

How Data are Retrieved, Entered, and Organized

www.iedb.org

Presented by: Randi Vita, M.D. Lead Ontology and Quality Manager

IEDB Scope

- Infectious Diseases, Allergy, Autoimmunity, Transplant
 - HIV, cancer, etc. only curated as structural data or when presented with above subjects as per NIH/NIAID
- Published literature and direct submissions
- Experimentally confirmed, no predictions, no reviews
- Negative data and supplemental data included
- Binding of an adaptive immune receptor to an epitope (T cell, B cell, MHC binding, MHC ligand elution)
- Must be epitope-specific
 - All tested antigens are curated for epitope-specific receptors

Minimal Criteria for Epitope Inclusion

- Linear peptide <50 amino acids in length
- Tested as an immunogen or an antigen
- Discontinuous residues shown to be important in recognition
- Non-peptidic epitopes <5,000 Daltons
- Minimal information required (sequence, outcome, host, etc.)

Literature Curation Process

PubMed / PDB

- Complex query
- Bi-weekly

240K retrieved

2020 IEDB User Workshop

Classifier

- Content based categories
- Retrained annually

151K epitope related

Infectious Disease 48,376 refs

Autoimmunity 19,299 refs

Transplantation

13,988 refs

Allergy 9,220 refs

Other 60,508

Abstract Review

- Manual scan
- Confirmation of classification

44K likely curatable

Manual Curation

- Assigned to curators
- Peer review

21K curated

Infectious Disease

11,263 refs

Autoimmunity

5,144 refs

Allergy

1,646 refs

Transplantation

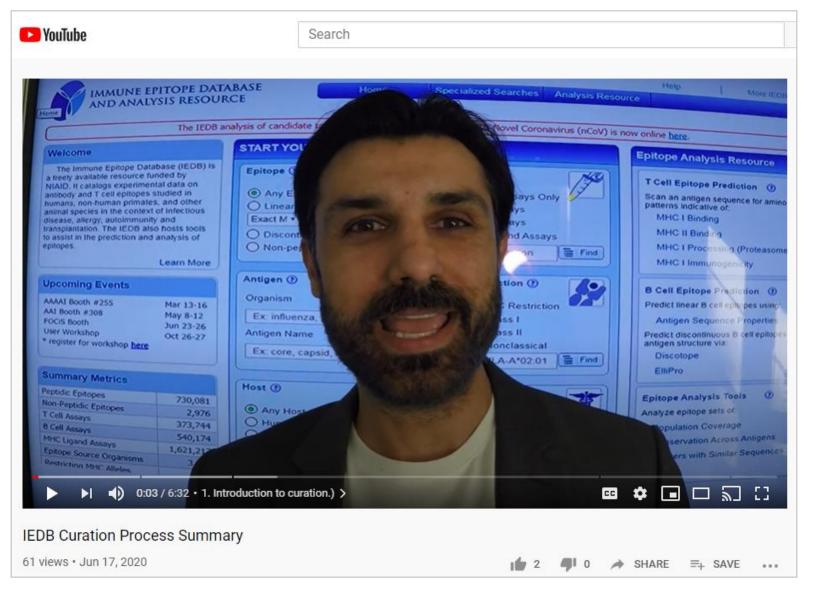
846 refs

Other

2,331 refs

2,331 Tels

Literature Curation Process: Video



Consistency and Quality Control Measures

- Manually curated by a team of PhD-level scientists with specific expertise
- Formal curation guidelines and peer review
 <u>Curation Manual</u>: http://curationwiki.iedb.org/wiki/index.php/Main_Page
- External immunological experts
- Built in validation in the curation application

Data Submissions

- Primarily sourced through NIAID Epitope Discovery contracts
- Data deposition is open to the general research community on a case-by-case basis

As of October, 2020:

- Data from 306 submissions is publicly available & 96 submissions are in process or on-hold
- Submitted data comprises 28% of epitopes

Inquire by contacting: nblazeska@lji.org or support@iedb.org!

