IMMUNE EPITOPE DATABASE AND ANALYSIS RESOURCE

IEDB-3D 2.0

A new way to visualize 3D structures in the IEDB

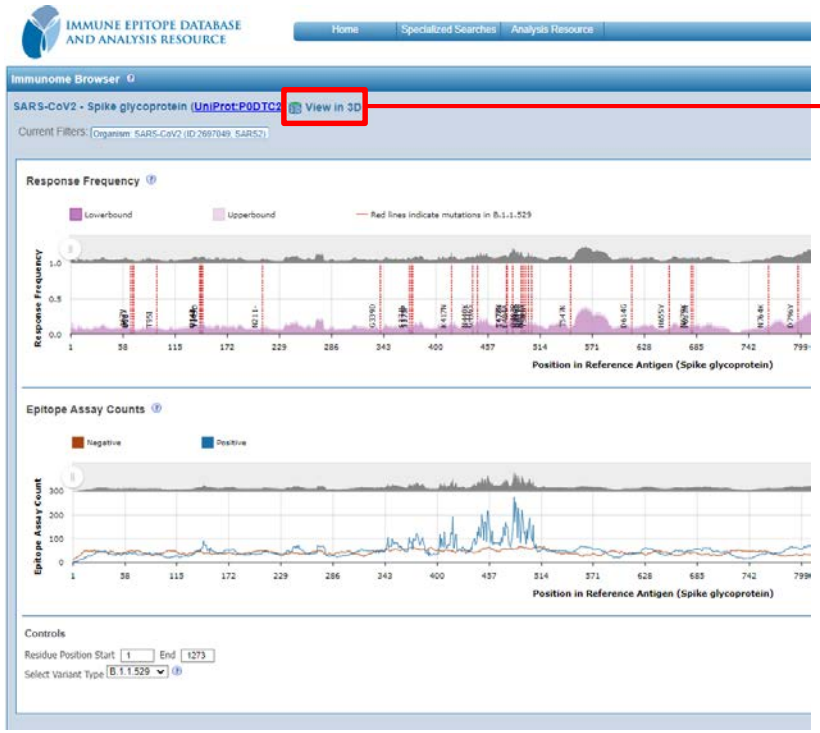
Presented by: Marcus Mendes, PhD, Bioinformatics Postdoc

