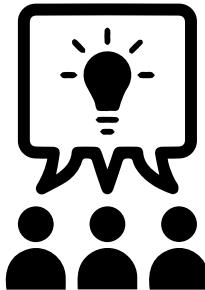


Closing Remarks & Survey

2022 IEDB Virtual User Workshop – Day 3

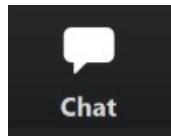
Friday, October 28, 2022

We want to hear from you!



Improve our resources
through user feedback

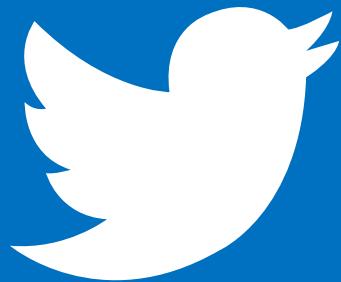
Daily and post-event
feedback survey



<https://www.surveymonkey.com/r/BYQV6VK>



**Please take some time to
complete the survey now**



#iedbuw2022

Follow us @iedb_

Recap of Day 2



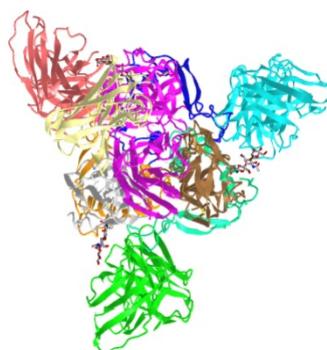
IMMUNE EPITOPE DATABASE AND ANALYSIS RESOURCE

IEDB-3D 2.0: Visualizing Structures in the IEDB



Dr. Marcus Mendes

Bioinformatics Postdoctoral Researcher



Structure Tools: LYRA & SCEptRe



Dr. Paolo Marcatili

DTU Associate Professor



Structure Tools

LYRA (Lymphocyte Receptor Automated Modelling)

The LYRA server predicts structures for either T-Cell Receptors (TCR) or B-Cell Receptors (BCR). Framework templates are selected based on BLOSUM score, and complementary determining regions needed based on a canonical structure model and grafted onto the framework templates.

SCEptRe: Structural Complexes of Epitope Receptor

SCEPteRe provides weekly updated, non-redundant, user customized benchmark datasets with its features for receptor-specific epitope predictions. This tool extracts weekly updated 3D complex and MHC-ligand from the Immune Epitope Database (IEDB) and clusters them based on antigen generate benchmark datasets. Users can customize structural quality and clustering parameters (epitope or epitope sequence identity) to generate these datasets based on their need.

Recap of Day 2



IMMUNE EPITOPE DATABASE
AND ANALYSIS RESOURCE

IEDB Query API (IQ-API)



Dr. Jason Greenbaum
Bioinformatics Core Director

The screenshot shows the IEDB Query API (IQ-API) documentation page. At the top, it displays the title "IEDB Query API (IQ-API) 0.1" and the URL "https://query-api.iedb.org/docs/swagger/edb_api.json". Below this, there's a note about PostgREST-based API for IEDB queries and a link to detailed documentation. A dropdown menu for "Schemes" is set to "HTTPS". The main content area is titled "Introspection" and shows a "GET / OpenAPI description (this document)" endpoint. Another section titled "antigen_search" shows a "GET /antigen_search" endpoint with a detailed description: "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, boell_search on boell_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."

Recap of Day 3



NIH Resources for Researchers: The LANL HIV Databases



Dr. Elizabeth-Sharon Fung
Annotator, Editor



Jennifer Macke
Research Technologist

HIV sequence database

DATABASES SEARCH ALIGNMENTS TOOLS PUBLICATIONS GUIDES search site Search

News Archive

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

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

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

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

HIV sequence database

DATABASES SEARCH TOOLS PRODUCTS PUBLICATIONS [Database](#) [Search](#) [Tools](#) [Products](#) [Publications](#)

HIV Molecular Immunology Database

Search Interfaces

- CTLCDB+
- T-Helper/CD4+
- Antibody
- Patient Search

Database API

- API Guide
- API Guide PDF
- API Reference
- API Reference (ReDoc)
- API Reference (JSON)

Experimental Methods and Outcome Measures

Author

Country

Keywords

Note

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

Recap of Day 2



IMMUNE EPITOPE DATABASE
AND ANALYSIS RESOURCE

The Cancer Epitope Database and Analysis Resource (CEDAR)



Dr. Alessandro Sette
Principal Investigator

CEDAR Home Specialized Searches Analysis Resource Help More CEDAR

This site is currently in test alpha. Many features are not fully functional and the data may not be accurate or up to date. Please email your feedback or comments to cedar@iit.org.

Welcome

The Cancer Epitope Database and Analysis Resource (CEDAR) is a freely available resource for the analysis of experimental data on antibody and T cell specificities against cancer antigens in humans, primates, and other animal species in the context of MHC molecules. It also contains tools to assist in the prediction and analysis of epitopes. The CEDAR database is part of the Immune Epitope Database (IEDB), which is the largest collection of epitopes from infectious disease, allergy, autoimmunity and cancer.