Direct Submission Process

Submission

 Investigators submit files via IEDB data submission tool



Review

 Automated validation and manual curator review check data consistency

Submitter confirms final approval

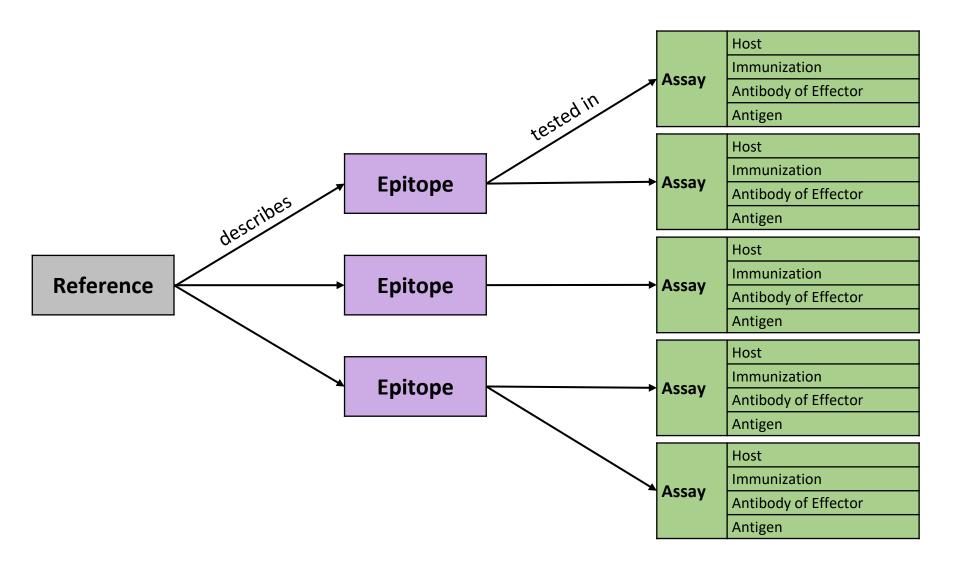


Release

Public release date set by submitter



Data Structure: A Database of Experiments



Collaborations with Ontologies

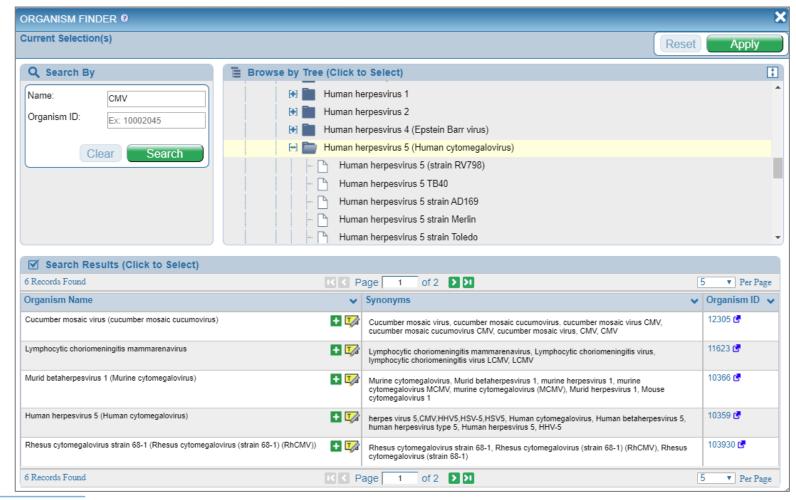
- Provides standardized nomenclature, definitions, synonyms, and hierarchical relationships
- Makes curation easier → Finders
- Enhances user experience → Finders
- Ensures consistency and accuracy
- Finds errors
- Facilitates interoperability

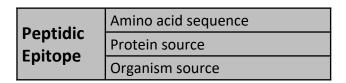
Peptidic Epitope Amino acid sequence Protein source Organism source



Human herpesvirus 5 (HHV-5)

