IEDB

Immune Epitope Database & Tools

Closing Remarks & Survey

2023 IEDB Virtual User Workshop Day 2

Thursday, November 2, 2023

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/7BTDN8W

SurveyMonkey

Please take some time to complete the survey now

#iedbuw2023

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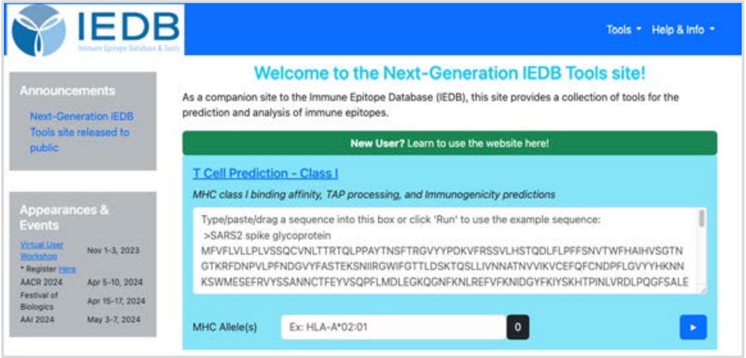
Recap of Day 2

IEDB Next-Generation Tools Introduction

Dr. Jason Greenbaum
Bioinformatics Core Director



Welcome to the Next-Generation IEDB Tools site!

As a companion site to the Immune Epitope Database (IEDB), this site provides a collection of tools for the prediction and analysis of immune epitopes.

New User? Learn to use the website here!

T Cell Prediction - Class I

MHC class I binding affinity, TAP processing, and Immunogenicity predictions

```
Type/paste/drag a sequence into this box or click 'Run' to use the example sequence:
 >SARS2 spike glycoprotein
MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTN
GTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLLIVNNATNVVIKVCEFQFCNDPFLGVYYHKNN
KSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALE
```

MHC Allele(s): Ex: HLA-A*02:01 — 0

Announcements

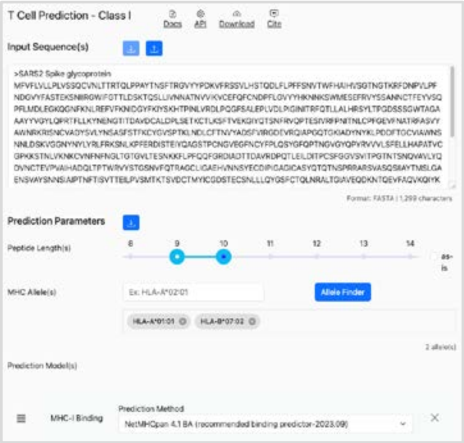
Next-Generation IEDB Tools site released to public

Appearances & Events

Virtual User Workshop * Register Here	Nov 1-3, 2023
AACR 2024	Apr 5-10, 2024
Festival of Biologics	Apr 15-17, 2024
AAI 2024	May 3-7, 2024

T Cell Class I Tools (Binding, Processing, Immunogenicity)

Dr. Jason Greenbaum
Bioinformatics Core Director



>SARS2 Spike glycoprotein

Format: FASTA | 1,299 characters

Peptide Length(s): 9, 10

MHC Allele(s): Ex: HLA-A*02:01

HLA-A*01:01, HLA-B*07:02

2 allele(s)

Prediction Model(s)

MHC-I Binding — Prediction Method: NetMHCpan 4.1 BA (recommended binding predictor-2023.09)

Recap of Day 2

Next-Generation Tool Pipelines - Cluster & PEPMatch

Dr. Bjoern Peters

Co-Principal Investigator

Interactive Cluster Visualization

Visualize a selected sub-cluster: All

3

PEPMatch

Prediction Parameters

Maximum number of mismatches: 0 1 2 3 4 5 (3 selected)

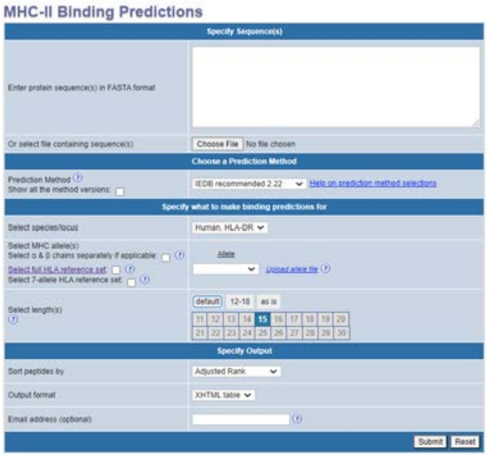
Proteome: Human

Include all matches or best match per peptide:
● Best match per peptide
○ All matches

