How Data are Retrieved, Entered, and Organized

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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
- 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



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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 <5000 Daltons
- Minimal information required (sequence, outcome, host, etc)



Data Sources

- IEDB does not create data. We capture experimentally generated data
- Published literature ~19,500
- Direct submissions 330



Literature Curation Process



Complex query (~2 wks)

Epitope Related >220,000

Automated classifier

Infectious Disease 44977 refs

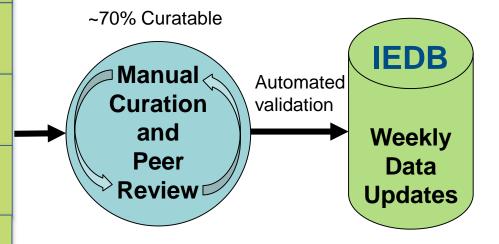
> Allergy 8733 refs

Autoimmunity 17882 refs

Transplant 13842 refs

Other 137370 refs

AND ANALYSIS RESOURCE



Consistency and quality control measures

- Manually curated by a team of 8 PhD level scientists at LJI and Chemical Entities of Biological Interest (ChEBI) with specific expertise
- Formal curation guidelines and peer review
- External immunological experts
- Built in validation in the curation application



Submission Community

- Primarily Epitope Discovery Contract Holders
- P. vivax, P. falciparum, Dengue, JEV, RVFV,
 Oropouche virus, Influenza, Ricin, Ebola, HCV, S. aureus (MRSA), HHV-6, Lassa, Vaccinia, VZV,
 common allergens
- David Fremont, James Crowe, Nicholas Mantis, Ben Doranz, Gregg Silverman, Alex Sette, Lawrence Stern, Michael Oldstone, David Koelle, William Kwok



Submission Process







ND ANALYSIS RESOURCE

Submit files via IEDB data submission tool

Automated validation

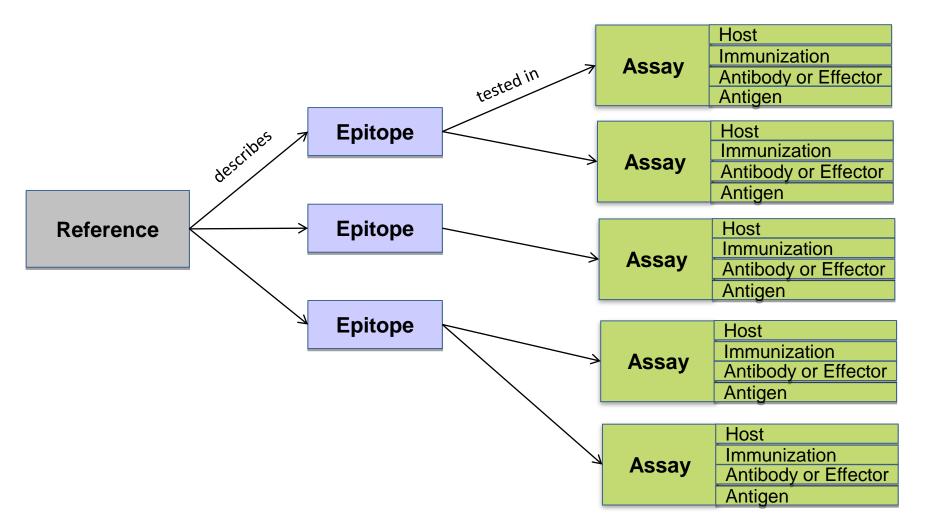
Curator review and submitter approval

Automated validation

Release date set by submitter

Data Structure

A database of experiments





Collaborations with ontologies

Provides standardized nomenclature, definitions, synonyms, and hierarchical relationships