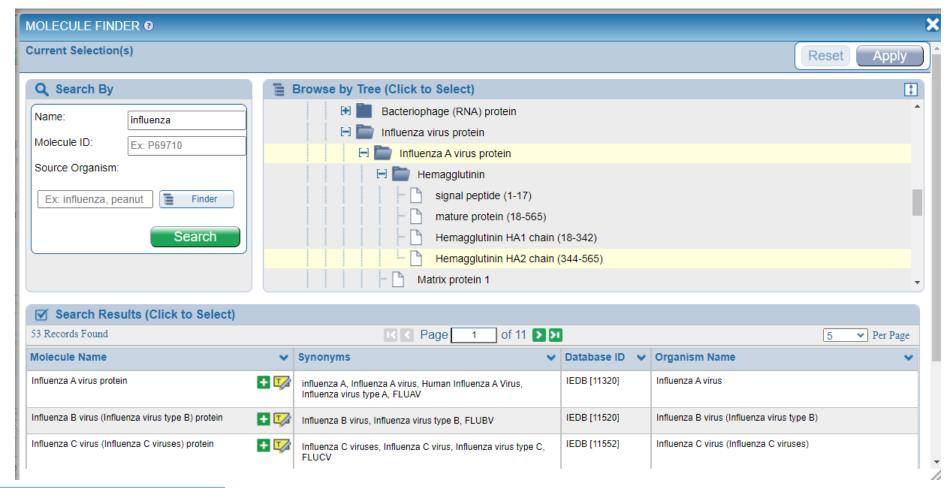
taxon:10359







PKYVKQNTLKLAT hemagglutinin HA1 GenBank/UniProt GI:AAL62329.1—UniProt:Q8V285



Non-peptidic Epitope Structure name Source structure Organism source



 α -L-Fucp- $(1\rightarrow 3)$ -[β -D-Galp- $(1\rightarrow 4)$]- β -D-GlcpNAc

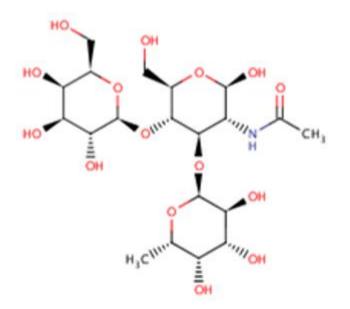
CHEBI:59294

Lipopolysaccharide

CHEBI:16412



NCBI taxon:210 Helicobacter pylori



ChEBI Name	α-L-Fucp-(1→3)-[β-D-Galp-(1→4)]-β-D-GlcpNAc
ChEBI ID	CHEBI:59294
ChEBI ASCII Name	alpha-L-Fucp-(1->3)-[beta-D-Galp-(1->4)]-beta-D-GlcpNAc
Definition	An α-L-Fucp-(1→3)-[β-D-Galp-(1→4)]-D-GlcpNAc where the glucosamine at the reducing end has β-configuration at its anomeric centre. Commonly known as Lewis x trisaccharide or Le ^x .
Stars	** This entity has been manually annotated by the ChEBI Team.

Immunization | Host | Immunogen | Administration | Disease |



Homo sapiens (human)

NCBI

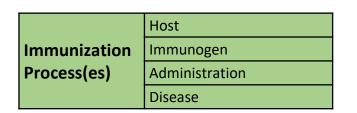
taxon:9606



Peanut allergy DO DOID:4378



Metadata		⁰ / ₀₁₀ Visualize
DOID	DOID:4378	
Name	peanut allergic reaction	
Definition	A food allergy that is an allergy or hypersensifrom peanuts causing an overreaction of the small percentage of people may lead to seven http://en.wikipedia.org/wiki/Allergy#Foods	immune system which in a
Synonyms	Allergy to peanuts (disorder) [EXACT] Peanut allergy [EXACT]	
Xrefs	MSH:D021183 SNOMEDCT_US_2015_03_01:213021008 SNOMEDCT_US_2015_03_01:91935009 UMLS_CUI:C0559470	
Relationships	is_a <u>food allergy</u>	



