

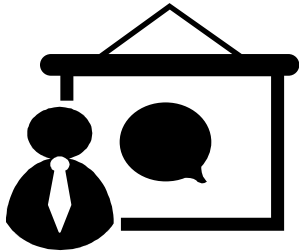
**Welcome to the**

**2022 IEDB Virtual User  
Workshop – Day 3**

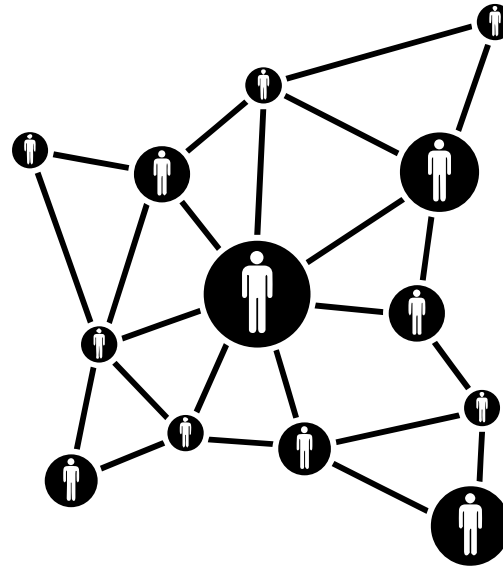
*Friday, October 28, 2022*

# Annual IEDB User Workshop – Why?

## 3 Day Event



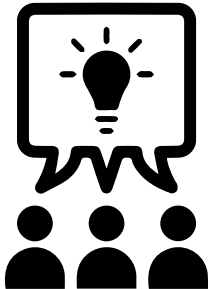
IEDB and tools overview with research examples and specialized topics



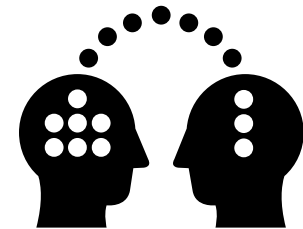
Engage with global user community



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    
 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, myosin

**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

# Who You'll Hear From



**Dr. Marcus Mendes**  
*Bioinformatics Postdoctoral  
Researcher*



**Dr. Paolo Marcatili**  
*DTU Associate Professor*



**Dr. Jason Greenbaum**  
*Bioinformatics Core Director*



**Dr. Alessandro Sette**  
*Principal Investigator*



**Dr. Zeynep Koşaloğlu-Yalçın**  
*Instructor*



**Dr. Bjoern Peters**  
*Co-Principal Investigator*

# Who You'll Hear From

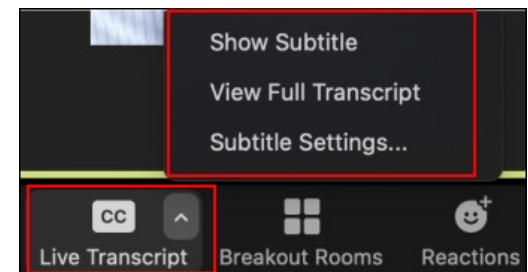
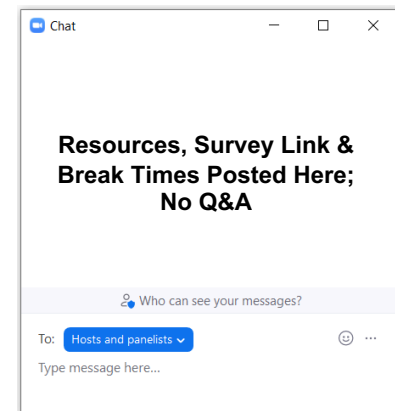
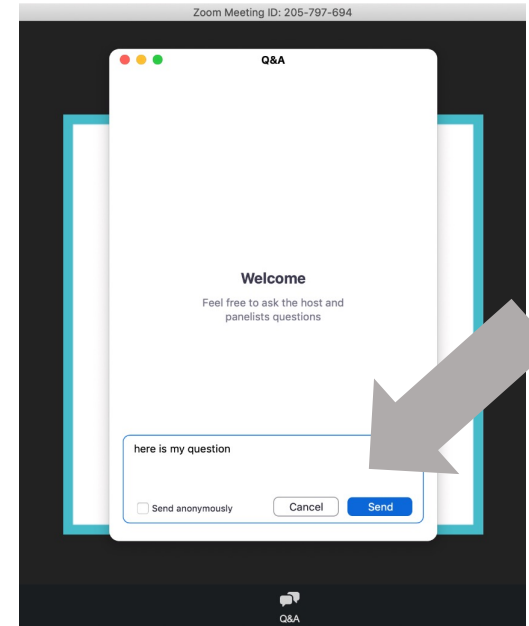
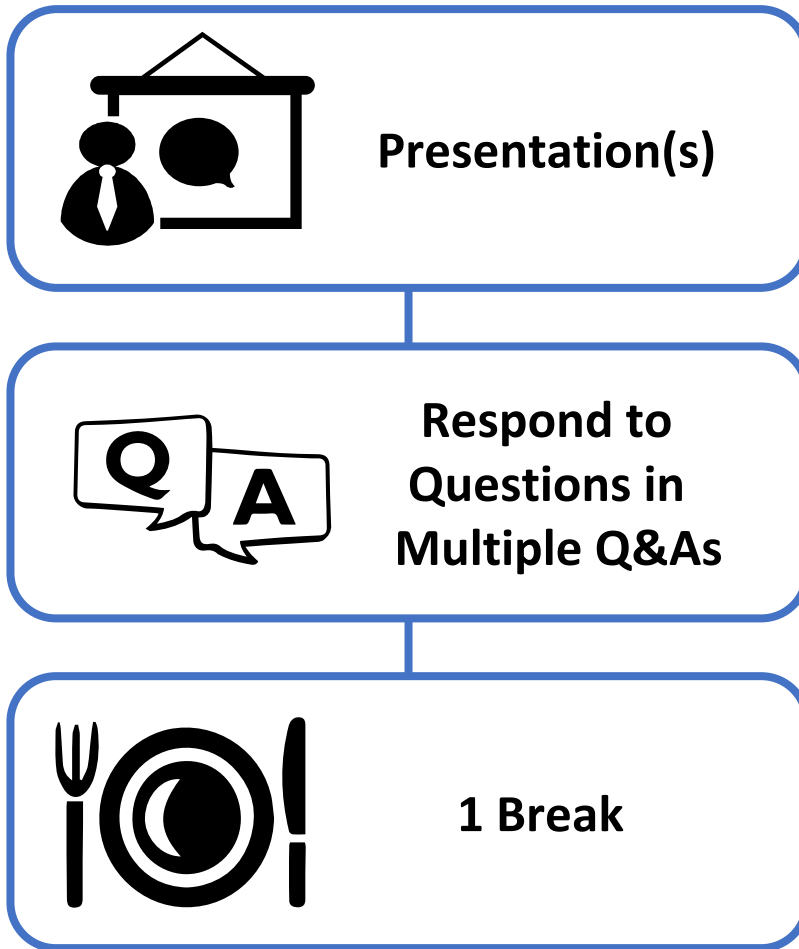


