Closing Remarks & Survey

2021 IEDB Virtual User Workshop – Day 1

Wednesday, November 3, 2021

We want to hear from you!

SurveyMonkey

Improve our resources through user feedback

Daily and post-event feedback survey

Chat

https://www.surveymonkey.com/r/QSKBF25

SurveyMonkey

Please take some time to complete the survey now

#iedbuw2021

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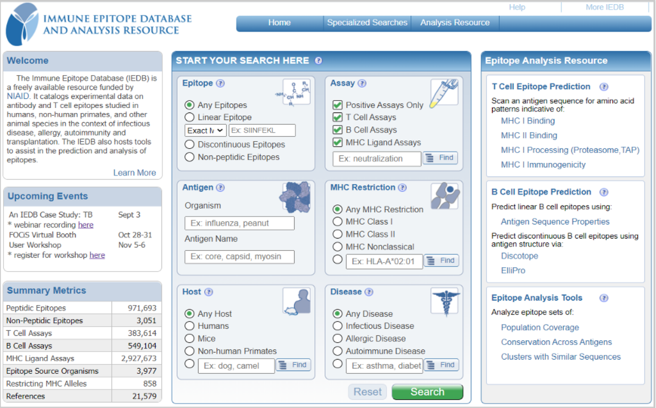
Recap of Day 1

IMMUNE EPITOPE DATABASE
AND ANALYSIS RESOURCE

Database Overview

Dr. Alessandro Sette
Principal Investigator



IMMUNE EPITOPE DATABASE AND ANALYSIS RESOURCE

Welcome

The Immune Epitope Database (IEDB) is a freely available resource funded by NIAID. It catalogs experimental data on antibody and T cell epitopes studied in humans, non-human primates, and other animal species in the context of infectious disease, allergy, autoimmunity and transplantation. The IEDB also hosts tools to assist in the prediction and analysis of epitopes.

Learn More

Upcoming Events

An IEDB Case Study: TB	Sept 3
* webinar recording here	
FOCiS Virtual Booth	Oct 28-31
User Workshop	Nov 5-6
* register for workshop here	

Summary Metrics

Peptidic Epitopes	971,693
Non-Peptidic Epitopes	3,051
T Cell Assays	383,614
B Cell Assays	549,104
MHC Ligand Assays	2,927,673
Epitope Source Organisms	3,977
Restricting MHC Alleles	858
References	21,579

START YOUR SEARCH HERE

Epitope
- ● Any Epitopes
- ○ Linear Epitope
- Exact M | Ex: SIINFEKL
- ○ Discontinuous Epitopes
- ○ Non-peptidic Epitopes

Assay
- ☑ Positive Assays Only
- ☑ T Cell Assays
- ☑ B Cell Assays
- ☑ MHC Ligand Assays
- Ex: neutralization | Find

Antigen
- Organism: Ex: influenza, peanut
- Antigen Name: Ex: core, capsid, myosin

MHC Restriction
- ● Any MHC Restriction
- ○ MHC Class I
- ○ MHC Class II
- ○ MHC Nonclassical
- ○ Ex: HLA-A*02:01 | Find

Host
- ● Any Host
- ○ Humans
- ○ Mice
- ○ Non-human Primates
- ○ Ex: dog, camel | Find

Disease
- ● Any Disease
- ○ Infectious Disease
- ○ Allergic Disease
- ○ Autoimmune Disease
- ○ Ex: asthma, diabet | Find

Reset | Search

Epitope Analysis Resource

T Cell Epitope Prediction

Scan an antigen sequence for amino acid patterns indicative of:
- MHC I Binding
- MHC II Binding
- MHC I Processing (Proteasome,TAP)
- MHC I Immunogenicity

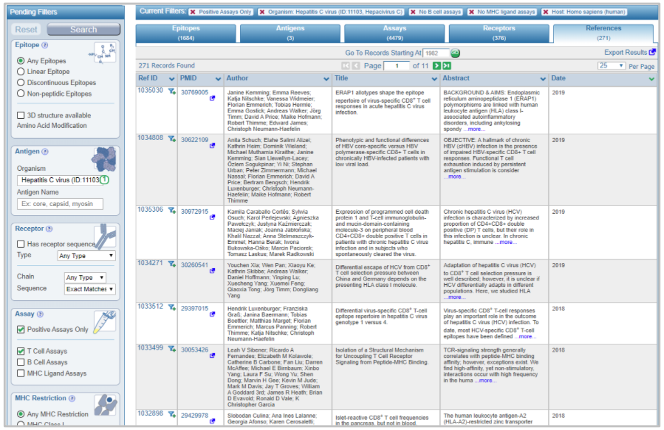
B Cell Epitope Prediction

Predict linear B cell epitopes using:
- Antigen Sequence Properties

Predict discontinuous B cell epitopes using antigen structure via:
- Discotope
- ElliPro

Epitope Analysis Tools

Analyze epitope sets of:
- Population Coverage
- Conservation Across Antigens
- Clusters with Similar Sequences