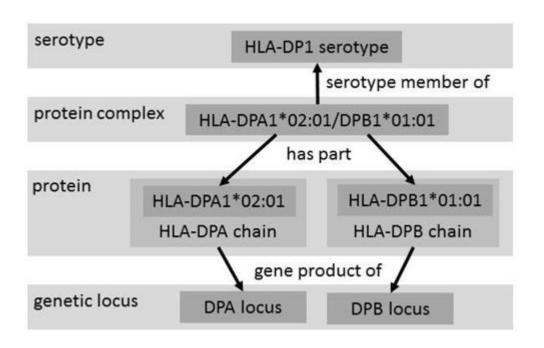


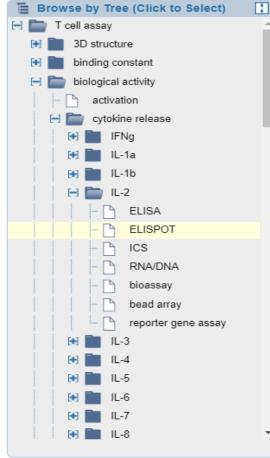
ELISA IL-2 release OBI OBI:1110152





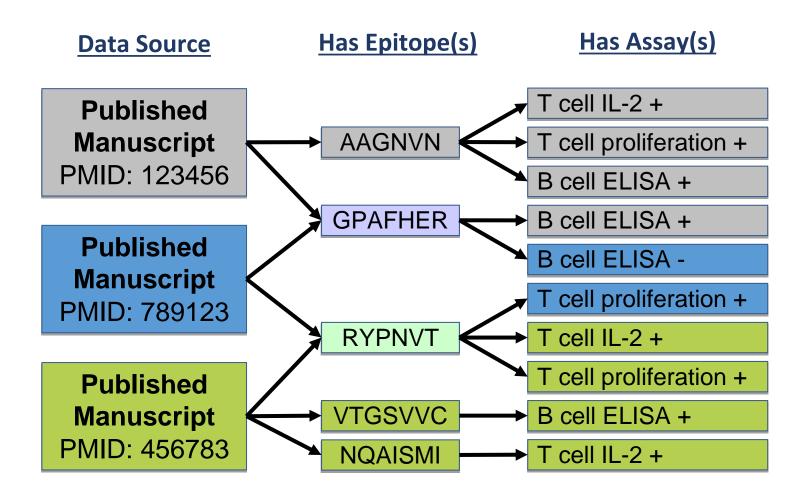
MHC Restriction Ontology (MRO)



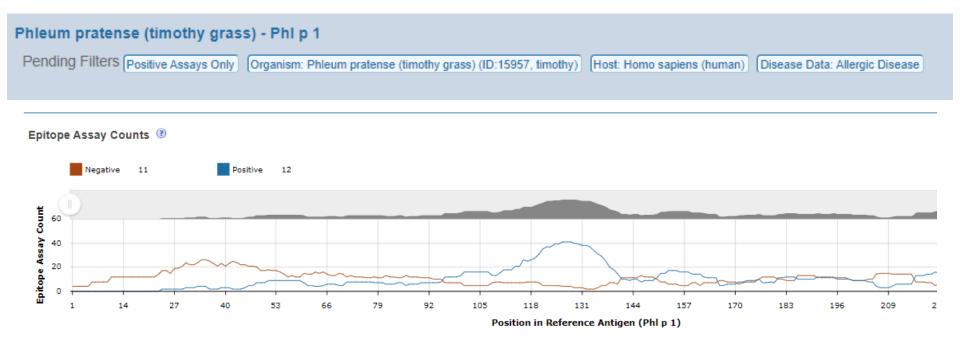


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Data Aggregation



Data Aggregation





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.

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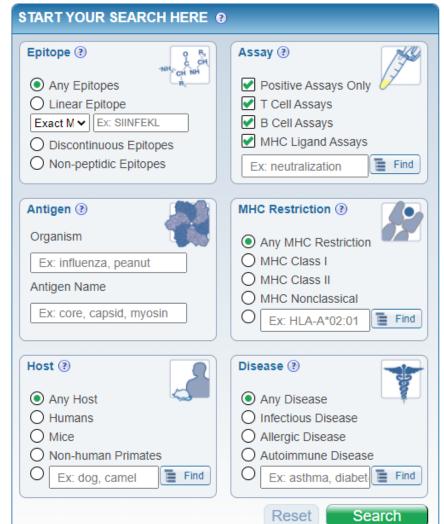
* webinar recording here

FOCiS Virtual Booth Oct 28-31

User Workshop Nov 5-6

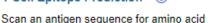
* register for workshop here

Summary Metrics	
Peptidic Epitopes	971,496
Non-Peptidic Epitopes	3,051
T Cell Assays	383,184
B Cell Assays	549,059
MHC Ligand Assays	2,927,353
Epitope Source Organisms	3,974
Restricting MHC Alleles	860
References	21,564





T Cell Epitope Prediction (?)