T Cell Class II Tools (Binding, Processing, Immunogenicity)

Dr. Bjoern Peters

Co-Principal Investigator



MHC-II Binding Predictions

Specify Sequence(s)

Enter protein sequence(s) in FASTA format

Or select file containing sequence(s): Choose File No file chosen

Choose a Prediction Method

Prediction Method: IEDB recommended 2.22

Show all the method versions: ☐

Specify what to make binding predictions for

Select species/locus: Human, HLA-DR

Select MHC allele(s)

Select α & β chains separately if applicable: ☐

Select full HLA reference set: ☐

Select 7-allele HLA reference set: ☐

Allele

Upload allele file

Select length(s): default 12-18 as is

11	12	13	14	**15**	16	17	18	19	20
21	22	23	24	25	26	27	28	29	30

Specify Output

Sort peptides by: Adjusted Rank

Output format: XHTML table

Email address (optional):

Recap of Day 2

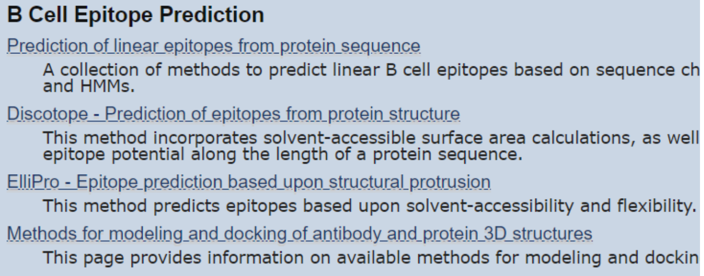
B Cell Epitope Prediction

Receptor Tools - TCRMatch

Dr. Eve Richardson
Bioinformatics Postdoctoral Researcher

Dr. Raphael Trevizani
Bioinformatics Postdoctoral Researcher

Dr. Mahita Jarjapu
Bioinformatics Postdoctoral Researcher



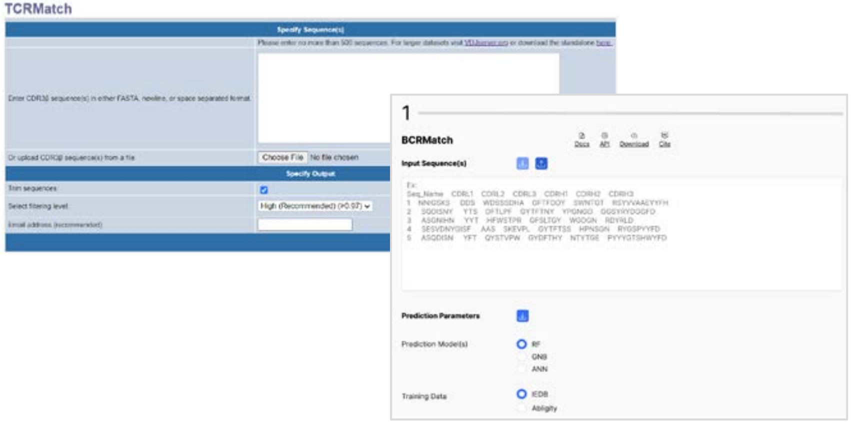
B Cell Epitope Prediction

Prediction of linear epitopes from protein sequence
A collection of methods to predict linear B cell epitopes based on sequence ch and HMMs.

Discotope - Prediction of epitopes from protein structure
This method incorporates solvent-accessible surface area calculations, as well epitope potential along the length of a protein sequence.

ElliPro - Epitope prediction based upon structural protrusion
This method predicts epitopes based upon solvent-accessibility and flexibility.

Methods for modeling and docking of antibody and protein 3D structures
This page provides information on available methods for modeling and dockin



TCRMatch

Specify Sequence(s)

Please enter no more than 500 sequences. For larger datasets visit VDJserver.org or download the standalone here.

Enter CDR3β sequence(s) in either FASTA, newline, or space separated format.