Ensures consistency and accuracy

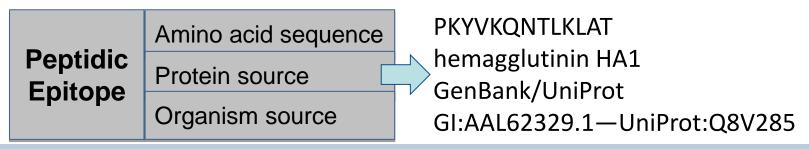
Finds errors

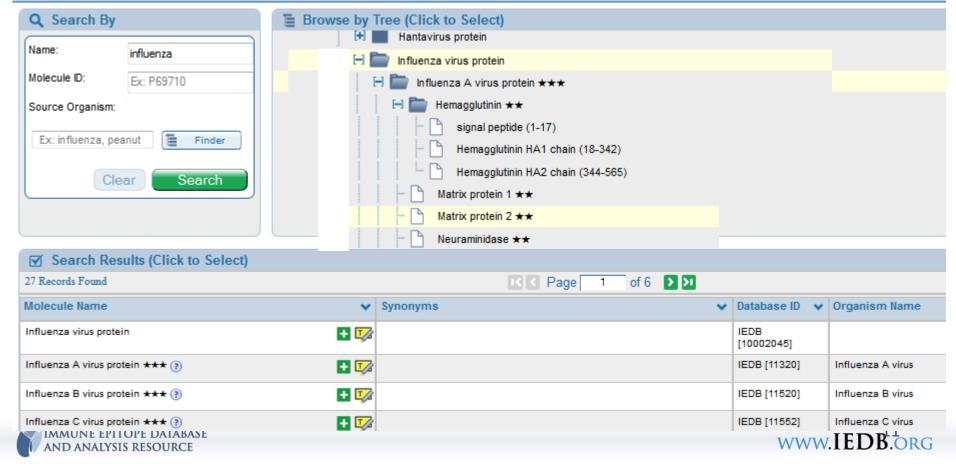
Makes curation easier

Enhances user experience

Facilitates interoperability



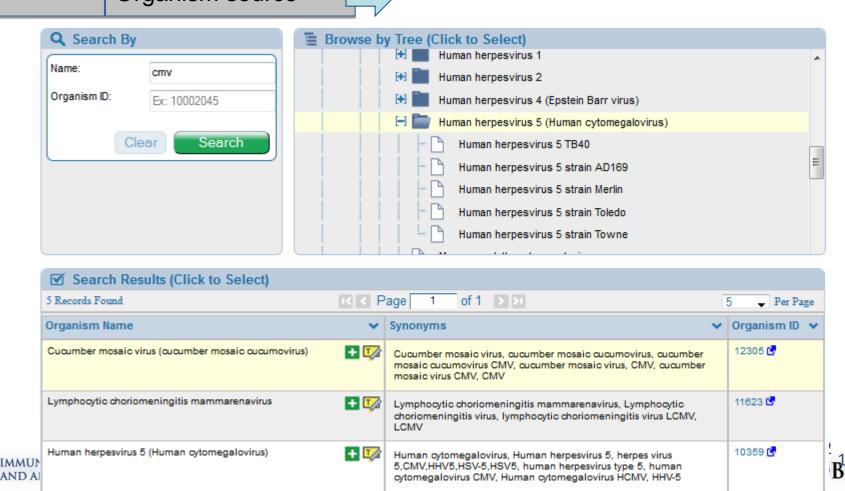




Peptidic Epitope Amino acid sequence Protein source Organism source

Human herpesvirus 5 (HHV-5) NCBI

taxon:10359



Non-peptidic Epitope Structure name

Source structure

Organism source

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

CHEBI:59294

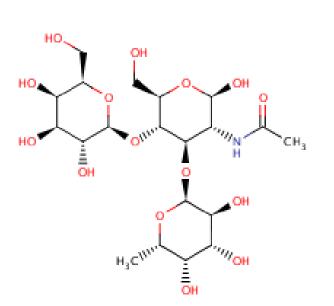
Lipopolysaccharide

CHEBI:16412



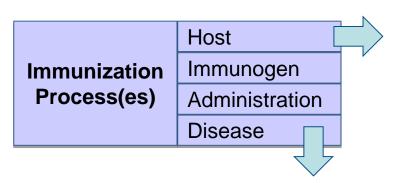
NCBI taxon:210

Helicobacter pylori



| ChEBI Name | α-L-Fuc p -(1→3)-[$β$ -D-Gal p -(1→4)]- $β$ -D-Glc p NAc |
|------------------|---|
| ChEBI ID | CHEBI:59294 |
| ChEBI ASCII Name | alpha-L-Fucp-(1->3)-[beta-D-Galp-(1->4)]-beta-D-GlcpNAc |
| Definition | An $\sigma\text{-L-Fuc}p\text{-}(1\to 3)\text{-}[\beta\text{-D-Gal}p\text{-}(1\to 4)]\text{-D-Glc}pNAc}$ where the glucosamine at the reducing end has $\beta\text{-configuration}$ at its anomeric centre. Commonly known as Lewis x trisaccharide or Le*. |
| Stars | ★★★ This entity has been manually annotated by the ChEBI Team. |