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:

Antigen Sequence Properties

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

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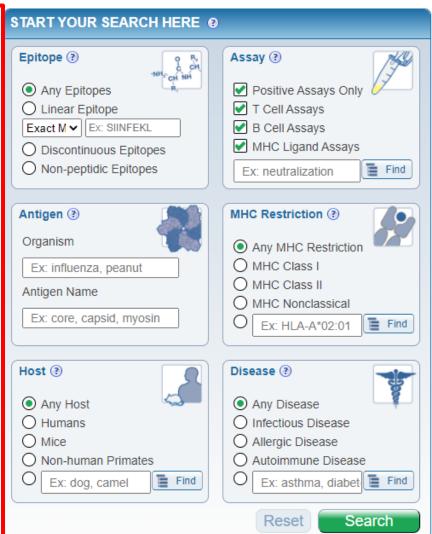
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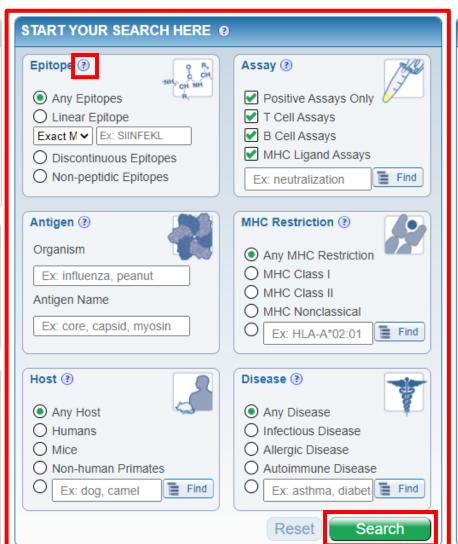
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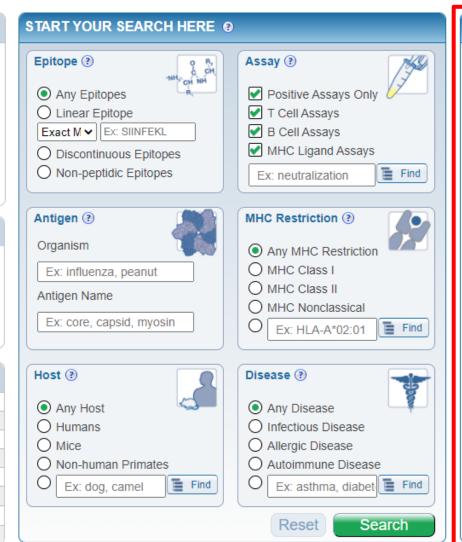
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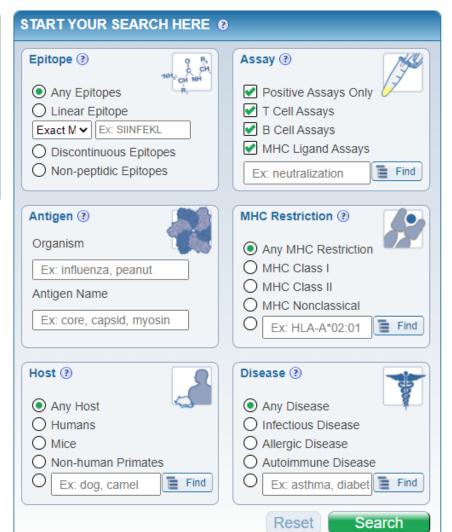
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Summany Matrice