Pending Filters

Reset | Search

Epitope
- ● Any Epitopes
- ○ Linear Epitope
- ○ Discontinuous Epitopes
- ○ Non-peptidic Epitopes
- ☐ 3D structure available
- Amino Acid Modification

Antigen
- Organism: Hepatitis C virus (ID:11103 ①
- Antigen Name: Ex: core, capsid, myosin

Receptor
- ☐ Has receptor sequence
- Type: Any Type
- Chain: Any Type
- Sequence: Exact Matches

Assay
- ☑ Positive Assays Only
- ☑ T Cell Assays
- ☐ B Cell Assays
- ☐ MHC Ligand Assays

MHC Restriction
- ● Any MHC Restriction

Current Filters: ☒ Positive Assays Only ☒ Organism: Hepatitis C virus (ID:11103, Hepacivirus C) ☒ No B cell assays ☒ No MHC ligand assays ☒ Host: Homo sapiens (human)

Go To Records Starting At 1982 | Export Results

271 Records Found | Page 1 of 11 | 25 Per Page

Ref ID	PMID	Author	Title	Abstract	Date
1035030	30769005	Janine Kemming; Emma Reeves; Katja Nitschke; Vanessa Widmeier; Florian Emmerich; Tobias Hermle; Emma Gostick; Andreas Walker; Jörg Timm; David A Price; Maike Hofmann; Robert Thimme; Edward James; Christoph Neumann-Haefelin	ERAP1 allotypes shape the epitope repertoire of virus-specific $CD8^+$ T cell responses in acute hepatitis C virus infection.	BACKGROUND & AIMS: Endoplasmic reticulum aminopeptidase 1 (ERAP1) polymorphisms are linked with human leukocyte antigen (HLA) class I-associated autoinflammatory disorders, including ankylosing spondy ...more...	2019
1034808	30622109	Anita Schuch; Elahe Salimi Alizei; Kathrin Heim; Dominik Wieland; Michael Muthamia Kiraithe; Janine Kemming; Sian Llewellyn-Lacey; Özlem Sogukpinar; Yi Ni; Stephan Urban; Peter Zimmermann; Michael Nassal; Florian Emmerich; David A Price; Bertram Bengsch; Hendrik Luxenburger; Christoph Neumann-Haefelin; Maike Hofmann; Robert Thimme	Phenotypic and functional differences of HBV core-specific versus HBV polymerase-specific CD8+ T cells in chronically HBV-infected patients with low viral load.	OBJECTIVE: A hallmark of chronic HBV (cHBV) infection is the presence of impaired HBV-specific CD8+ T cell responses. Functional T cell exhaustion induced by persistent antigen stimulation is consider ...more...	2019
1035306	30972915	Kamila Caraballo Cortés; Sylwia Osuch; Karol Perlejewski; Agnieszka Pawełczyk; Justyna Kaźmierczak; Maciej Janiak; Joanna Jabłońska; Khalil Nazzal; Anna Stelmaszczyk-Emmel; Hanna Berak; Iwona Bukowska-Ośko; Marcin Paciorek; Tomasz Laskus; Marek Radkowski	Expression of programmed cell death protein 1 and T-cell immunoglobulin- and mucin-domain-containing molecule-3 on peripheral blood CD4+CD8+ double positive T cells in patients with chronic hepatitis C virus infection and in subjects who spontaneously cleared the virus.	Chronic hepatitis C virus (HCV) infection is characterized by increased proportion of CD4+CD8+ double positive (DP) T cells, but their role in this infection is unclear. In chronic hepatitis C, immune ...more...	2019
1034271	30260541	Youchen Xia; Wen Pan; Xiaoyu Ke; Kathrin Skibbe; Andreas Walker; Daniel Hoffmann; Yinping Lu; Xuecheng Yang; Xuemei Feng; Qiaoxia Tong; Jörg Timm; Dongliang Yang	Differential escape of HCV from $CD8^+$ T cell selection pressure between China and Germany depends on the presenting HLA class I molecule.	Adaptation of hepatitis C virus (HCV) to $CD8^+$ T cell selection pressure is well described; however, it is unclear if HCV differentially adapts in different populations. Here, we studied HLA ...more...	2019
1033512	29397015	Hendrik Luxenburger; Franziska Graß; Janina Baermann; Tobias Boettler; Matthias Marget; Florian Emmerich; Marcus Panning; Robert Thimme; Katja Nitschke; Christoph Neumann-Haefelin	Differential virus-specific $CD8^+$ T-cell epitope repertoire in hepatitis C virus genotype 1 versus 4.	Virus-specific $CD8^+$ T-cell responses play an important role in the outcome of hepatitis C virus (HCV) infection. To date, most HCV-specific $CD8^+$ T-cell epitopes have been defined ...more...	2018
1033499	30053426	Leah V Sibener; Ricardo A Fernandes; Elizabeth M Kolawole; Catherine B Carbone; Fan Liu; Darren McAffee; Michael E Birnbaum; Xinbo Yang; Laura F Su; Wong Yu; Shen Dong; Marvin H Gee; Kevin M Jude; Mark M Davis; Jay T Groves; William A Goddard 3rd; James R Heath; Brian D Evavold; Ronald D Vale; K Christopher Garcia	Isolation of a Structural Mechanism for Uncoupling T Cell Receptor Signaling from Peptide-MHC Binding.	TCR-signaling strength generally correlates with peptide-MHC binding affinity; however, exceptions exist. We find high-affinity, yet non-stimulatory, interactions occur with high frequency in the huma ...more...	2018
1032898	29429978	Slobodan Culina; Ana Ines Lalanne; Georgia Afonso; Karen Cerosaletti;	Islet-reactive $CD8^+$ T cell frequencies in the pancreas, but not in blood	The human leukocyte antigen-A2 (HLA-A2)-restricted zinc transporter	2018