Upcoming Events & News

Antibody Booth
SDCS Fall Meeting, Boston, MA, Oct 26-29
Virtual User Workshops
regular data
IEDB SARS-CoV-2 Epitope Analysis Video

Summary Metrics

Peptide Epitopes	1,210,866
Non-Peptide Epitopes	57
T Cell Assays	9,299
ELISpot	99,240
MHC Ligand Assays	3,833,304
Epitope Source Organisms	1,459
Restricting HLA Alleles	628
References	3,940

SEARCH

START YOUR SEARCH HERE

Epitope Any Linear peptide Exact M^{*} Ex: AGGAGTV Discontinuous Non-peptide

Assay Any Cell Cytotoxicity MHC Ligand Ex: Cytotoxicity Outcome: Positive Negative

Epitope Source Any Ex: KRAS MHC Restriction Any Class I Class II Nonclassical Ex: HLA-A*02:01

MHC Human Mouse Rat

Immune Exposure Any Naturally occurring disease Animal model of cancer Vaccination

Reset **Search**

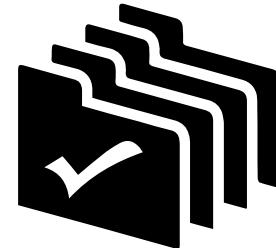
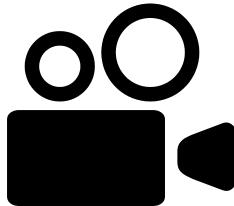
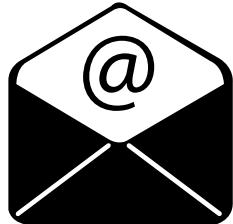
CEDAR Prostate Cancer Meta-analysis



Dr. Alessandro Sette
Principal Investigator

Protein	Abbreviation	Species	Protein Accession	References	Protein Length	Epitopes [†]							Epitopes					
						T cell	Human	Host	Human	Host	Mouse	Fc ^{II}	T cell	T cell	Class I	Class II	MHC Binding	MHC Edition
Prostatic acid phosphatase	PAP [*] PAP-C	human, mouse, rat	P15309, Q8CE08, A0ADG2K4B4	30	381	67	35	34	11	64	31	33	20	2	73			
Prostate-specific antigen	PSA [*]	KLK3 human	P07288	44	261	78	39	47	52	51	33	18	22	1	82			
Prostate-specific membrane antigen	PSMA [*]	human, mouse, rat	Q04609, Q5409	32	750	51	39	17	34	34	27	6	23	1	60			
Prostsein (Solute carrier family 45 member 3)	PROS [*]	human, mouse, rat	Q96J72, Q8KH07, D3ZP95	5	553	42	42	0	38	4	4	0	6	2	48			
Prostate stem cell antigen	PSCA [*]	human	O43653	6	114	18	18	1	7	17	17	0	12	2	20			
Metalloreductase STEAP1	STEAP [*]	human, mouse	Q9UHE8, Q9CW7R	8	339	15	7	10	0	15	13	2	2	5	19			
Transient receptor potential cation channel subfamily M member 8	Trp-p8	human, mouse	Q7Z2W7, Q8R4D5	2	1104	2	1	1	0	2	2	0	5	9	14			
TCR gamma alternate reading frame protein	TARP [*]	human	A2JGV3.1	5	58	5	6	0	0	5	3	2	3	1	6			
Total				132	278	187	110	142	192	130	61		93	21	322			

Post-Event Details



You will receive a post-event email next week

Workshop recording will be shared with you

All presentations will be shared with you



Participation certificates will be provided upon request



Post-event feedback survey

User Workshop Structure

Day 1

START YOUR SEARCH HERE

Epitope Any Linear peptide Discontinuous Non-peptidic
Exact M Ex: SIINFEKL

Assay T Cell B Cell MHC Ligand
Ex: neutralization
Outcome: Positive Negative

Epitope Source Organism
Ex: influenza, peanut
Antigen
Ex: core, capsid, myo

MHC Restriction Any Class I Class II Non-classical
Ex: HLA-A*02:01

Host Any Human Mouse Non-human primate
Ex: dog, camel

Disease Any Infectious Allergic Autoimmune
Ex: asthma

Process Overview and Database

Day 2

IEDB Analysis Resource

[Overview](#) [T Cell Tools](#) [B Cell Tools](#) [Analysis Tools](#) [Tools-API](#) [Usage](#) [Download](#) [Data](#)

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

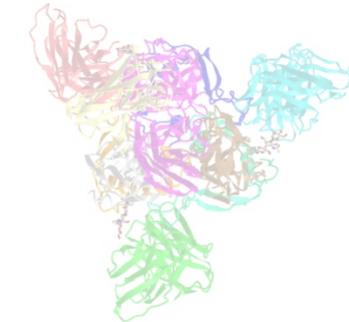
The tools here are intended to predict regions of proteins that are likely to be recognized as epitopes in the context of a B cell response.

Analysis Tools

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

Analysis Resource – Processing & Prediction Tools

Day 3



Specialized Topics – 3D Structures, Cancer, HIV



Additional Questions?

Email us at help@iedb.org



Thank you!

We appreciate your time and interest in the IEDB!