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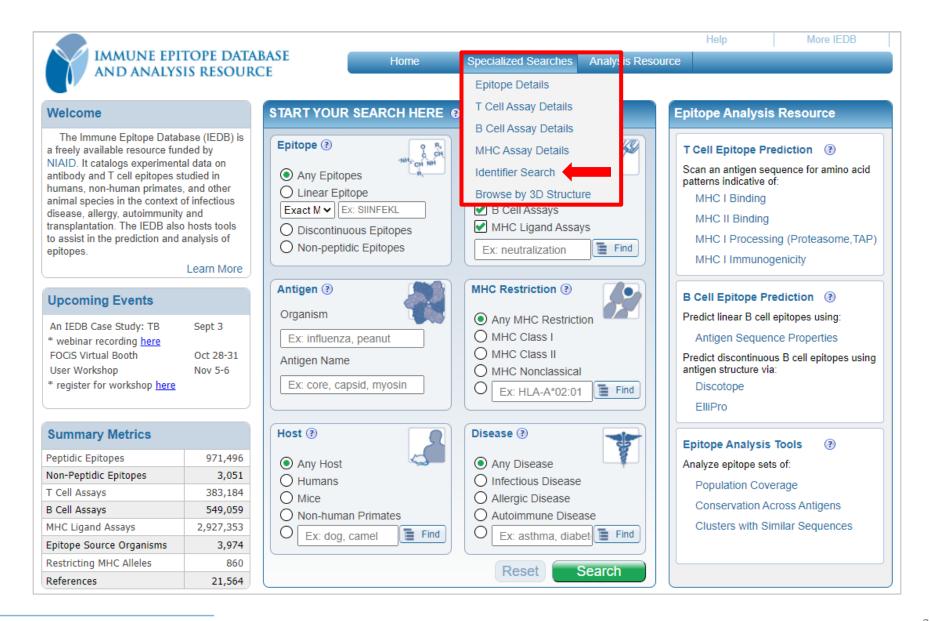
Conservation Across Antigens

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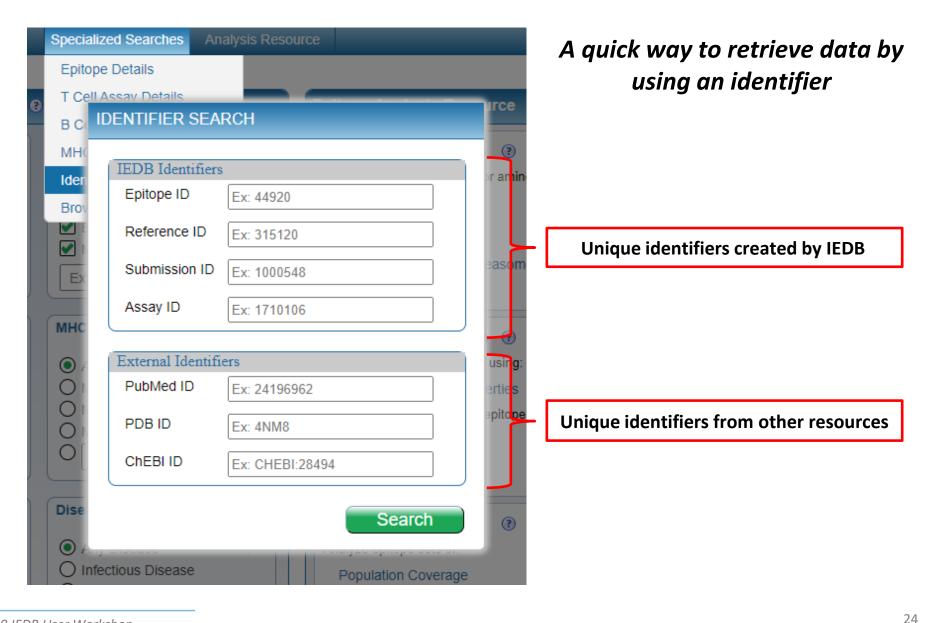
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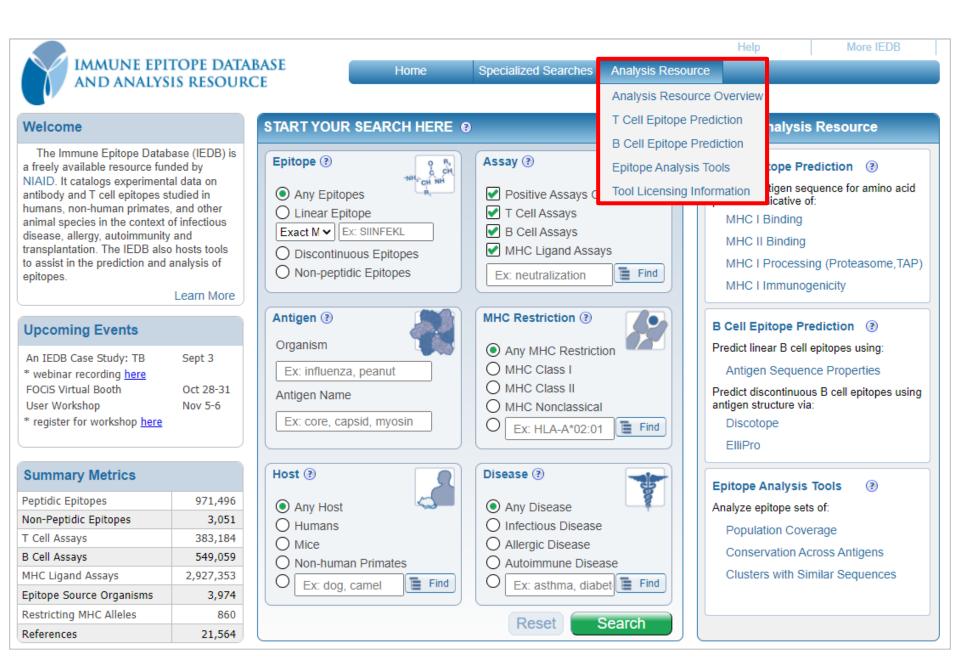
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Identifier Search