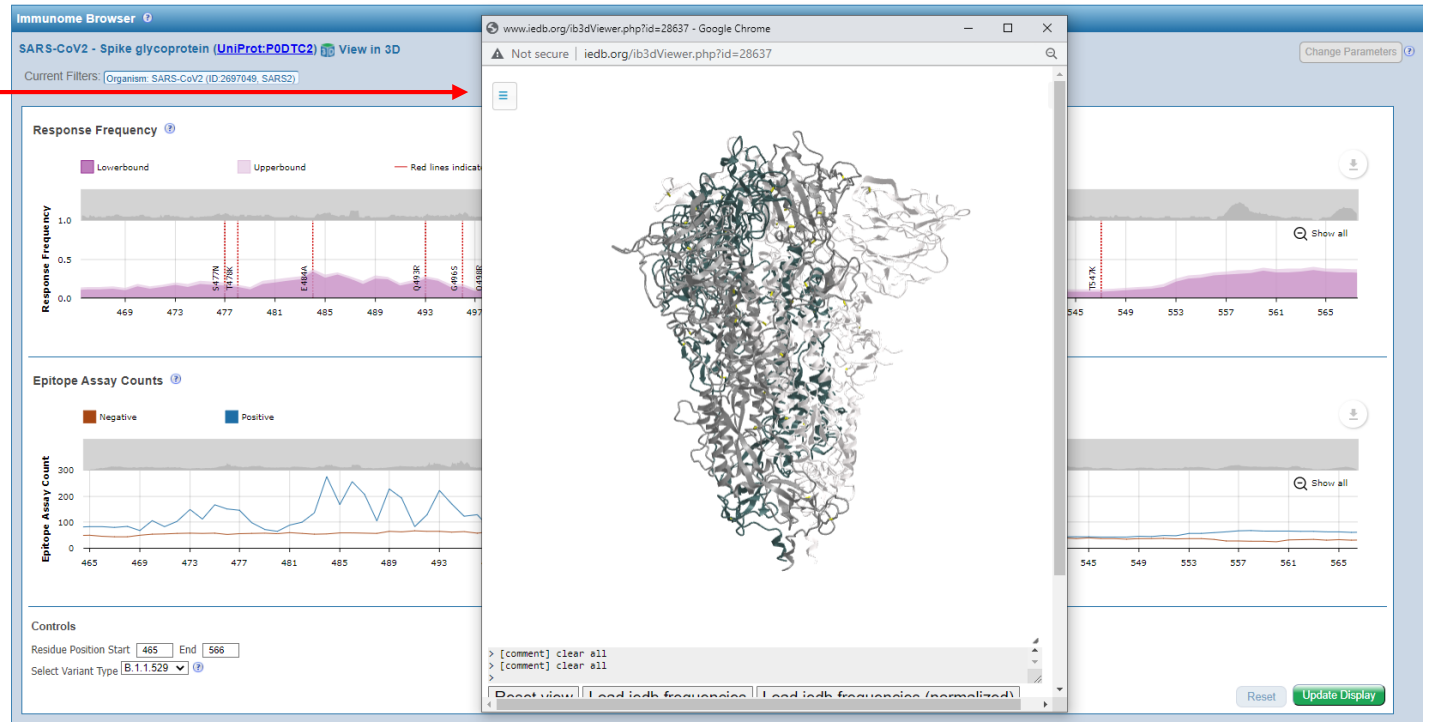
IEDB-3D 2.0 Viewer Project

Background

NIH requested the IEDB to capture SARS-CoV-2 mutations:

- Displays each amino acid mutation on the Immunome Browser for the spike glycoprotein antigen
- Utilized iCn3D to display the spike glycoprotein (and the mutations) in the Immunome Browser

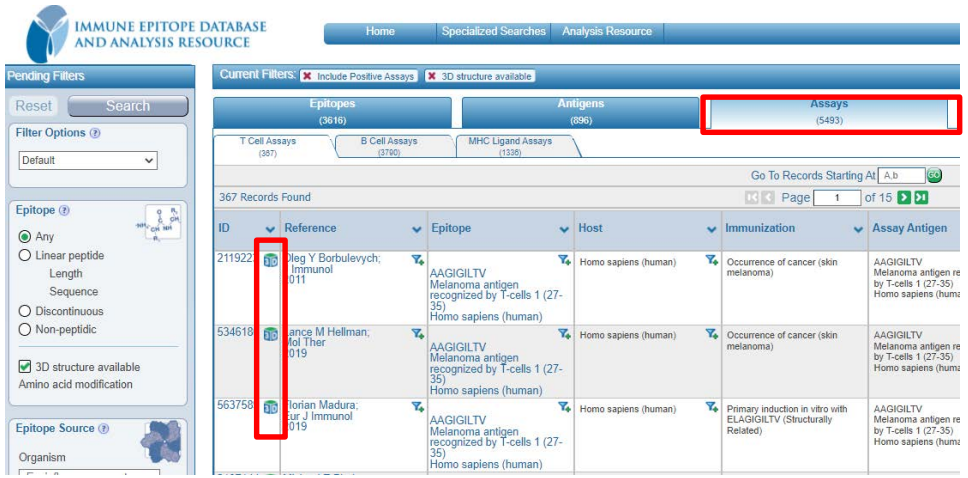




IEDB-3D 2.0 Viewer Project

(1) Assays Tab

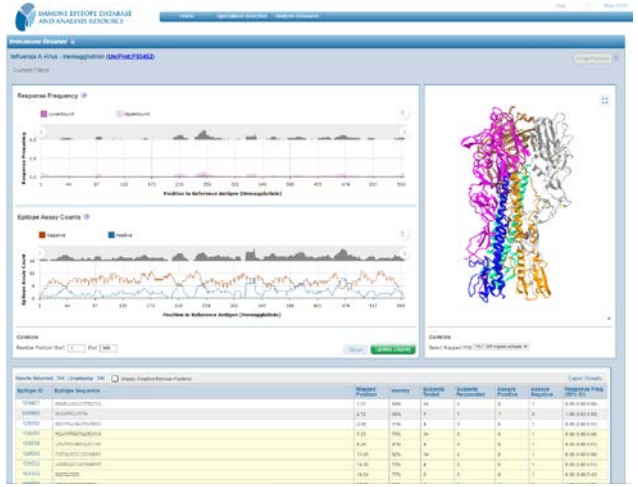
Displays experimentally determined 3D structures from PDB, directly showing epitope recognition. Depending on the assay, it can show an epitope bound to MHC, MHC & TCR or an antibody with pre-calculated contacts