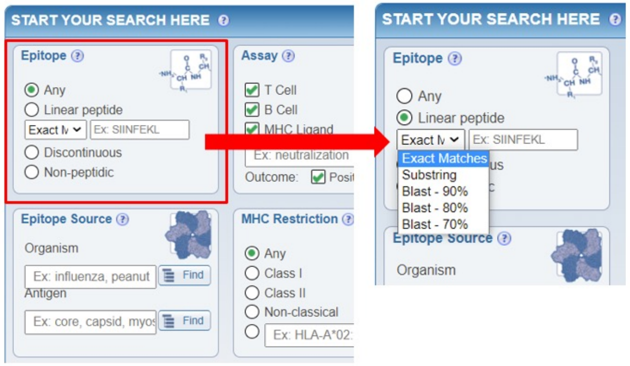
Recap of Day 1

IMMUNE EPITOPE DATABASE
AND ANALYSIS RESOURCE

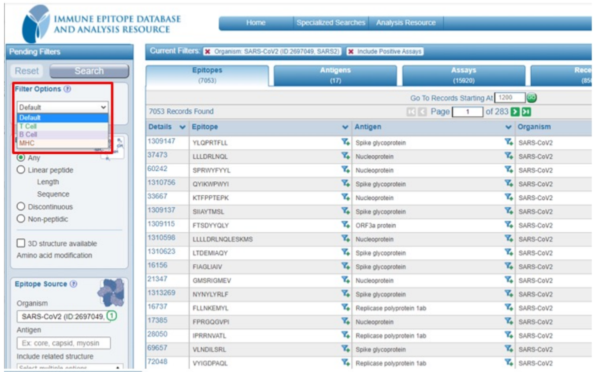
Accessing the Data: Query, Reporting and Examples

Epitope Search Pane

Search by epitope sequence



Results Page: Pending Filters/Filter Options



Current Filters: Organism: SARS-CoV2 (ID:2697049, SARS2) | Include Positive Assays

Organism: SARS-CoV2 (ID:2697049, ①

Go To Records Starting At 1200

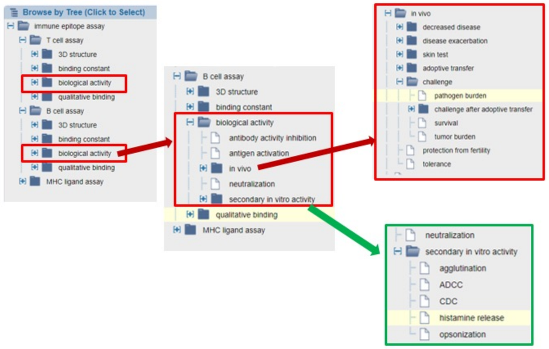
7053 Records Found — Page 1 of 283

Details	Epitope	Antigen	Organism
1309147	YLQPRTFLL	Spike glycoprotein	SARS-CoV2
37473	LLLDRLNQL	Nucleoprotein	SARS-CoV2
60242	SPRWYFYYL	Nucleoprotein	SARS-CoV2
1310756	QYIKWPWYI	Spike glycoprotein	SARS-CoV2
33667	KTFPPTEPK	Nucleoprotein	SARS-CoV2
1309137	SIIAYTMSL	Spike glycoprotein	SARS-CoV2
1309115	FTSDYYQLY	ORF3a protein	SARS-CoV2
1310598	LLLLDRLNQLESKMS	Nucleoprotein	SARS-CoV2
1310623	LTDEMIAQY	Spike glycoprotein	SARS-CoV2
16156	FIAGLIAIV	Spike glycoprotein	SARS-CoV2
21347	GMSRIGMEV	Nucleoprotein	SARS-CoV2
1313269	NYNYLYRLF	Spike glycoprotein	SARS-CoV2
16737	FLLNKEMYL	Replicase polyprotein 1ab	SARS-CoV2
17385	FPRGQGVPI	Nucleoprotein	SARS-CoV2
28050	IPRRNVATL	Replicase polyprotein 1ab	SARS-CoV2
69657	VLNDILSRL	Spike glycoprotein	SARS-CoV2
72048	VYIGDPAQL	Replicase polyprotein 1ab	SARS-CoV2

Dr. Randi Vita

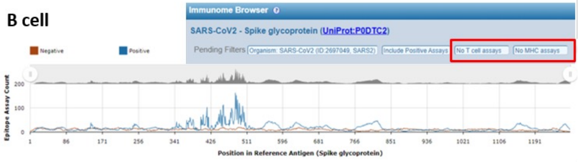
Lead Ontology & Quality Manager

User Queries: How can we assess the protective capability of the epitopes of the database?

