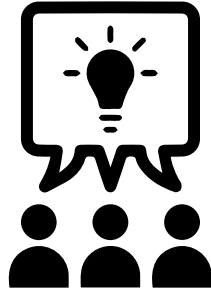


# Closing Remarks & Survey

## 2020 IEDB Virtual User Workshop – Day 1

*Thursday, November 5, 2020*

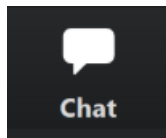
# We want to hear from you!



Improve our resources  
through user feedback



Daily and post-event  
feedback survey



<https://www.surveymonkey.com/r/YLZMS9B>



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

# Recap of Day 1

## Database Overview



Dr. Alessandro Sette  
Principal Investigator

The screenshot shows the IEDB homepage with various search filters and navigation options. Key sections include:

- Welcome:** Overview of the IEDB as a freely available resource for antibody and T cell epitopes.
- START YOUR SEARCH HERE:**
  - Epitope:** Any Epitopes, Linear Epitope, Discontinuous Epitopes, Non-peptidic Epitopes.
  - Assay:** Positive Assays Only, T Cell Assays, B Cell Assays, MHC Ligand Assays, MHC I Binding, MHC I Processing (Proteasome, TAP), MHC I Immunogenicity.
- Antigen:** Organism (e.g., influenza, peanut), Antigen Name (e.g., core, capsid, myosin).
- MHC Restriction:** Any MHC Restriction, MHC Class I, MHC Class II, MHC Nonclassical, Ex. HLA-A\*02:01.
- Host:** Any Host, Humans, Mice, Non-human Primates, Ex. dog, camel.
- Disease:** Any Disease, Infectious Disease, Allergic Disease, Autoimmune Disease, Ex. asthma, diabetes.

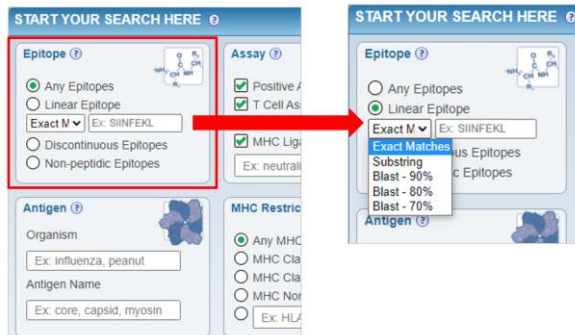
The screenshot displays a search results table with the following columns: ID, Author, Title, and Date. The table lists various research entries, such as:

- 163603:** Epitopes of the influenza A virus hemagglutinin...
- 163608:** Phenotypic and functional differences of CD4+ T cells...
- 163606:** Expression of programmed cell death protein 1 and its ligand...
- 1634271:** Differential escape of HCV from CD8+ T cell selection...
- 1636512:** Virus specific CD8+ T cell responses to hepatitis C virus infection...
- 1636499:** Isolation of a T helper 1 mechanism for controlling T cell response...
- 1636596:** The human hepatitis A antigen A2-12-restricted T cell epitope...