Homo sapiens (human)

NCBI

taxon:9606

Peanut allergy

DO

DOID:4378

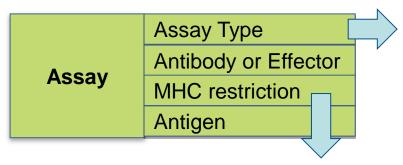
Metadata

🔐 Visualize



| DOID | DOID:4378 |
|---------------|---|
| Name | peanut allergic reaction |
| Definition | A food allergy that is an allergy or hypersensitivity to dietary substances from peanuts causing an overreaction of the immune system which in a small percentage of people may lead to severe physical symptoms. http://en.wikipedia.org/wiki/Allergy#Foods |
| 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> |



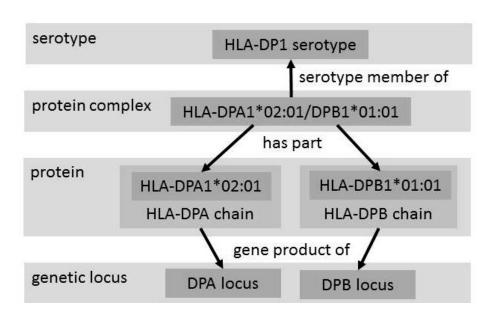


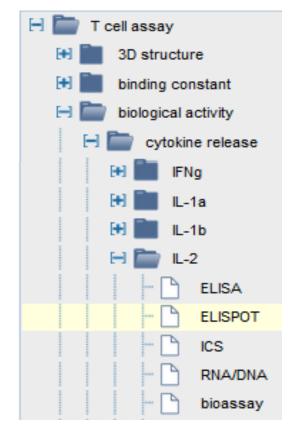
ELISA IL-2 release OBI

OBI:1110152



MHC Restriction Ontology (MRO)



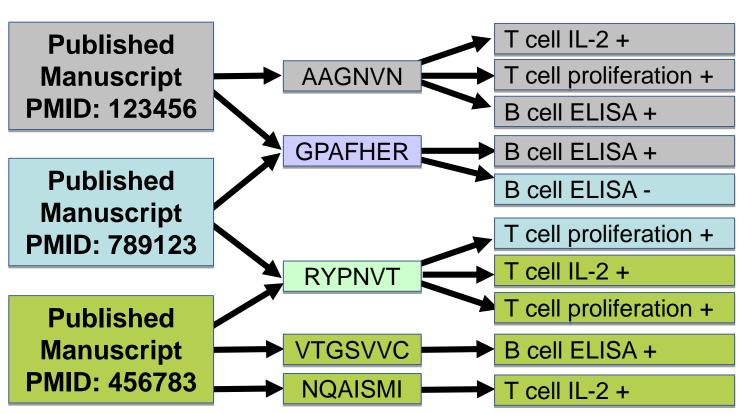




Data Aggregation

A database of experiments

data source has epitope(s) has assay(s)