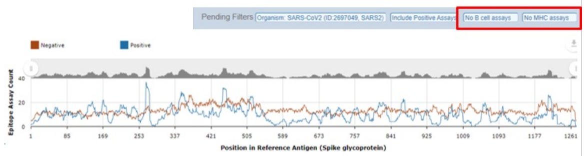


User Queries: How to see the differences between B and T cell responses

B cell



T cell

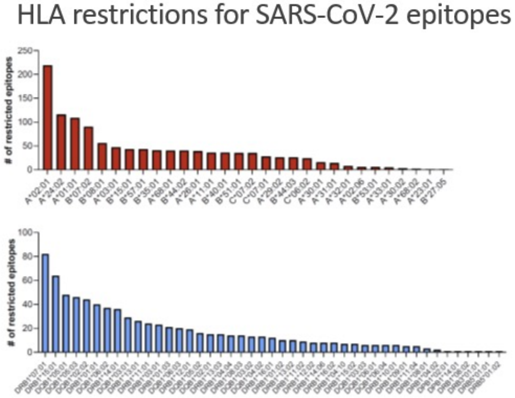


Recap of Day 1

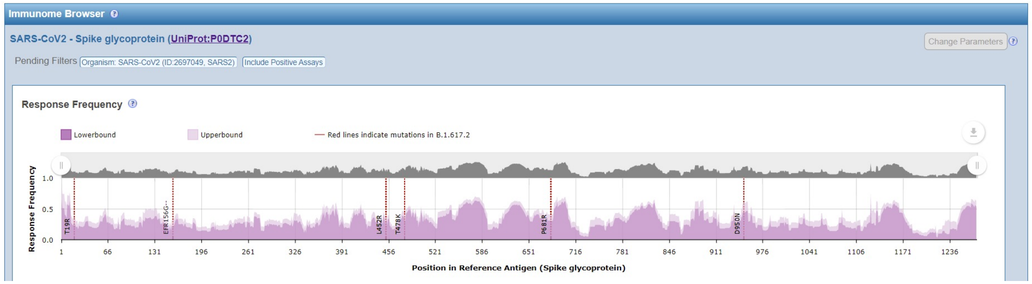
IMMUNE EPITOPE DATABASE
AND ANALYSIS RESOURCE

SARS-CoV-2 and the ImmunomeBrowser

Dr. Alba Grifoni
LJI Research Faculty/Instructor



HLA restrictions for SARS-CoV-2 epitopes



Immunome Browser

SARS-CoV2 - Spike glycoprotein (UniProt:P0DTC2)

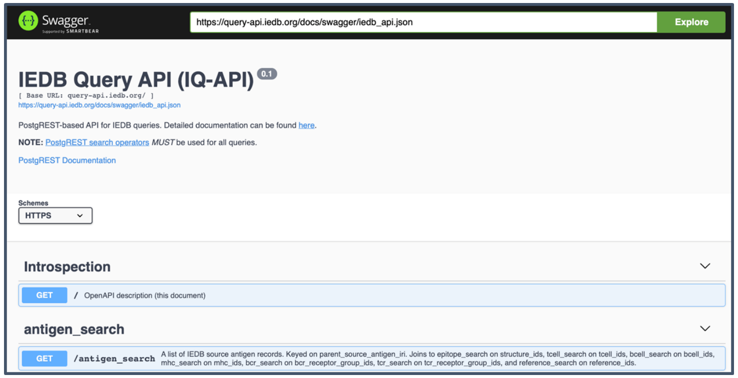
Pending Filters: Organism: SARS-CoV2 (ID:2697049, SARS2) | Include Positive Assays

Recap of Day 1

IMMUNE EPITOPE DATABASE
AND ANALYSIS RESOURCE

New Database Features - Query API

Dr. Jason Greenbaum
Bioinformatics Core Director



IEDB Query API (IQ-API)

[Base URL: query-api.iedb.org/]
https://query-api.iedb.org/docs/swagger/iedb_api.json

PostgREST-based API for IEDB queries. Detailed documentation can be found here.

NOTE: PostgREST search operators *MUST* be used for all queries.

PostgREST Documentation

Schemes: HTTPS

Introspection

GET / OpenAPI description (this document)

antigen_search

GET /antigen_search A list of IEDB source antigen records. Keyed on parent_source_antigen_iri. Joins to epitope_search on structure_ids, tcell_search on tcell_ids, bcell_search on bcell_ids, mhc_search on mhc_ids, bcr_search on bcr_receptor_group_ids, tcr_search on tcr_receptor_group_ids, and reference_search on reference_ids.