Or upload CDR3β sequence(s) from a file: Choose File No file chosen

Specify Output

Trim sequences: ☑

Select filtering level: High (Recommended) (>0.97)

Email address (recommended):

1

BCRMatch

Input Sequence(s)

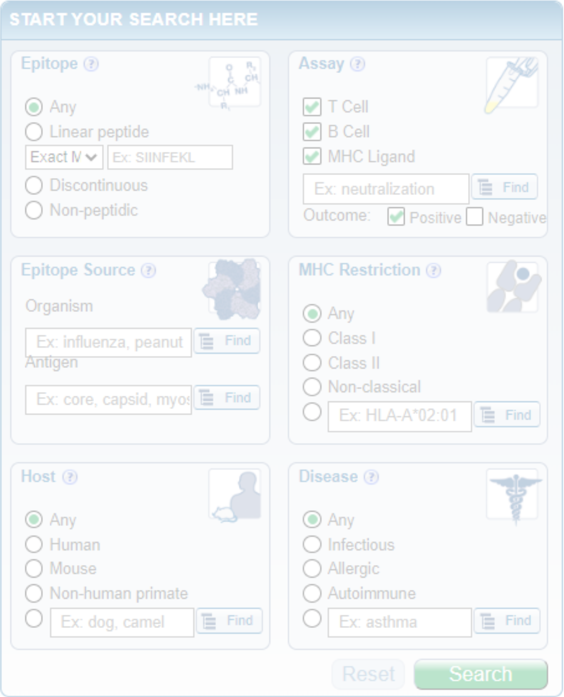
Prediction Parameters

Prediction Model(s): ● RF ○ GNB ○ ANN

Training Data: ● IEDB ○ Abligity

User Workshop Structure

Day 1



START YOUR SEARCH HERE

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

Assay
- ☑ T Cell
- ☑ B Cell
- ☑ MHC Ligand
- Ex: neutralization | Find
- Outcome: ☑ Positive ☐ Negative

Epitope Source
- Organism: Ex: influenza, peanut | Find
- Antigen: Ex: core, capsid, myos | Find

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

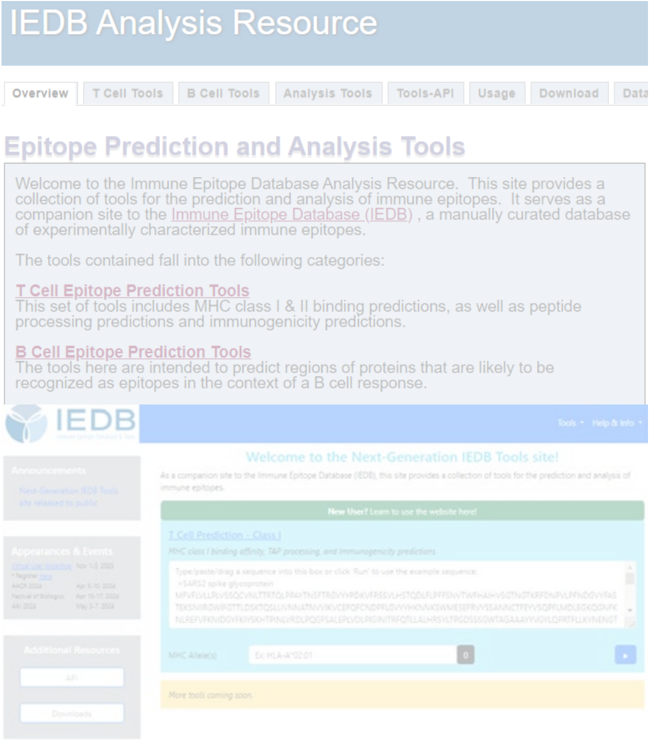
Host
- ● Any
- ○ Human
- ○ Mouse
- ○ Non-human primate
- ○ Ex: dog, camel | Find

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

Reset | Search

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.

IEDB

Welcome to the Next-Generation IEDB Tools site!

New User? Learn to use the website here!

T Cell Prediction - Class I

MHC class I binding affinity, TAP processing, and immunogenicity predictions

More tools coming soon.

Next-Generation Tools & Analysis Resource

Day 3

CEDAR
Cancer Epitope Database and Analysis Resource

Los Alamos
NATIONAL LABORATORY

Specialized Topics – 3D Structures, Cancer, HIV

Preview of Day 3

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

Preview of Day 3

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

Additional Questions?

Email us at help@iedb.org

Thank you!

See you tomorrow for Day 3

We appreciate your time and interest in the IEDB!