**Dr. Elizabeth-Sharon Fung**  
*Annotator, Editor*



**Jennifer Macke**  
*Research Technologist*

# User Workshop Structure



Subtitles

Live Transcript

Breakout Rooms

Reactions

# Agenda – Day 3

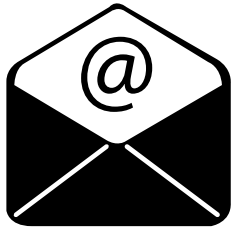
Start Time	End Time	Topic	Speaker
08:00	08:05	Welcome	Nina Blazeska <i>IEDB Project Manager</i>
08:05	08:30	IEDB-3D 2.0: Visualizing Structures in the IEDB	Marcus Mendes <i>Bioinformatics Postdoctoral Researcher</i>
08:30	09:00	Structure Tools: LYRA & SCEptRe	Paolo Marcatili (Recording) <i>DTU Associate Professor</i>
09:00	09:15	<u>Section 1</u> : Q&A with Drs. Mendes and Peters (in lieu of Dr. Marcatili)	
09:15	09:35	IEDB Query API (IQ-API)	Jason Greenbaum <i>Bioinformatics Core Director</i>
09:35	10:05	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>
10:05	10:20	<u>Section 2</u> : Q&A with Drs. Greenbaum, Fung and Macke	
10:20	10:45	Break	

# Agenda – Day 3

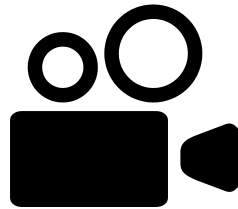
Start Time	End Time	Topic	Speaker
10:45	11:15	The Cancer Epitope Database and Analysis Resource (CEDAR)	Alessandro Sette <i>IEDB Principal Investigator</i>  In the absence of Zeynep Koşaloğlu-Yalçın <i>Instructor Cancer Bioinformatics</i>
11:15	11:35	CEDAR Prostate Cancer Meta-analysis	Alessandro Sette <i>IEDB Principal Investigator</i>
11:35	11:50	<u>Section 3</u> : Q&A with Drs. Sette and Peters	
11:50	12:00	Closing Remarks & Feedback Survey	Nina Blazeska <i>IEDB Project Manager</i>
	12:00	<b>End of Session</b>	



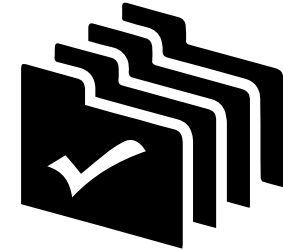
# Other Event Logistics



You will receive a post-event email next week



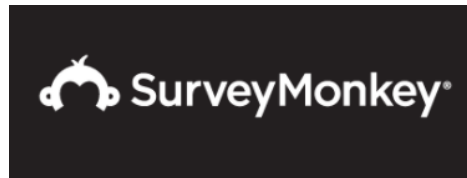
Workshop recording will be shared with you



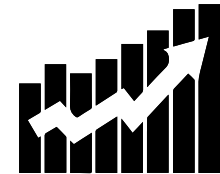
All presentations will be shared with you



Participation certificates will be provided upon request



Daily and post-event feedback survey



Be aware of IEDB slowness due to increased traffic



**#iedbuw2022**

**Follow us @iedb\_**

# Without further ado...



**Dr. Marcus Mendes**  
*Bioinformatics Postdoctoral  
Researcher*

## **IEDB-3D 2.0: Visualizing Structures in the IEDB**