New Database Features - Custom Exports

Kelly Wheeler
Senior Software Engineer

CUSTOM FILE EXPORT

File Format: .XLS
Header Count: Double Headers
Field Set: Full Export

- ☑ Antigen
  - ☑ Antigen Name
  - ☑ Antigen ID
  - ☑ Organism Name
  - ☑ Organism ID
  - ☑ # Epitopes
  - ☑ # Assays
  - ☑ # References

Recap of Day 1

NIH Resources for Researchers:
The LANL HIV Sequence Database

Dr. Brian Foley
Research Scientist

Tutorials and Basic Informatio

Tutorials

HIV Database presentations from conference workshops

FAQs about the HIV Sequence Database

FAQs about the HIV Immunology Database

Sequence quality control explains several common problems with sets of viral sequences

How to make a phylogenetic tree explains how to build a phylogenetic tree

HIV numbering relative to reference strain HXB2

SIV numbering relative to reference strain SIVmm239

Articles

3D views of HIV macromolecular structures provides links to 3D views of HIV proteins

Stalking the AIDS Virus [PDF] article from LANL Research Quarterly (Fall 2003) about HIV Database research on the HIV-immune system interaction as a step toward an AIDS vaccine

Los Alamos research fundamental to first efficacy study for mosaic HIV-1 preventive vaccine 2017 LANL news release about the HIV mosaic vaccine

Reference Inform

Circulating recombinan etails about all documented CRFs

HIV-1 gene map illustr of HIV-1, including HXB2 breakpoints

HXB2 annotated spreadsheet (.xls) provides a fully-annotated sequence of HXB2 with base-by-base detail

HIV and SIV subtype nomenclature gives an overview of HIV and SIV subtype nomenclature, particularly HIV-1 groups and subtypes

Primate immunodeficiency virus nomenclature lists SIV species and nomenclature

How the HIV database classifies sequences explains how recombinants are named and annotated

Common sequence formats for alignments shows examples of common sequence formats for alignments

How to cite this Database explains how to cite this website and the printed HIV compendia

Codes and symbols in sequences decodes the symbols and IUPAC codes that appear in sequences and alignments

Codon table gives the translation of nucleotides into amino acids

Links HIV/AIDS resources and bioinformatics tools on other websites

last modified: Wed Feb 28 14:38 2018

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

All kinds of basic information about HIV and about our database

Previous workshop presentations

Yes! We do respond to this e-mail address!

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 nucleotidealignment 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

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_{50} and/or IC_{80} 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

🟪 Epilign (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

Some of our tools are specific to HIV or lentiviruses, most can be used on DNA or Protein sequences from any organism.

Color-coded square indicates whether a given tool is specific to HIV or not.

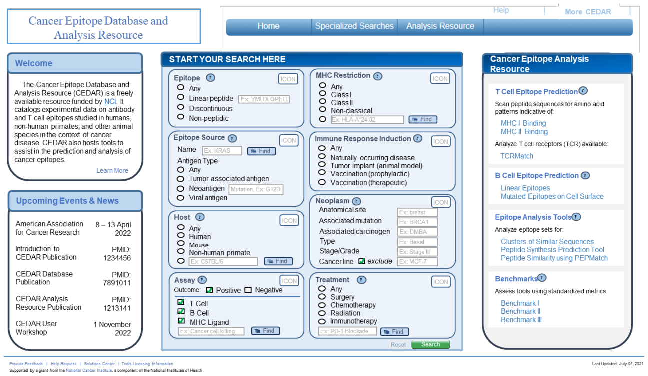
Tools are listed alphabetically and organized into general categories.

Write to seq-info@lanl.gov for additional help, or to report problems or suggest new tools or features.

Recap of Day 1

IMMUNE EPITOPE DATABASE
AND ANALYSIS RESOURCE

The Cancer Epitope Database and Analysis Resource (CEDAR)



Cancer Epitope Database and Analysis Resource

Help | More CEDAR

Home | Specialized Searches | Analysis Resource

Welcome

The Cancer Epitope Database and Analysis Resource (CEDAR) is a freely available resource funded by NCI. It catalogs experimental data on antibody and T cell epitopes studied in humans, non-human primates, and other animal species in the context of cancer disease. CEDAR also hosts tools to assist in the prediction and analysis of cancer epitopes.

Learn More

Upcoming Events & News

American Association for Cancer Research	8 – 13 April 2022
Introduction to CEDAR Publication	PMID: 1234456
CEDAR Database Publication	PMID: 7891011
CEDAR Analysis Resource Publication	PMID: 1213141
CEDAR User Workshop	1 November 2022

START YOUR SEARCH HERE

Epitope ? ICON
○ Any
○ Linear peptide Ex: YMLDLQPETT
○ Discontinuous
○ Non-peptidic

MHC Restriction ? ICON
○ Any
○ Class I
○ Class II
○ Non-classical
○ Ex: HLA-A*24:02 Find

Epitope Source ? ICON
Name Ex: KRAS Find
Antigen Type
○ Any
○ Tumor associated antigen
○ Neoantigen Mutation, Ex: G12D
○ Viral antigen

Immune Response Induction ? ICON
○ Any
○ Naturally occurring disease
○ Tumor implant (animal model)
○ Vaccination (prophylactic)
○ Vaccination (therapeutic)