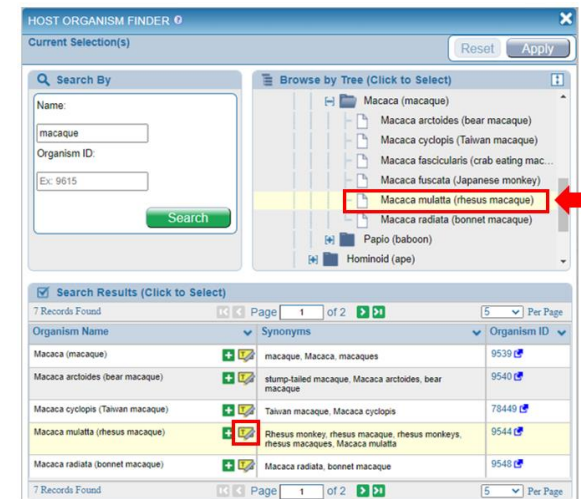
# Recap of Day 1

How Data are Retrieved,  
Entered, Organized, and  
Accessing the Data

## Epitope Search Pane

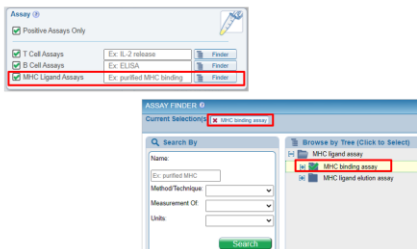



**Dr. Randi Vita**  
Lead Ontology & Quality  
Manager



Organism Name	Synonyms	Organism ID
Macaca (macaque)	macaque, Macaca, macaques	9539
Macaca arctoides (bear macaque)	stump-tailed macaque, Macaca arctoides, bear macaque	9540
Macaca cyclops (Taiwan macaque)	Taiwan macaque, Macaca cyclops	78440
Macaca mulatta (rhesus macaque)	rhesus monkey, rhesus macaque, rhesus monkeys, rhesus macaques, Macaca mulatta	9544
Macaca radiata (bonnet macaque)	Macaca radiata, bonnet macaque	9548

**User Query:** How can we search or analyze the allergen peptides binding to MHC class I or class II molecules?



**User Query:** Full analysis of Ebola virus



# Recap of Day 1

**A resource for SARS-CoV-2 mutation tracking and analysis:  
The LANL/GISAID COVID pipeline**



**Dr. Bette Korber**  
*Laboratory Fellow*



**Dr. Will Fischer**  
*Staff Scientist*

# Recap of Day 1

## Analysis Resource Overview

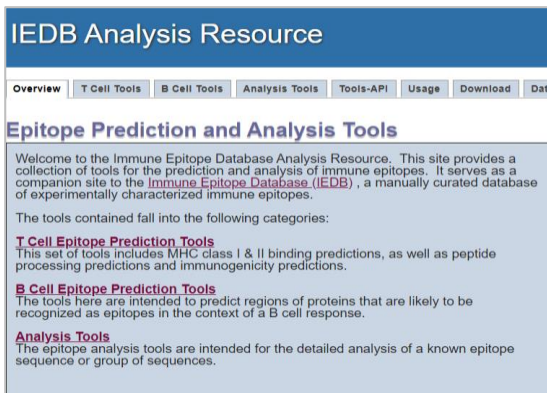


**Dr. Bjoern Peters**  
*Co-Principal Investigator*

## Analysis Tools



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



**IEDB Analysis Resource**

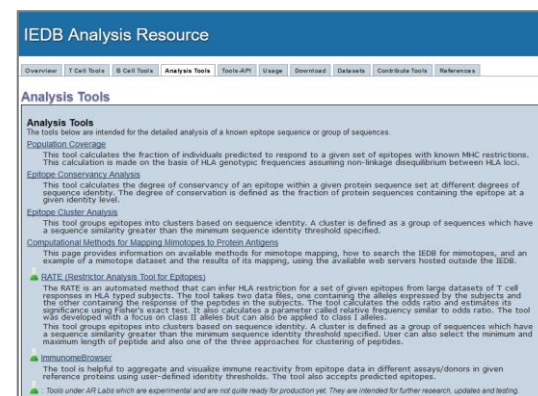
Overview | T Cell Tools | B Cell Tools | Analysis Tools | Tools-API | Usage | Download | Data

### 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.



**IEDB Analysis Resource**

Overview | T Cell Tools | B Cell Tools | Analysis Tools | Tools-API | Usage | Download | Database | Contribute Tools | References

### Analysis Tools

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

**Epitope Coverage**  
This tool calculates the fraction of individuals predicted to respond to a given set of epitopes with known MHC restrictions. The 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 conservancy 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 (Restriction 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.
- Immunogenicity**  
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.
- Immunogenicity**  
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.