Overview of 3 Viewers

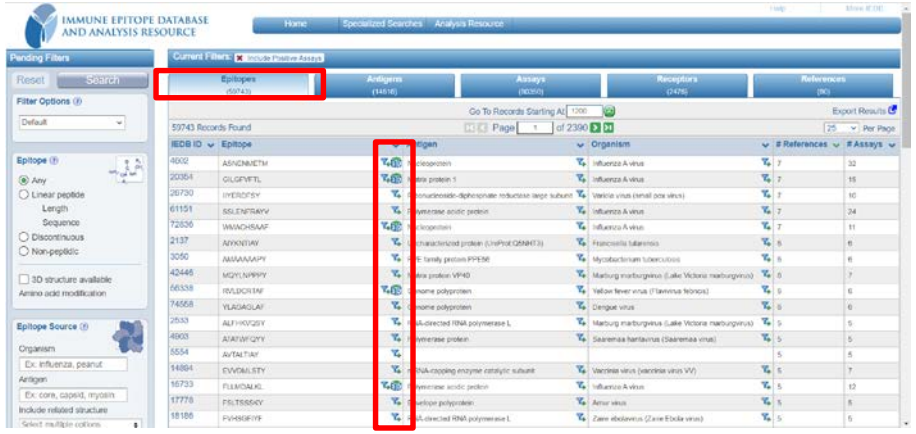
(3) ImmunomeBrowser

Maps set of epitopes to an antigen, highlighting immunogenic regions.



(2) Epitopes Tab

Displays individual epitope in its source antigen, either from PDB or AlphaFold



IEDB-3D 2.0 Viewer Project

- **Assay Viewer** - Displays experimentally determined 3D structures from PDB, directly showing epitope recognition.

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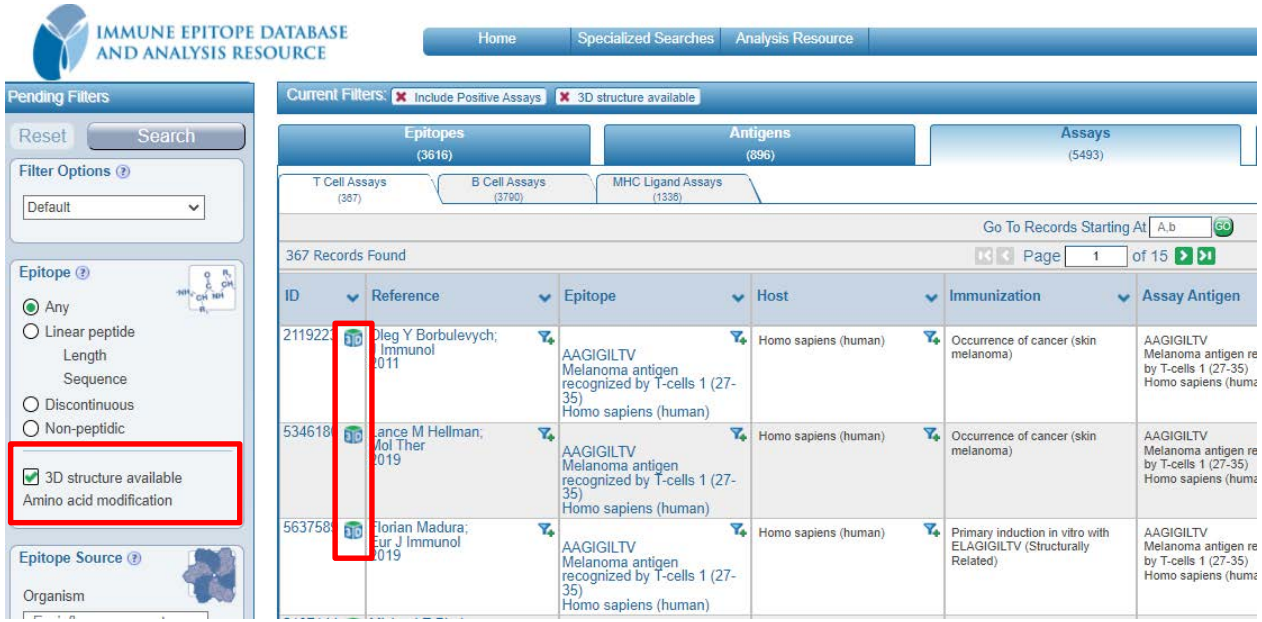

The IEDB has just launched its updated 3D viewers! Learn more via our help article here.