Host ? ICON
○ Any
○ Human
○ Mouse
○ Non-human primate
○ Ex: C57BL/6 Find

Neoplasm ? ICON
Anatomical site Ex: breast
Associated mutation Ex: BRCA1
Associated carcinogen Ex: DMBA
Type Ex: Basal
Stage/Grade Ex: Stage III
Cancer line ☑ *exclude* Ex: MCF-7

Assay ? ICON
Outcome: ☑ Positive ☐ Negative
☑ T Cell
☑ B Cell
☑ MHC Ligand
Ex: Cancer cell killing Find

Treatment ? ICON
○ Any
○ Surgery
○ Chemotherapy
○ Radiation
○ Immunotherapy
Ex: PD-1 Blockade Find

Reset Search

Cancer Epitope Analysis Resource

T Cell Epitope Prediction ?
Scan peptide sequences for amino acid patterns indicative of:
MHC I Binding
MHC II Binding
Analyze T cell receptors (TCR) available:
TCRMatch

B Cell Epitope Prediction ?
Linear Epitopes
Mutated Epitopes on Cell Surface

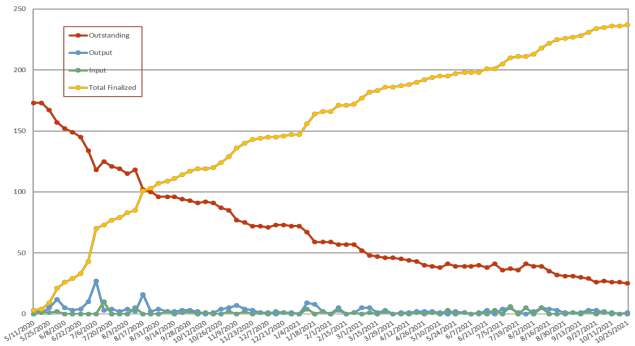
Epitope Analysis Tools ?
Analyze epitope sets for:
Clusters of Similar Sequences
Peptide Synthesis Prediction Tool
Peptide Similarity using PEPMatch

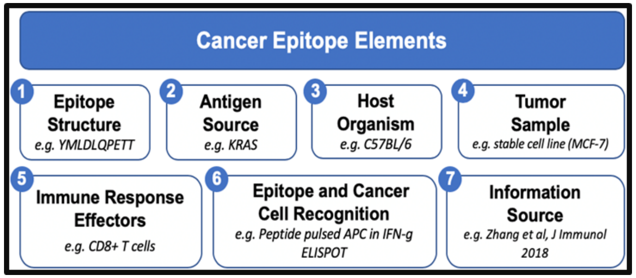
Benchmarks ?
Assess tools using standardized metrics:
Benchmark I
Benchmark II
Benchmark III

Provide Feedback | Help Request | Solutions Center | Tools Licensing Information
Supported by a grant from the National Cancer Institute, a component of the National Institutes of Health

Last Updated: July 04, 2021

Dr. Zeynep Koşaloğlu-Yalçın
Instructor





Cancer Epitope Elements

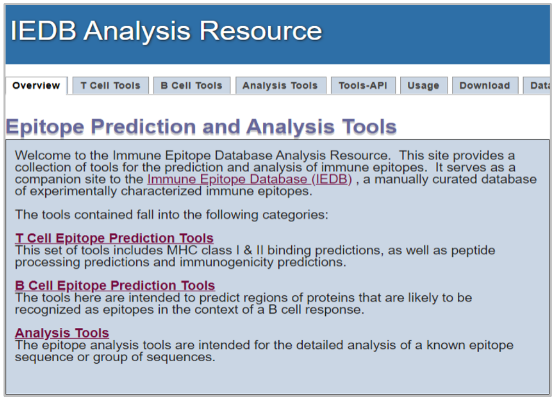
1. **Epitope Structure** *e.g. YMLDLQPETT*
2. **Antigen Source** *e.g. KRAS*
3. **Host Organism** *e.g. C57BL/6*
4. **Tumor Sample** *e.g. stable cell line (MCF-7)*
5. **Immune Response Effectors** *e.g. CD8+ T cells*
6. **Epitope and Cancer Cell Recognition** *e.g. Peptide pulsed APC in IFN-g ELISPOT*
7. **Information Source** *e.g. Zhang et al, J Immunol 2018*

Recap of Day 1

IMMUNE EPITOPE DATABASE
AND ANALYSIS RESOURCE

Analysis Resource Overview

Dr. Bjoern Peters
Co-Principal Investigator



Epitope Prediction and Analysis Tools

Welcome to the Immune Epitope Database Analysis Resource. This site provides a collection of tools for the prediction and analysis of immune epitopes. It serves as a companion site to the Immune Epitope Database (IEDB) , a manually curated database of experimentally characterized immune epitopes.