# Recap of Day 1

## Using the IEDB-AR to Identify Candidates in SARS-CoV-2



**Dr. Alba Grifoni**  
*LJI Research Faculty/Instructor*



### DiscoTope: Structure-based Antibody Prediction

Step 1: Please enter the 4-letter PDB ID  (example: 1z40)  
Or upload a PDB file  No file chosen

Step 2: Please enter PDB Chain ID

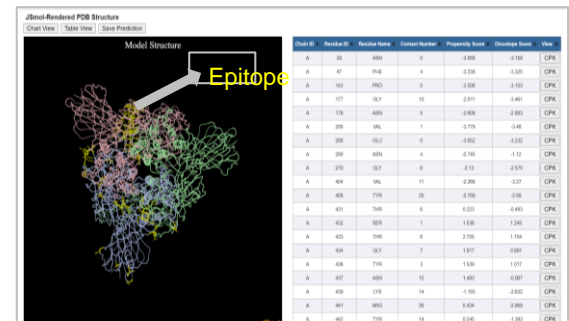
Step 3: Select version

Current Filters:  Positive Assays Only

Organism: Severe acute respiratory syndrome-related coronavirus (Human coronavirus (strain SARS)) (ID:684009\_SARS)

No B cell assays  No MHC ligand assays  MHC Restriction Type: Class II

Epitopes (90)	Antigens (3)	Assays (178)	Receptors (0)	References (14)	
90 Records Found					
Go To Records Starting At 1200					
Export Results					
Page 1 of 4					
25 Per Page					
Details	Epitope	Antigen	Organism	# References	# Assays
32340	KMKELSPRWY FYLLG	Nucleoprotein	Severe acute respiratory syndrome-related coronavirus (Human coronavirus (strain SARS))	2	2
46680	NYNYKYRYLR	Spike glycoprotein	Severe acute respiratory syndrome-related coronavirus (Human coronavirus (strain SARS))	2	3





# User Workshop Structure

## Day 1

START YOUR SEARCH HERE ?

### Epitope ?

- Any Epitopes
- Linear Epitope

Exact Iv  Ex: SIINFEKL

- Discontinuous Epitopes
- Non-peptidic Epitopes



### Assay ?

- Positive Assays Only
- T Cell Assays
- B Cell Assays
- MHC Ligand Assays

Ex: neutralization



### 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



### Host ?

- Any Host
- Humans
- Mice
- Non-human Primates
- Ex: dog, camel



### Disease ?

- Any Disease
- Infectious Disease
- Allergic Disease
- Autoimmune Disease
- Ex: asthma, diabet



Process Overview and Database

## Day 2

## IEDB Analysis Resource

[Overview](#)

[T Cell Tools](#)

[B Cell Tools](#)

[Analysis Tools](#)

[Tools-API](#)

[Usage](#)

[Download](#)

[Data](#)

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### 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
08:00	08:05	Welcome	Nina Blazeska <i>IEDB Project Manager</i>
08:05	09:05	MHC Binding Predictions	Bjoern Peters <i>IEDB Co-Principal Investigator</i>
09:05	09:20	<u>Section 1</u> : Q&A	
09:20	09:30	<b>Break</b>	
09:30	10:00	T Cell Processing & Immunogenicity Predictions	Bjoern Peters <i>IEDB Co-Principal Investigator</i> Austin Crinklaw <i>Tools Research Technician</i>
10:00	10:15	T Cell Tool Spotlight: TCRMatch	Will Chronister <i>Bioinformatics Postdoctoral Researcher</i>
10:15	10:45	Structure Tools: LYRA & SCEptRe	Paolo Marcatili <i>DTU Associate Professor</i>
10:45	11:00	<u>Section 2</u> : Q&A	
11:00	11:30	<b>Break</b>	

# Preview of Day 2

Start Time	End Time	Topic	Speaker
11:00	11:30	Break	
11:30	12:00	NIH Resources for Researchers: HIV Sequence & Immunology Databases	Brian Foley & Elizabeth-Sharon Fung Los Alamos National Laboratory
12:00	12:10	<u>Section 3</u> : Q&A	
12:10	12:55	B Cell Epitope Prediction	Bjoern Peters IEDB Co-Principal Investigator
12:55	13:10	IEDB Tools 3.0: Future of Tools	Jason Greenbaum Bioinformatics Core Director
13:10	13:20	<u>Section 4</u> : Q&A	
13:20	13:30	Closing Remarks & Feedback Survey	Nina Blazeska IEDB Project Manager
13:30	14:00	<u>Optional Q&amp;A Session</u> 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**