Welcome

The Immune Epitope Database (IEDB) is a freely available resource funded by NIAID. It catalogs experimental data on antibody and T cell epitopes studied in humans, non-human primates, and other animal species in the context of infectious disease, allergy, autoimmunity and transplantation. The IEDB also hosts tools to assist in the prediction and analysis of epitopes.

Learn More

Upcoming Events & News

AAI Exhibitor Booth	May 6-10
FOCiS Exhibitor Booth	June 21-24
Virtual User Workshop	Oct 26-28

* register here

IEDB SARS-CoV-2 Epitope Analysis Videos

Summary Metrics

Peptidic Epitopes	1,539,170
Non-Peptidic Epitopes	3,146
T Cell Assays	443,509
B Cell Assays	1,332,364
MHC Ligand Assays	4,631,827
Epitope Source Organisms	4,234
Restricting MHC Alleles	970
References	23,297

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
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- Autoimmune
- Ex: asthma — Find

Reset | Search

Epitope Analysis Resource

T Cell Epitope Prediction

Scan an antigen sequence for amino acid patterns indicative of:

- MHC I Binding
- MHC II Binding
- MHC I Processing (Proteasome,TAP)
- MHC I Immunogenicity

B Cell Epitope Prediction

Predict linear B cell epitopes using:

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Predict discontinuous B cell epitopes using antigen structure via:

- Discotope
- ElliPro

Epitope Analysis Tools

Analyze epitope sets of:

- Population Coverage
- Conservation Across Antigens
- Clusters with Similar Sequences

Supported by a contract from the National Institute of Allergy and Infectious Diseases, a component of the National Institutes of Health in the Department of Health and Human Services.

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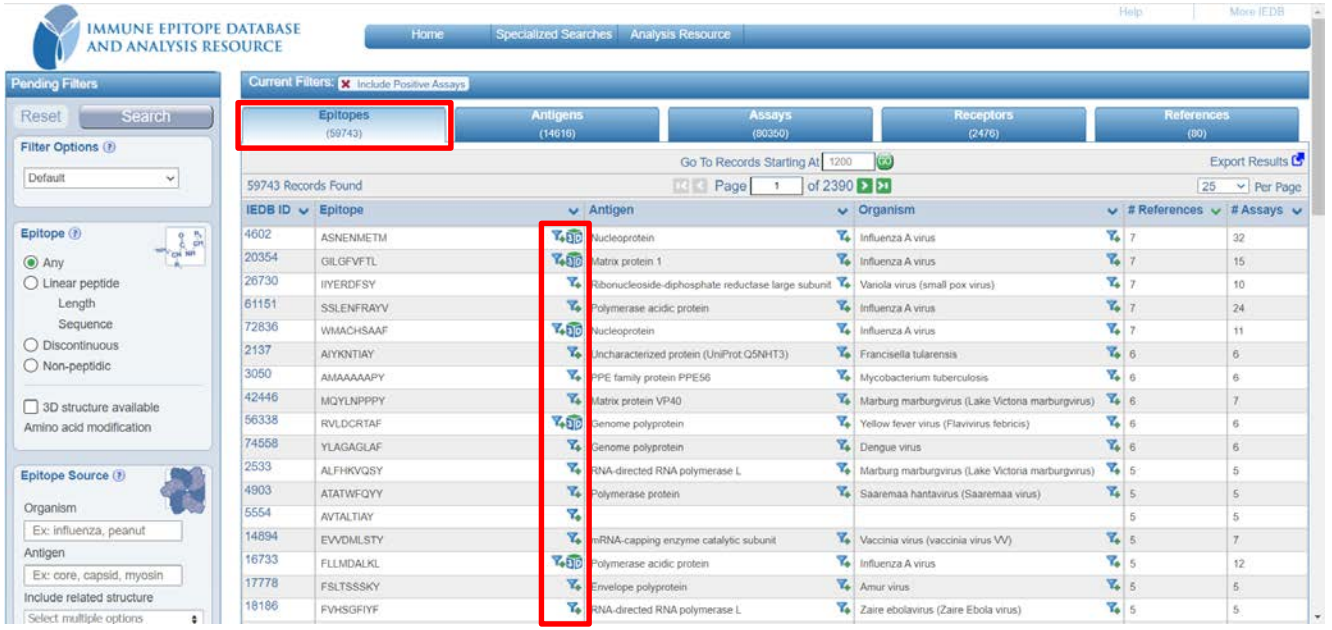