The tools contained fall into the following categories:

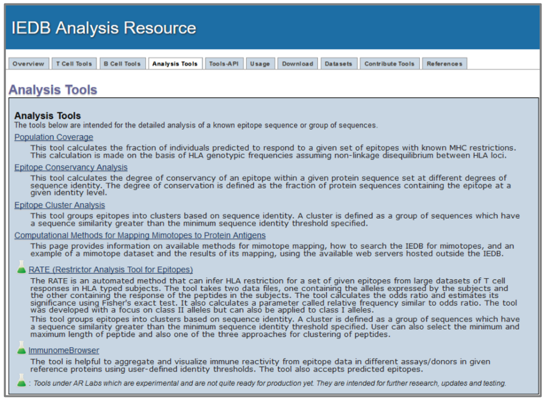
T Cell Epitope Prediction Tools
This set of tools includes MHC class I & II binding predictions, as well as peptide processing predictions and immunogenicity predictions.

B Cell Epitope Prediction Tools
The tools here are intended to predict regions of proteins that are likely to be recognized as epitopes in the context of a B cell response.

Analysis Tools
The epitope analysis tools are intended for the detailed analysis of a known epitope sequence or group of sequences.

Analysis Tools

Dr. Alessandro Sette
Principal Investigator



Analysis Tools

Analysis Tools
The tools below are intended for the detailed analysis of a known epitope sequence or group of sequences.

Population Coverage
This tool calculates the fraction of individuals predicted to respond to a given set of epitopes with known MHC restrictions. This calculation is made on the basis of HLA genotypic frequencies assuming non-linkage disequilibrium between HLA loci.

Epitope Conservancy Analysis
This tool calculates the degree of conservancy of an epitope within a given protein sequence set at different degrees of sequence identity. The degree of conservation is defined as the fraction of protein sequences containing the epitope at a given identity level.

Epitope Cluster Analysis
This tool groups epitopes into clusters based on sequence identity. A cluster is defined as a group of sequences which have a sequence similarity greater than the minimum sequence identity threshold specified.

Computational Methods for Mapping Mimotopes to Protein Antigens
This page provides information on available methods for mimotope mapping, how to search the IEDB for mimotopes, and an example of a mimotope dataset and the results of its mapping, using the available web servers hosted outside the IEDB.

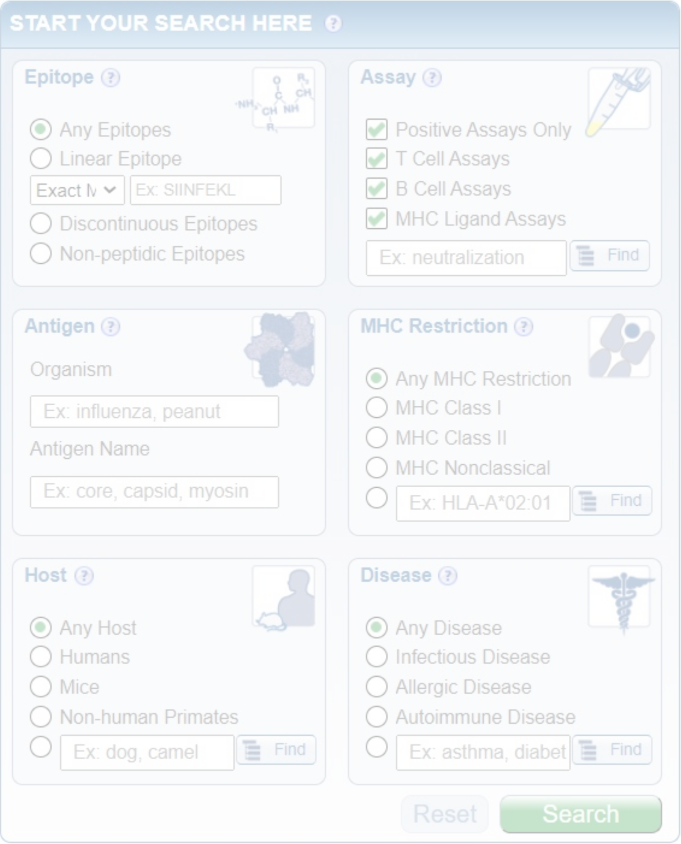
RATE (Restrictor Analysis Tool for Epitopes)
The RATE is an automated method that can infer HLA restriction for a set of given epitopes from large datasets of T cell responses in HLA typed subjects. The tool takes two data files, one containing the alleles expressed by the subjects and the other containing the response of the peptides in the subjects. The tool calculates the odds ratio and estimates its significance using Fisher's exact test. It also calculates a parameter called relative frequency similar to odds ratio. The tool was developed with a focus on class II alleles but can also be applied to class I alleles.
This tool groups epitopes into clusters based on sequence identity. A cluster is defined as a group of sequences which have a sequence similarity greater than the minimum sequence identity threshold specified. User can also select the minimum and maximum length of peptide and also one of the three approaches for clustering of peptides.

ImmunomeBrowser
The tool is helpful to aggregate and visualize immune reactivity from epitope data in different assays/donors in given reference proteins using user-defined identity thresholds. The tool also accepts predicted epitopes.

: Tools under AR Labs which are experimental and are not quite ready for production yet. They are intended for further research, updates and testing.