Identifier Search







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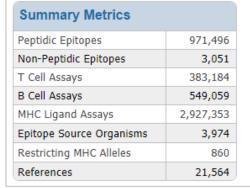
An IEDB Case Study: TB Sept 3

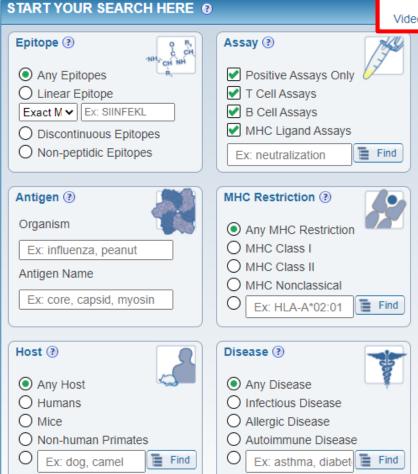
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Help

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B Cell Epitope Prediction (3)



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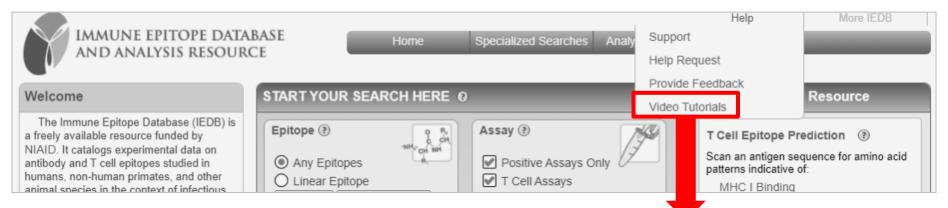
Conservation Across Antigens