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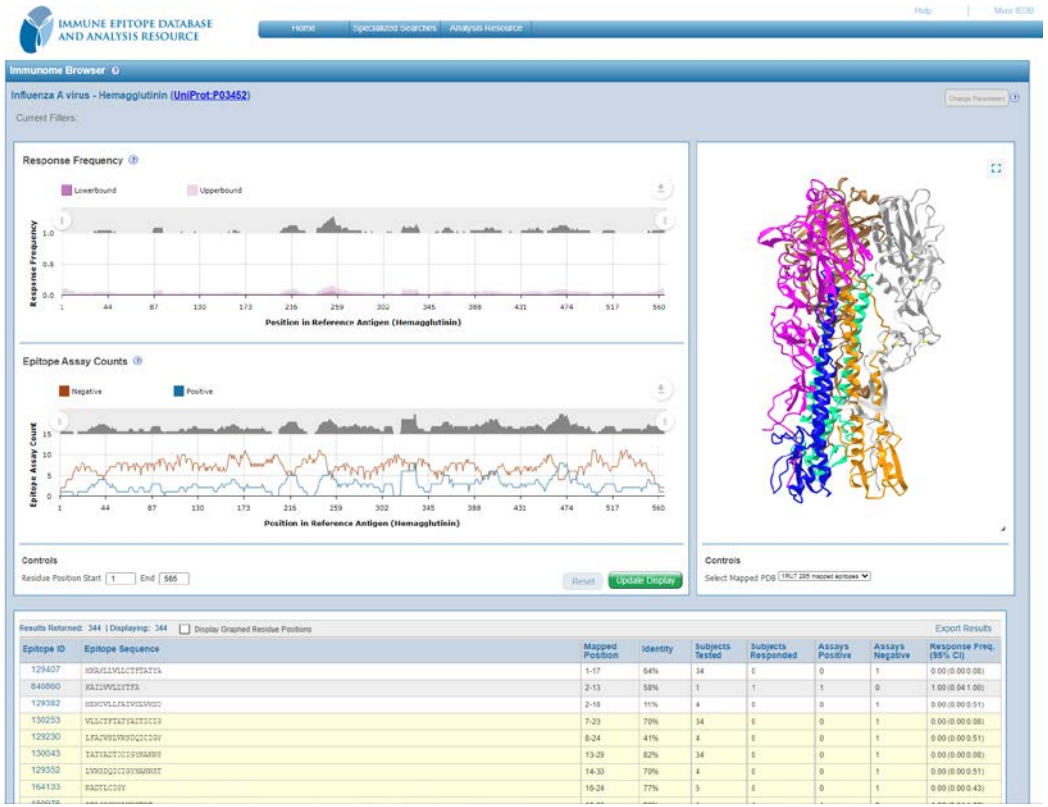
(3) Immunome Browser



