAlign

Purpose: Show weblogs, calculate frequency by position, and find variants in an alignment. [Explanation](#).

### Input

Alignment

Positions/range to analyze   
[Sample Input: ACE2 receptors] e.g., 1, 12-20, 450-end

Positions are coordinates of  DNA  Protein sequence

**Sequence filter**

Collection date   -

Host    
 Aonyx cinereus (Asian small-clawed otter)  
 Arctictis binturong (Bearcat)  
 Canis lupus familiaris (Dog)  
 Chaetophractus villosus (Big hairy armadillo)

Pango lineage designation in GISAID    
 Beta (B.1.351)  
 Gamma (P.1\*)  
 Delta (B.1.617.2 and AY.\*)  
 Omicron (B.1.1.529 + BA.\*)  
 BA.1\* + BD.\*  
 BA.1.1.\* + BC.1\*  
 BA.2\* + BH.\* + BJ.\*  
 BA.2.12.1 + BG.\*  
 BA.2.75 + BL.\*

Geographic region  **Continent**   
 Africa  
 Asia  
 Europe  
 North America  
 Oceania  
 South America  
**Country**  
 Afghanistan  
 Albania  
 Algeria  
 American Samoa

**Sub-country**   
 Afghanistan\_Kabul  
 Afghanistan\_Kabul\_Kabul  
 Afghanistan\_Kandahar  
 Afghanistan\_Kandahar\_Kandahar  
 Afghanistan\_Nangarhar  
 Afghanistan\_Nangarhar\_Jalalabad  
 Albania\_Bajram Curr  
 Albania\_Korce  
 Albania\_Krum  
 Albania\_Krume

Report results for all selected geographic regions as a single group  
 Report separate results for each selected geographic region

Same tool as AnalyzeAlign, with options specific to SARS-COV-2.

### Logo options

### Other options

### Output

Downloadable logo files  PDF  EPS  SVG

Combine logos for separate results into a page  Concatenate PDF or EPS logos as a  x  matrix (row x column)  
 Orientation:  Portrait  Landscape  
 Include logo of removed symbols, if option to remove symbols selected:

Email results

# Thank you for attending!

**We are happy to help with research questions on the use of our tools and database.**

**We are thrilled to get ideas for further tool development!**

**Contact us:**

[seq-info@lanl.gov](mailto:seq-info@lanl.gov) or [immuno@lanl.gov](mailto:immuno@lanl.gov)