



Welcome to the

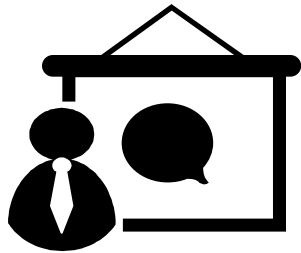
2023 IEDB Virtual User Workshop

Day 3

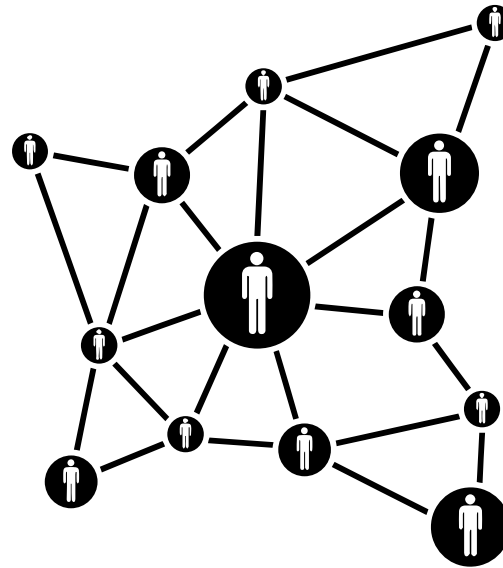
Friday, November 3, 2023

Annual IEDB User Workshop – Why?

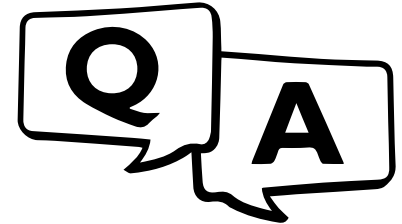
3 Day Event



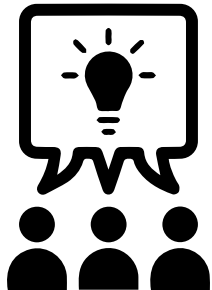
IEDB and tools overview with research examples and specialized topics



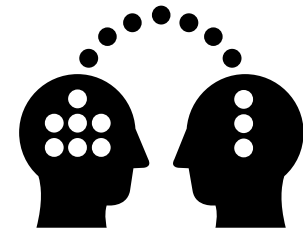
Engage with global user community



Answer user questions to facilitate learning



Improve our resources through user feedback



Share ideas to further scientific research

User Workshop Structure

Day 1

START YOUR SEARCH HERE

Epitope

Any
 Linear peptide
Exact N
 Discontinuous
 Non-peptidic

Assay

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

Epitope Source

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

Host

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

MHC Restriction

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

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.

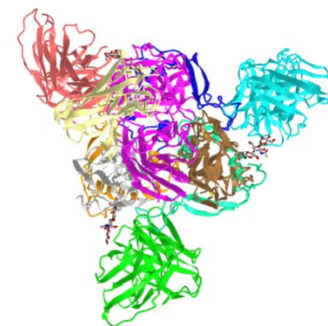
B Cell Epitope Prediction Tools

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.

The screenshot shows the IEDB Analysis Resource homepage. At the top is the IEDB logo and navigation tabs for Overview, T Cell Tools, B Cell Tools, Analysis Tools, Tools-API, Usage, Download, and Data. Below the navigation is a welcome message and a list of tool categories. A 'T Cell Prediction - Class I' tool is highlighted, showing a search box with the example sequence 'YIAREU spike glycoprotein' and a search button. Below the search box is a text area containing the amino acid sequence: 'MPFVSLRSLVSSGCVNTRTGLRRAVTVTRVYVDFVRSLSLSTQDLRFFPNVTRWNAHVSQNTARFQVLPVDFVYAS TIKDHWQVWPTLSLQKFGDQVNNATVYVWVCKPFCNDFRFDVYVWNAKSNMREFRVYSAKCTEYVYGFVLDLRGQDPA NLSFRVAVDCHFRVSKVTRVYVLDLQVLSLRLVLDLQVTRTLLAARVTRVCSGGVWASAAHVVYDGLRTELVKINDEUT'. The MHC Allele is set to 'HLA-A*02:01'. There are also sections for Announcements, Appearances & Events, and Additional Resources.