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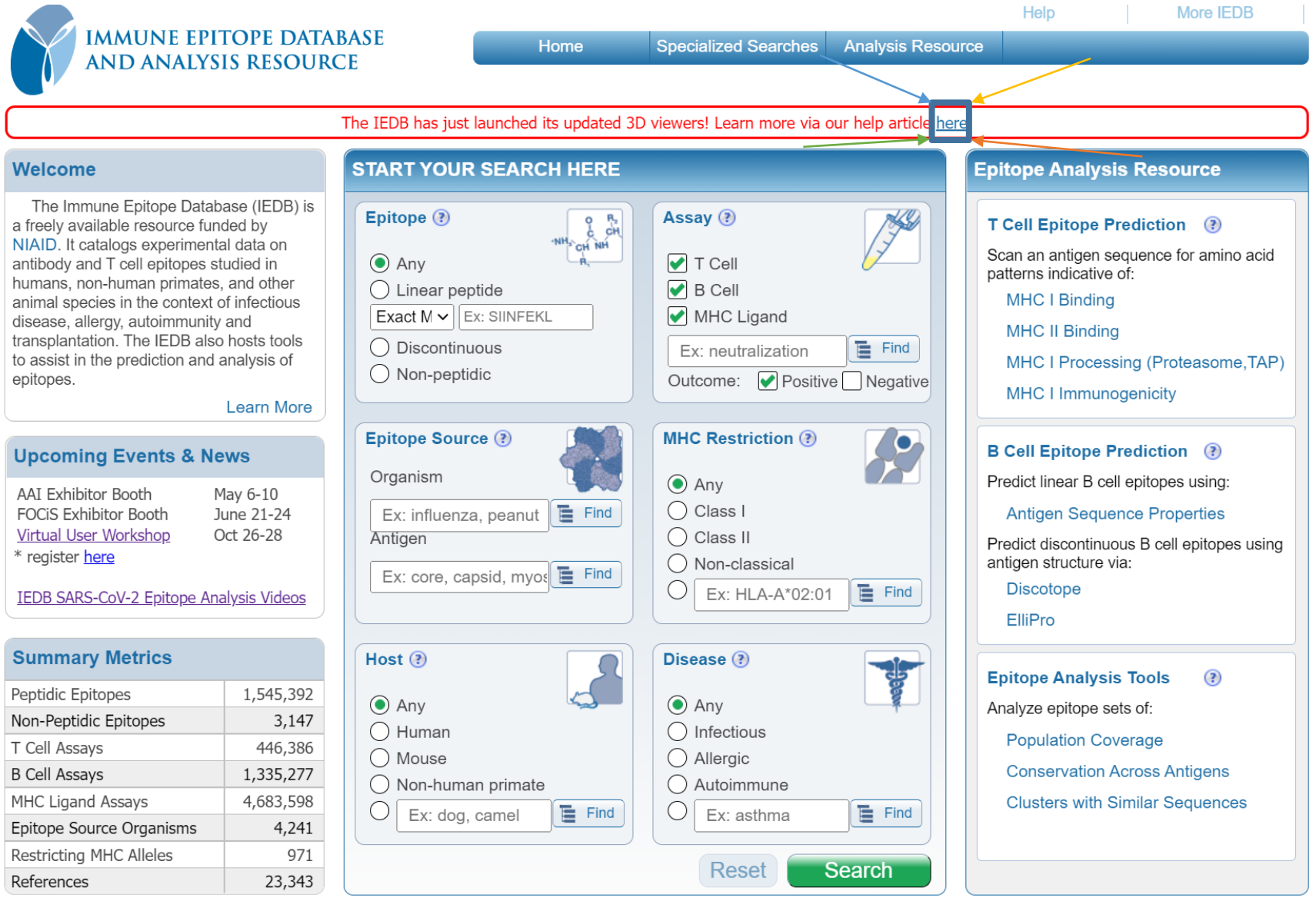