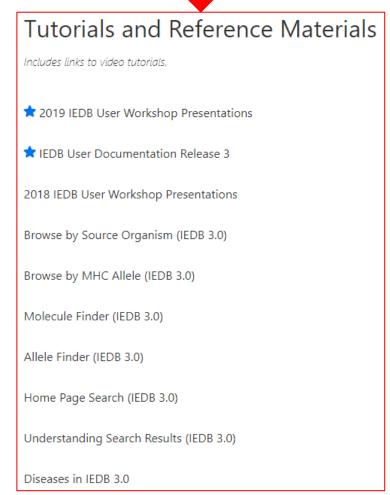
Clusters with Similar Sequences

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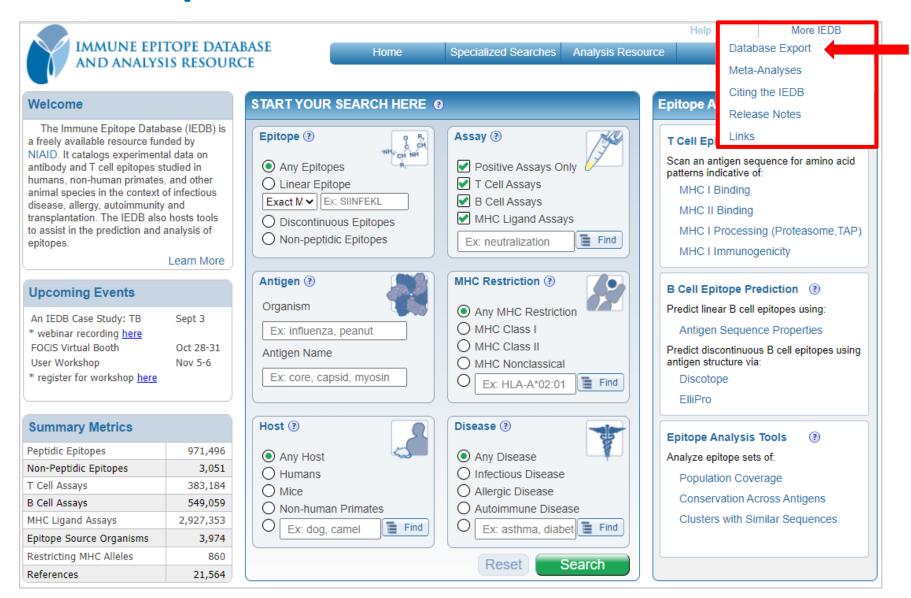
Reset

Search





More Exports



More Exports

http://www.iedb.org/database_export_v3

XML Database Export	
Complete Database Export	323MB
<u>ledbAccessionList.zip</u>	49kB
MhcAlleleNameList.zip	34kB
<u>OrganismList.zip</u>	35MB
<u>AssayTypeList zip</u>	5kB
GeoLocList zip	3kB

IEDB Schema		
Curation.xsd (Primary IEDB schema)	48kB	
<u>CurationSimpleTypes.xsd</u>	303kB	
<u>ledbAccessionList.xsd</u>	909B	
MhcAlleleNameList.xsd	1kB	
<u>OrganismList.xsd</u>	751B	
<u>AssayTypeList.xsd</u>	771B	
GeoLocList.xsd	642B	

MySQL Database Export	
SQL Statement Export	379MB
MyISAM Binary Export	819MB

Physical Entity Relationship Diagram	
iedb public erd.pdf	31kB

65MB
2MB
28MB
36MB
168MB
12MB
5MB
3МВ

Stable ID Exports	
Linkout IDs Compact	21MB
Linkout IDs Full	40MB
ChEBI to Epitope ID Maps	158kB
PDB to Epitope ID Maps	51kB
Epitope ID to Linear Seg Maps	11MB

Receptor_full Export

- Receptor_full contains exports of all antibody and T cell sequences in the IEDB
- Provides nucleotide and protein full length sequences
- Includes CDR1, 2, and 3 sequences
- Includes gene usage
- Listed by each epitope that they were shown to recognize

ledb_3d_full Export

- iedb_3d_full contains exports of all 3D structures in the IEDB
- Antibody, MHC, and T cell are in separate spreadsheets
- Provides structural details on receptor-Antigen interactions (inter-molecular contacts)
- Include PDB IDs and resolutions of complexes, PDB chain IDs of antibody, TCR, MHC, and antigen chains
- Includes full length receptor and antigen sequences
- Can be combined with receptor export to get information on CDRs and VDJ gene usage

After the Break

- How to query the data in the IEDB
- Your submitted questions

But first...