Next-Generation Tools & Analysis Resource

Day 3



CEDAR
Cancer Epitope Database and Analysis Resource

Los Alamos
NATIONAL LABORATORY

Specialized Topics – 3D Structures, Cancer, HIV

Who You'll Hear From



Dr. Marcus Mendes
*Bioinformatics Postdoctoral
Researcher*



Dr. Jason Greenbaum
Bioinformatics Core Director



Dr. Zeynep Koşaloğlu-Yalçın
Instructor



Dr. Alessandro Sette
Principal Investigator



Dr. Randi Vita
Lead Ontology & Quality Manager

Who You'll Hear From



Jennifer Mamrosh
Principal Investigator

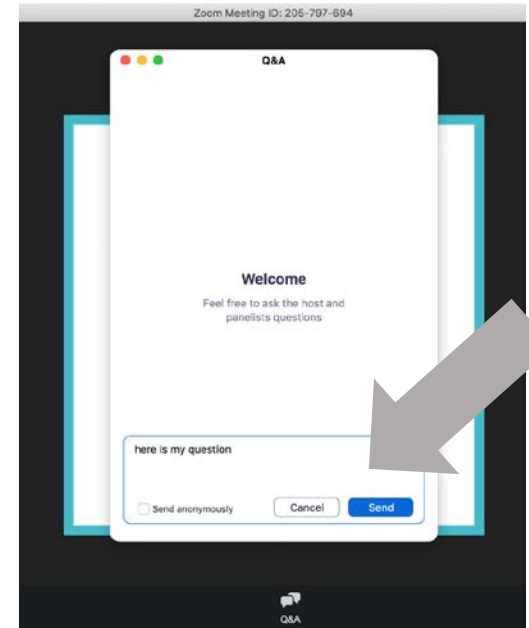
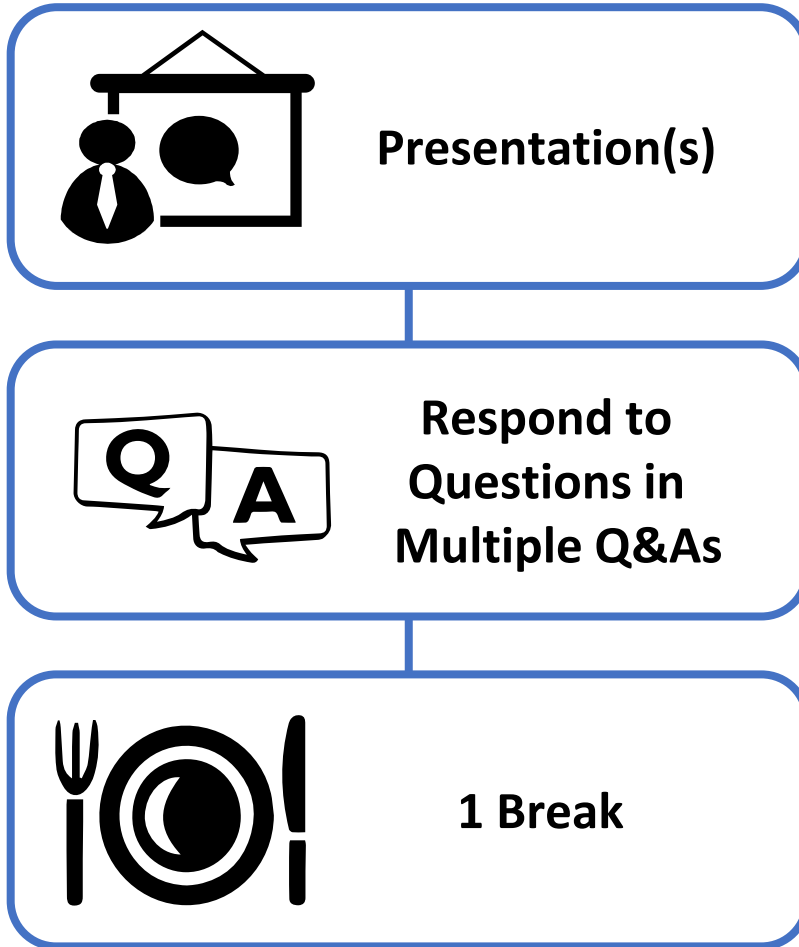