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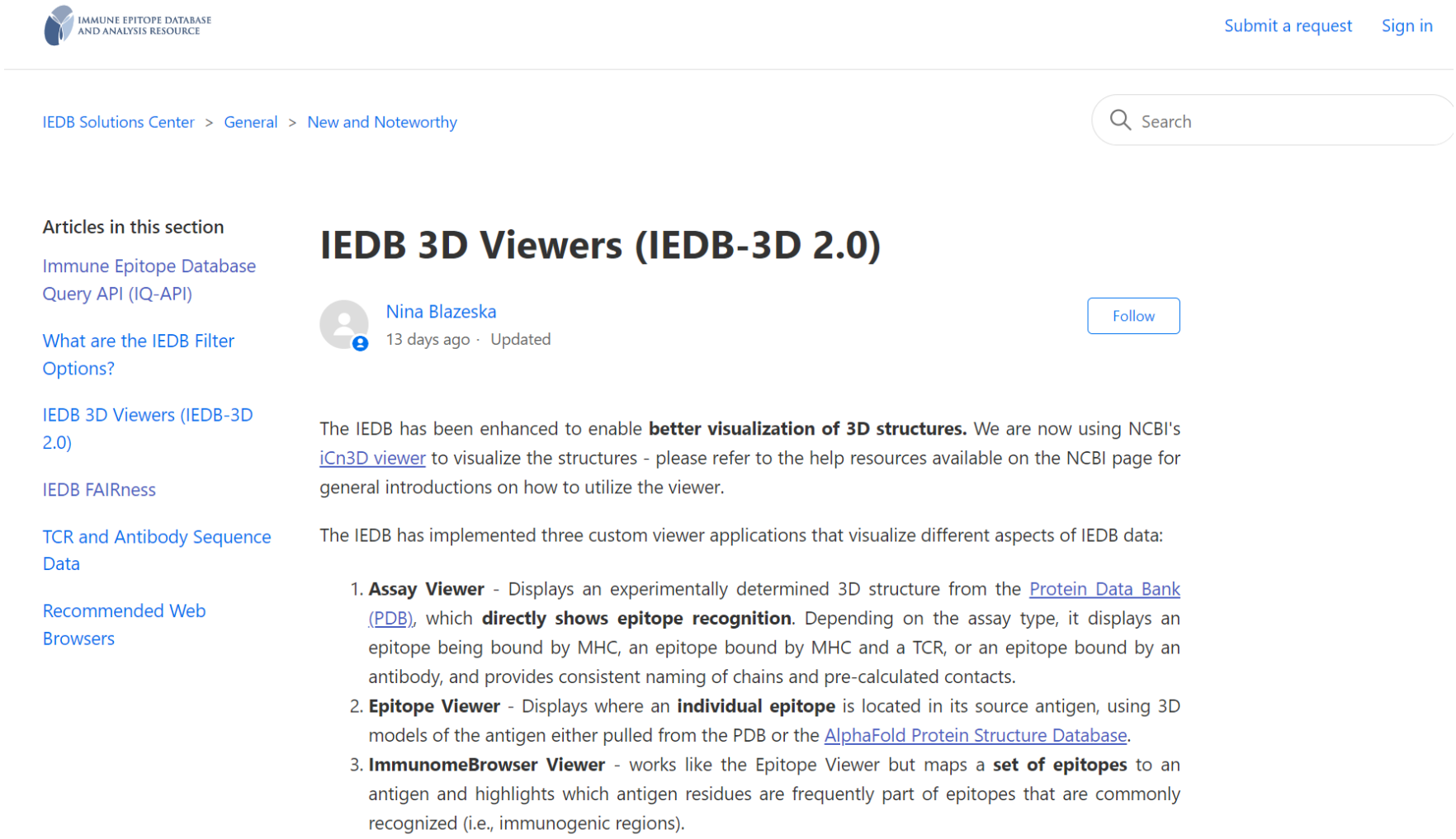

IMMUNE EPITOPE DATABASE AND ANALYSIS RESOURCE

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- IEDB 3D Viewers (IEDB-3D 2.0)
- IEDB FAIRness
- TCR and Antibody Sequence Data
- Recommended Web Browsers

IEDB 3D Viewers (IEDB-3D 2.0)

Nina Blazeska
13 days ago · Updated

Follow

The IEDB has been enhanced to enable **better visualization of 3D structures.** We are now using NCBI's iCn3D viewer to visualize the structures - please refer to the help resources available on the NCBI page for general introductions on how to utilize the viewer.

The IEDB has implemented three custom viewer applications that visualize different aspects of IEDB data:

1. **Assay Viewer** - Displays an experimentally determined 3D structure from the Protein Data Bank (PDB), which **directly shows epitope recognition**. Depending on the assay type, it displays an epitope being bound by MHC, an epitope bound by MHC and a TCR, or an epitope bound by an antibody, and provides consistent naming of chains and pre-calculated contacts.
2. **Epitope Viewer** - Displays where an **individual epitope** is located in its source antigen, using 3D models of the antigen either pulled from the PDB or the AlphaFold Protein Structure Database.
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https://help.iedb.org/hc/en-us/articles/6339160938523

Thanks!