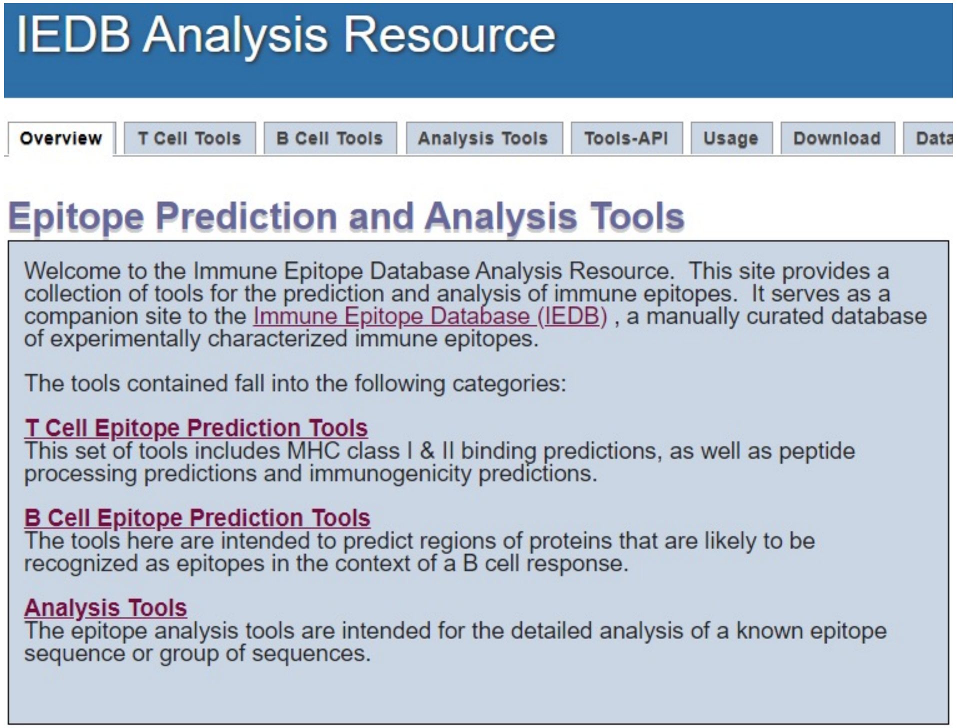
User Workshop Structure

Day 1



Process Overview and Database

Day 2



Epitope Prediction and Analysis Tools

Welcome to the Immune Epitope Database Analysis Resource. This site provides a collection of tools for the prediction and analysis of immune epitopes. It serves as a companion site to the Immune Epitope Database (IEDB) , a manually curated database of experimentally characterized immune epitopes.

The tools contained fall into the following categories:

T Cell Epitope Prediction Tools
This set of tools includes MHC class I & II binding predictions, as well as peptide processing predictions and immunogenicity predictions.

B Cell Epitope Prediction Tools
The tools here are intended to predict regions of proteins that are likely to be recognized as epitopes in the context of a B cell response.

Analysis Tools
The epitope analysis tools are intended for the detailed analysis of a known epitope sequence or group of sequences.

Analysis Resource

Preview of Day 2

Start Time	End Time	Topic	Speaker
14:00	**14:05**	Welcome	Nina Blazeska *IEDB Project Manager*
14:05	**15:00**	MHC Binding Predictions	Raphael Trevizani *Bioinformatics Postdoctoral Researcher* Bjoern Peters *IEDB Co-Principal Investigator*
15:00	**15:20**	T Cell Processing & Immunogenicity Predictions	Austin Crinklaw *Bioinformatics Research Technician* Bjoern Peters *IEDB Co-Principal Investigator*
15:20	**15:35**	Section 1: Q&A with Drs. Trevizani, Peters and Crinklaw	
15:35	**15:45**	**Break**	
15:45	**16:00**	T Cell Tool Spotlight: TCRMatch	Will Chronister *Bioinformatics Postdoctoral Researcher*
16:00	**16:30**	Structure Tools: LYRA & SCEptRe	Paolo Marcatili *DTU Associate Professor*
16:30	**16:45**	PEPMatch: Homology of SARS-CoV-2 Spike Sequences to Myocarditis Antigens	Daniel Marrama *Bioinformatics Research Technician*
16:45	**17:00**	Section 2: Q&A with Drs. Chronister, Peters and Marrama	
17:00	**17:30**	**Break**	

Preview of Day 2

Start Time	End Time	Topic	Speaker
17:30	**18:00**	NIH Resources for Researchers: The LANL HIV Immunology Database	Elizabeth-Sharon Fung *Los Alamos National Laboratory*
18:00	**18:10**	Section 3: Q&A with Dr. Fung and Dr. Fischer	
18:10	**18:45**	B Cell Epitope Prediction	Marcus Mendes *Bioinformatics Postdoctoral Researcher*
18:45	**19:05**	IEDB Tools 3.0: Future of Tools	Jason Greenbaum *Bioinformatics Core Director*
19:05	**19:20**	Section 4: Q&A with Drs. Mendes and Greenbaum	
19:20	**19:30**	Closing Remarks & Feedback Survey	Nina Blazeska *IEDB Project Manager*
19:30	**20:00**	**Optional Q&A Session** This will be to answer any remaining questions from the day	

Optional Q&A

This will be to answer any remaining questions from the day