Elizabeth-Sharon Fung
Annotator, Editor

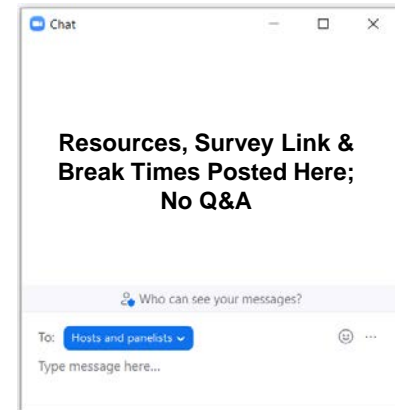


Jennifer Macke
Annotator

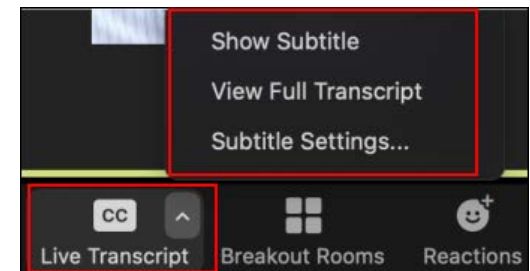
User Workshop Structure



Q&A



Chat



Subtitles

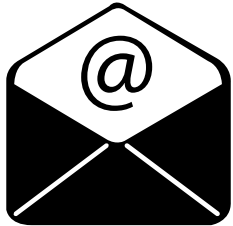
Agenda – Day 3

Start Time	End Time	Topic	Speaker
08:00	08:05	Welcome	Nina Blazeska <i>IEDB Senior Project Manager</i>
08:05	08:30	IEDB-3D 2.0: Visualizing Structures in the IEDB	Marcus Mendes <i>Bioinformatics Postdoctoral Researcher</i>
08:30	08:50	IEDB Query API (IQ-API)	Jason Greenbaum <i>Bioinformatics Core Director</i>
08:50	09:05	<u>Section 1</u> : Q&A with Drs. Mendes and Greenbaum	
09:05	09:35	The Cancer Epitope Database and Analysis Resource (CEDAR)	Zeynep Koşaloğlu-Yalçın <i>Instructor Cancer Bioinformatics</i>
09:35	09:55	CEDAR Prostate Cancer Meta-analysis	Alessandro Sette <i>IEDB Principal Investigator</i>
09:55	10:10	<u>Section 2</u> : Q&A with Drs. Koşaloğlu-Yalçın and Sette	
10:10	10:25	Break	

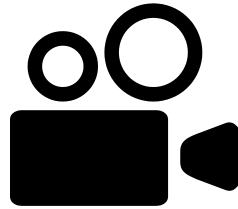
Agenda – Day 3

Start Time	End Time	Topic	Speaker
10:25	11:15	NIH Resources for Researchers: The LANL HIV Databases	Elizabeth-Sharon Fung <i>Los Alamos National Laboratory</i> Jennifer Macke <i>Los Alamos National Laboratory</i> Jennifer Mamrosh <i>Los Alamos National Laboratory</i>
11:15	11:35	IEDB, UniProt & Protein Ontology - A Collaboration	Randi Vita <i>Lead Ontology and Quality Manager</i>
11:35	11:50	<u>Section 3</u> : Q&A with Drs. Fung, Macke, Mamrosh and Vita	
11:50	12:00	Closing Remarks & Feedback Survey	Nina Blazeska <i>IEDB Senior Project Manager</i>
	12:00	End of Session	

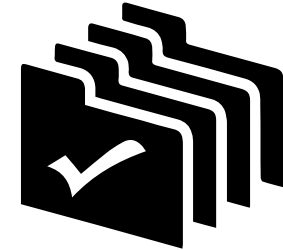
Other Event Logistics



You will receive a post-event email next week



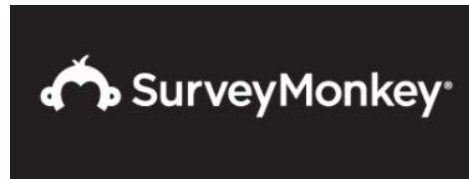
Workshop recording will be shared with you



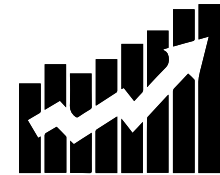
All presentations will be shared with you



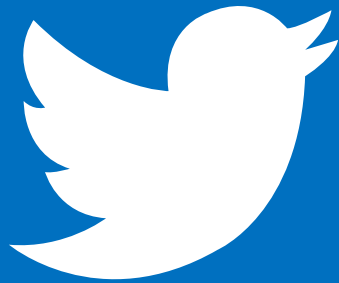
Participation certificates will be provided upon request



Daily and post-event feedback survey



Be aware of IEDB slowness due to increased traffic



#iedbuw2023

Follow us @iedb_

Without further ado...



Dr. Marcus Mendes
*Bioinformatics Postdoctoral
Researcher*

IEDB-3D 2.0: Visualizing Structures in the IEDB