Data Aggregation

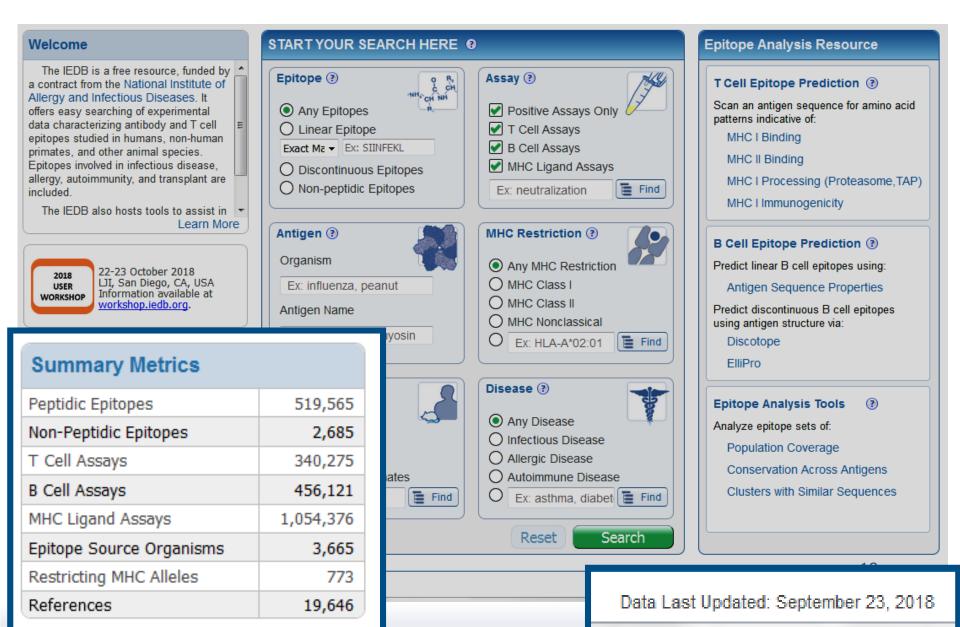


Position in Reference Antigen (Phl p 1)

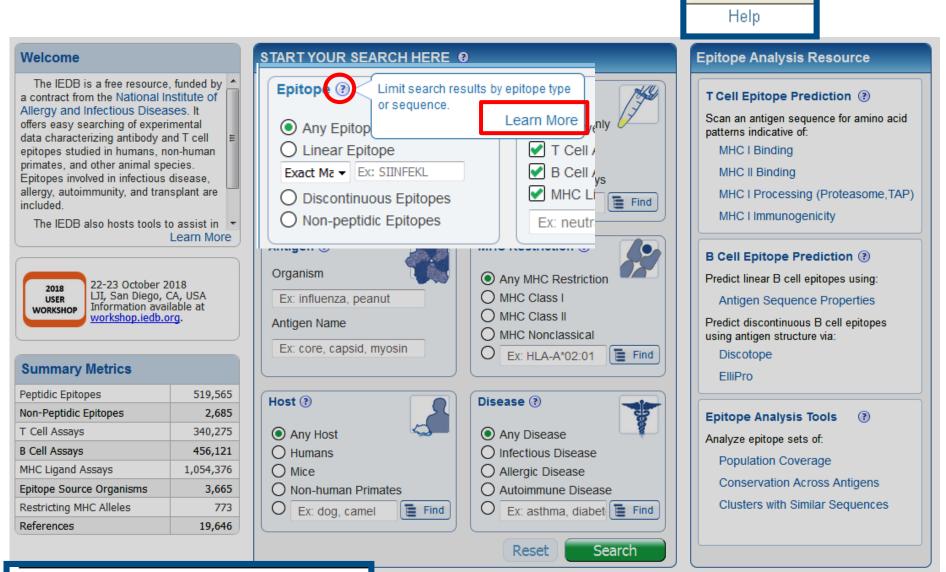
The human T cell response to Timothy grass Phl p 1 protein



Cumulative Data



Help and Feedback



Help and Feedback

IEDB Solutions Center > General > Tutorials and Reference Materials

Q Search

Articles in this section

IEDB User Documentation Release 3

How-To Videos

2015 IEDB User Workshop Presentations

Browse by Source Organism (IEDB 3.0)

Browse by MHC Allele (IEDB 3.0)

Molecule Finder (IEDB 3.0)

IEDB Epitopes



Randi Vita

11 months ago · Updated

Follow

In order to be consistent across all publications, the IEDB defines an epitope as peptides less than or equal to 50 amino acids in size and non-peptidic structures less than or equal to 5000 Daltons. These structures must be experimentally tested for binding to an adaptive immune receptor (T cell receptor (TCR), antibody or B cell receptor (BCR), or major histocompatibility complex (MHC)) or the receptor must be known and stated to be epitope specific in order to be included in the IEDB.

