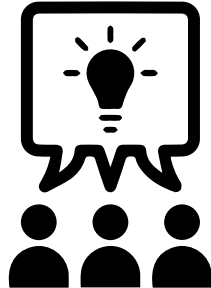


Closing Remarks & Survey

2022 IEDB Virtual User Workshop – Day 2

Thursday, October 27, 2022

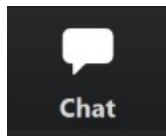
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through user feedback



Daily and post-event
feedback survey



<https://www.surveymonkey.com/r/BKKXK68>



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



#iedbuw2022

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Recap of Day 2

T Cell Processing & Immunogenicity Predictions



Dr. Bjoern Peters
Co-Principal Investigator

T Cell Epitopes - Processing Prediction

These tools predict epitope candidates based upon the processing of peptides in the cell.

[Proteasomal cleavage/TAP transport/MHC class I combined predictor](#)

This tool combines predictors of proteasomal processing, TAP transport, and MHC binding to produce an overall score for each peptide's intrinsic potential of being a T cell epitope.

[Neural network based prediction of proteasomal cleavage sites \(NetChop\) and T cell epitopes \(NetCTL and NetCTLpan\)](#)

NetChop is a predictor of proteasomal processing based upon a neural network. NetCTL and NetCTLpan are predictors of T cell epitopes along a protein sequence. It also employs a neural network architecture.

[MHC-NP: Prediction of peptides naturally processed by the MHC](#)

MHC-NP employs data obtained from MHC elution experiments in order to assess the probability that a given peptide is naturally processed and binds to a given MHC molecule. This tool was the winner of the [2nd Machine Learning Competition in Immunology](#).



[MHCII-NP:](#)

This tool utilizes MHC II ligand elution data to predict naturally processed MHC II ligands by scanning the given peptide sequences.

Recap of Day 2

PEPMatch



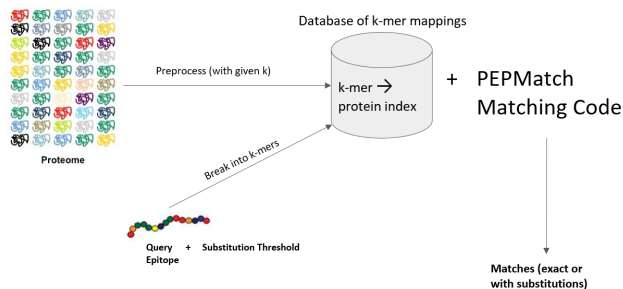
Daniel Marrama
Bioinformatics Research Technician

TCRMatch

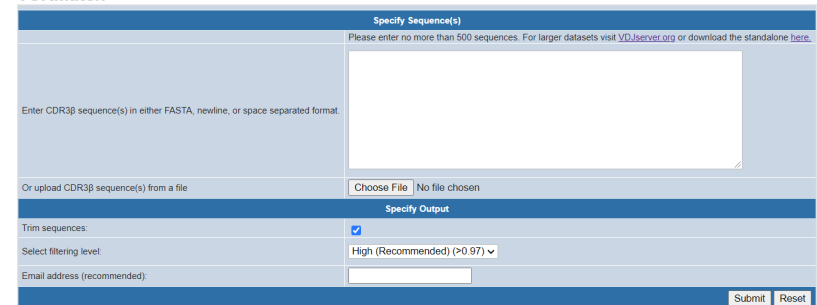


Dr. Raphael Trevizani
Bioinformatics Postdoctoral Researcher

PEPMatch Tool Overview



TCRMatch



The screenshot shows the TCRMatch web interface. It features a 'Specify Sequence(s)' section with a text input field for CDR3 sequences and a 'Choose File' button. Below this is a 'Specify Output' section with checkboxes for 'Trim sequences' and a dropdown for 'Select filtering level' (set to 'High (Recommended) (>0.97)'). An 'Email address (recommended)' field is also present. 'Submit' and 'Reset' buttons are at the bottom right.

Recap of Day 2

B Cell Epitope Prediction



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 and HMMs.

[Discotope - Prediction of epitopes from protein structure](#)

This method incorporates solvent-accessible surface area calculations, as well as 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.

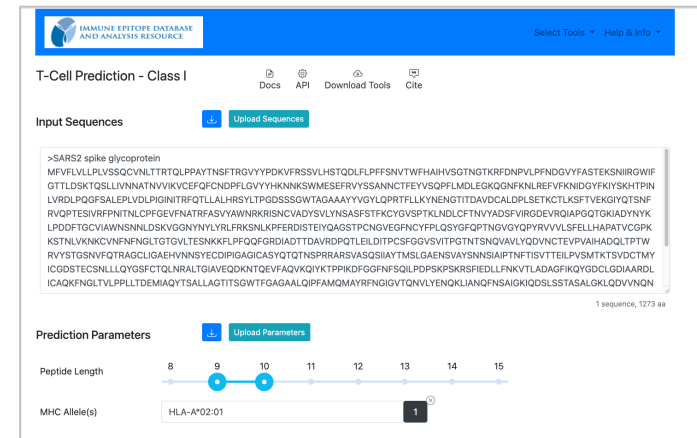
[Methods for modeling and docking of antibody and protein 3D structures](#)

This page provides information on available methods for modeling and docking.

IEDB Tools 3.0: Future of Tools



Dr. Jason Greenbaum
Bioinformatics Core Director




The screenshot shows the IEDB T-Cell Prediction - Class I interface. At the top, there is a navigation bar with the IEDB logo and links for 'Select Tools', 'Help & Info', 'Docs', 'API', 'Download Tools', and 'Cite'. Below the navigation bar, the page title is 'T-Cell Prediction - Class I'. There are two main input sections: 'Input Sequences' and 'Prediction Parameters'. The 'Input Sequences' section has an 'Upload Sequences' button and a text area containing a long protein sequence: '>SARS2 spike glycoprotein MFVFLVLLPLVSSQC...'. The 'Prediction Parameters' section has an 'Upload Parameters' button and a slider for 'Peptide Length' ranging from 8 to 15, with the value set to 10. Below the slider, there is a dropdown menu for 'MHC Allele(s)' with 'HLA-A*02:01' selected.


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, 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

Preview of 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	

Preview of Day 3

Start Time	End Time	Topic	Speaker
10:45	11:15	The Cancer Epitope Database and Analysis Resource (CEDAR)	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. Koşaloğlu-Yalçın & Sette	
11:50	12:00	Closing Remarks & Feedback Survey	Nina Blazeska <i>IEDB Project Manager</i>
	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!