Please see our full inclusion criteria at this link:

http://curationwiki.iedb.org/wiki/index.php/IEDB Inclusion Criteria

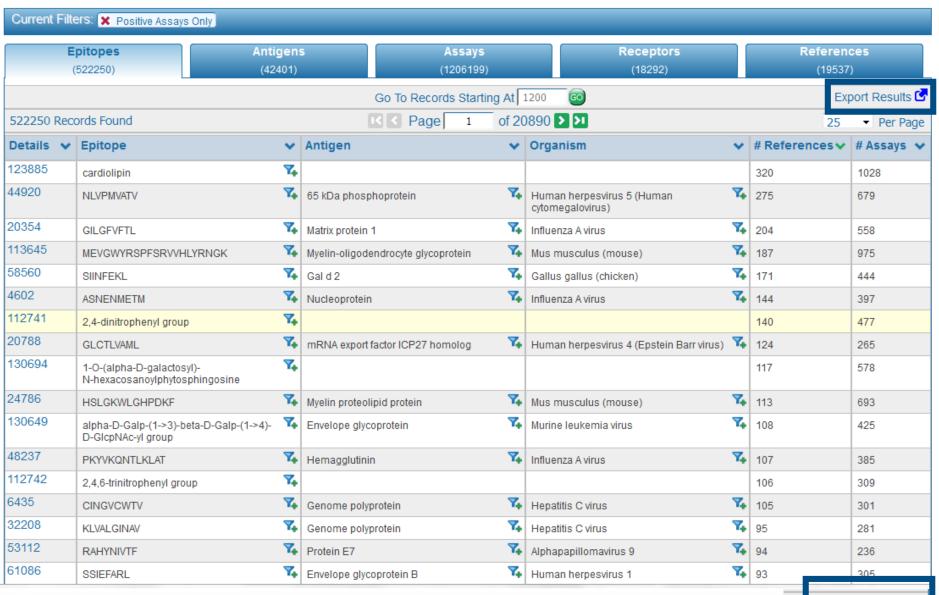
Users can easily narrow search results to include only linear peptidic epitopes, discontinuous peptidic epitopes, or non-peptidic epitopes. Peptidic epitopes may also be searched upon using any specific amino acid sequence, with the additional feature of being able to search for epitopes homologous to the input sequence at 70%, 80%, or 90% identity or using a substring match. Non-peptidic epitopes may be searched upon by textual name or via the Molecule Finder which presents all non-peptidic epitopes in a

Help and Feedback

- Respond to all help requests within 1 business day and resolve issue within 2 days for 85% of requests
 - Submit by email to help@iedb.org
- Knowledgebase available at https://help.iedb.org
- User Workshop sessions will be recorded and converted into video tutorials



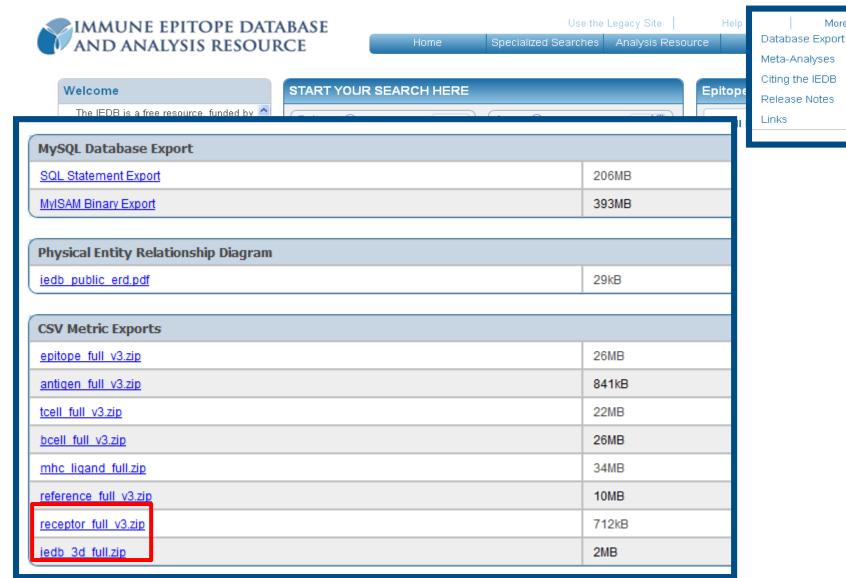
Exports



Export Results 6



Exports

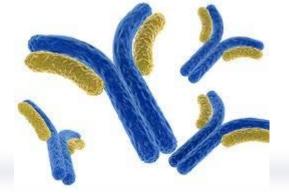




More IEDB

Receptor 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





3D 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-Ag interactions (intermolecular contacts)
- Include PDB IDs and resolutions of complexes, PDB chain IDs of antibody, TCR, MHC, and Ag chains
- Includes full length receptor and antigen sequences
- Can be combined with receptor export to get information on CDRs and VDJ gene usage

